

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 16, 2003, 11:19:02 ; Search time 6399.51 Seconds
(without alignments)
15794.017 Million cell updates/sec
Title: US-09-513-888c-1_COPY_871_4343
Perfect score: 3473
Sequence: 1 agctgcgcctggggcatct.....cgtggtggtcacgcctgca 3473

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0
Searched: 2054640 seqs, 14551402878 residues
Word size : 0
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 1000 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rtd.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sv.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3473	100.0	9108	9	AF123653	AF123653 Homo sapi
2	2462	70.9	173264	2	AC025853	AC025853 Homo sapi
3	757	21.8	1515	9	AF123656	AF123656 Homo sapi
4	757	21.8	1614	9	AF123655	AF123655 Homo sapi
5	757	21.8	1692	9	AF123657	AF123657 Homo sapi
6	757	21.8	1722	9	AF123658	AF123658 Homo sapi
7	757	21.8	5492	9	AF123659	AF123659 Homo sapi
8	214	6.2	633	9	AF123654	AF123654 Homo sapi
9	39	1.1	70707	9	AC093002	AC093002 Homo sapi
10	39	1.1	124882	9	AC090064	AC090064 Homo sapi
11	39	1.1	185929	2	AC017085	AC017085 Homo sapi
12	38	1.1	183342	9	AC087490	AC087490 Homo sapi
13	38	1.1	206030	9	AC021439	AC021439 Homo sapi
14	38	1.1	227884	2	AC114995	AC114995 Mus muscu
15	38	1.1	263546	2	AC099416	AC099416 Mus muscu
16	37	1.1	182676	2	AC104362	AC104362 Homo sapi
17	35	1.0	27399	9	AL713867	AL713867 Human DNA
18	35	1.0	160483	2	AC125977	AC125977 Rattus no
19	35	1.0	200761	10	AC122140	AC122140 Mus muscu
20	34	1.0	103	11	G38795	G38795 C12M105 Pla
21	34	1.0	4005	3	AF030690	AF030690 Plasmodiu
22	34	1.0	43593	2	AC131564	AC131564 Lytechinu
23	34	1.0	66074	2	AC119882	AC119882 Mus muscu
24	34	1.0	99537	2	AC111610	AC111610 Rattus no
25	34	1.0	109542	2	AC131398	AC131398 Rattus no
26	34	1.0	114113	2	AL160005	AL160005 Homo sapi
27	34	1.0	127815	2	AC103042	AC103042 Rattus no
28	34	1.0	158992	2	AC119377	AC119377 Rattus no
29	34	1.0	153550	2	AL354894	AL354894 Homo sapi
30	34	1.0	160483	2	AC125977	AC125977 Rattus no
31	34	1.0	170799	2	AC094997	AC094997 Rattus no
32	34	1.0	173523	2	AL513528	AL513528 Homo sapi
33	34	1.0	178273	2	AC005308	AC005308 Plasmodiu
34	34	1.0	180748	2	AC126872	AC126872 Rattus no
35	34	1.0	195734	2	AC126265	AC126265 Mus muscu
36	34	1.0	197171	9	CNS01DRD	AL117187 Human chr
37	34	1.0	198944	8	ATCHRIV38	AL161538 Arabidops
38	34	1.0	206606	8	ATFCA1	Z97335 Arabidops
39	34	1.0	219726	10	AC087556	AC087556 Mus muscu
40	34	1.0	222185	2	AC127697	AC127697 Mus muscu
41	34	1.0	321003	2	PFMAL4P3	AL035476 Plasmodiu
42	34	1.0	321003	2	PFMAL4P3	AL035476 Plasmodiu
43	33	1.0	135	11	AL823652	AL823652 Arabidops
44	33	1.0	11805	6	AX346651	AX346651 Sequence
45	33	1.0	16596	9	AL591590	AL591590 Human DNA
46	33	1.0	39969	9	HSJ645L19	AL049590 Human DNA
47	33	1.0	88518	2	AL391643	AL391643 Homo sapi
48	33	1.0	89944	9	AL591622	AL591622 Human DNA
49	33	1.0	100785	9	AP000617	AP000617 Homo sapi
50	33	1.0	101033	9	AC104090	AC104090 Homo sapi
51	33	1.0	104868	8	ATF15G16	AL132959 Arabidops
52	33	1.0	107135	2	AC128204	AC128204 Rattus no
53	33	1.0	107328	9	AL160057	AL160057 Human DNA
54	33	1.0	110000	2	PFMAL13P2_0	AL049185 Plasmodiu
55	33	1.0	110000	2	PFMAL13P2_0	AL049185 Plasmodiu
56	33	1.0	113333	2	AC096958	AC096958 Rattus no
57	33	1.0	116696	3	PFMAL3P3	Z98547 Plasmodiu
58	33	1.0	131132	9	AC103563	AC103563 Homo sapi
59	33	1.0	137169	2	AC015781	AC015781 Homo sapi
60	33	1.0	142001	8	ATF21F14	AL138642 Arabidops
61	33	1.0	147292	2	AC023010	AC023010 Homo sapi
62	33	1.0	147595	2	AC021778	AC021778 Homo sapi
63	33	1.0	148689	9	AC093168	AC093168 Homo sapi
64	33	1.0	149548	9	AC099066	AC099066 Homo sapi
65	33	1.0	150325	2	AC018535	AC018535 Homo sapi

66	33	1.0	152989	2	AC095122	AC095122 Rattus no	139	32	0.9	5908	6	AX277930	Sequence
67	33	1.0	153097	2	AC125750	AC125750 Rattus no	140	32	0.9	5908	6	AX323617	Sequence
68	33	1.0	153729	9	CNS01DWN	AL137785 Human chr	141	32	0.9	6197	6	AX344849	Sequence
69	33	1.0	157410	2	CNS013816	AL137785 Homo sapi	c 142	32	0.9	6216	6	AX348318	Sequence
70	33	1.0	158041	2	AC112587	AL137785 Rattus no	c 143	32	0.9	6216	6	AX348571	Sequence
71	33	1.0	158548	3	PFMAL13P2	AL034558 Plasmid	c 144	32	0.9	6769	6	AR004690	Sequence
72	33	1.0	161117	2	OSJN00245	AL731601 Oryza sat	c 145	32	0.9	6769	6	AR008176	Sequence
73	33	1.0	161284	9	AC016558	AC016558 Homo sapi	c 146	32	0.9	6769	6	AR136959	Sequence
74	33	1.0	162884	9	AC020936	AC020936 Homo sapi	c 147	32	0.9	6769	6	I76960	Sequence 20
75	33	1.0	165821	2	AC022005	AC022005 Homo sapi	c 148	32	0.9	6769	6	I80955	Sequence 20
76	33	1.0	167254	9	CNS05YDS	AL357093 Human chr	c 149	32	0.9	6769	6	I81051	Sequence 20
77	33	1.0	167390	9	AC007263	AC007263 Homo sapi	c 150	32	0.9	7238	6	AX346520	Sequence
78	33	1.0	168628	2	AC119391	AC119391 Rattus no	c 151	32	0.9	10917	8	AY090462	Oryza sat
79	33	1.0	169514	9	AC064869	AC064869 Homo sapi	c 152	32	0.9	11200	9	HSU40369	Human sperm
80	33	1.0	169546	2	AC004157	AC004157 Plasmid	c 153	32	0.9	12029	3	AE001372	Plasmid
81	33	1.0	169794	2	AC004688	AC004688 Plasmid	c 154	32	0.9	14613	3	AE001396	Plasmid
82	33	1.0	173456	9	AL158198	AL158198 Human DNA	c 155	32	0.9	19437	9	AC016671	Homo sapi
83	33	1.0	173456	9	AL158198	AL158198 Human DNA	c 156	32	0.9	24099	2	AC129023	Mus muscu
84	33	1.0	173456	9	AL158198	AL158198 Human DNA	c 157	32	0.9	25598	2	AC020801	Mus muscu
85	33	1.0	177250	2	AC025060	AC025060 Homo sapi	c 158	32	0.9	30465	2	AC017693	Drosophil
86	33	1.0	178274	2	AC022006	AC022006 Homo sapi	c 159	32	0.9	36463	9	AP001170	Homo sapi
87	33	1.0	178879	2	AC026883	AC026883 Homo sapi	c 160	32	0.9	36874	9	AC005336	Homo sapi
88	33	1.0	180420	2	AC123135	AC123135 Rattus no	c 161	32	0.9	38461	9	HSU165H7	Human DNA
89	33	1.0	180440	2	AC113570	AC113570 Canis fam	c 162	32	0.9	39877	9	AC020950	Mus muscu
90	33	1.0	181141	2	AC093621	AC093621 Homo sapi	c 163	32	0.9	41780	2	AC014811	Homo sapi
91	33	1.0	181503	10	AL662783	AL662783 Mouse DNA	c 164	32	0.9	42032	2	AC104949	Homo sapi
92	33	1.0	188717	9	CNS01DWR	AL138478 Human chr	c 165	32	0.9	47573	3	AF030694	Plasmid
93	33	1.0	190830	2	AC102136	AC102136 Mus muscu	c 166	32	0.9	55284	9	AL136318	Human DNA
94	33	1.0	196403	2	AL844139	AL844139 Mus muscu	c 167	32	0.9	62939	2	AC120369	Mus muscu
95	33	1.0	196715	2	AC094874	AC094874 Rattus no	c 168	32	0.9	63239	2	AC094243	Rattus no
96	33	1.0	197171	9	CNS01DRD	AL117187 Human chr	c 169	32	0.9	63971	2	AC121292	Mus muscu
97	33	1.0	199551	2	AC006281	AC006281 Plasmid	c 170	32	0.9	64682	2	AC121144	Mus muscu
98	33	1.0	206600	2	AC124496	AC124496 Mus muscu	c 171	32	0.9	64981	9	AL354738	Human DNA
99	33	1.0	214857	10	AC122899	AC122899 Mus muscu	c 172	32	0.9	67970	3	PFMAL13P3	Plasmid
100	33	1.0	224448	2	PFMAL4P4	AL035477 Plasmid	c 173	32	0.9	69020	2	AC125008	Mus muscu
101	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 174	32	0.9	70020	2	AC113529	Mus muscu
102	33	1.0	254775	2	AC091478	AC091478 Mus muscu	c 175	32	0.9	70020	2	AC113529	Mus muscu
103	33	1.0	256172	2	AC005139	AC005139 Plasmid	c 176	32	0.9	70197	2	AC102300	Mus muscu
104	33	1.0	287058	2	AC095595	AC095595 Rattus no	c 177	32	0.9	71004	2	AC119972	Mus muscu
105	33	1.0	310779	2	AC005140	AC005140 Plasmid	c 178	32	0.9	72115	2	AC119284	Mus muscu
106	33	1.0	318221	2	PFMAL13P3	AL049184 Plasmid	c 179	32	0.9	72115	2	AC119284	Mus muscu
107	33	1.0	339247	2	AC107252	AC107252 Rattus no	c 180	32	0.9	75004	9	AC012667	Homo sapi
108	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 181	32	0.9	75004	9	AC012667	Homo sapi
109	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 182	32	0.9	75251	2	AC018562	Homo sapi
110	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 183	32	0.9	75251	2	AC018562	Homo sapi
111	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 184	32	0.9	75251	2	AC018562	Homo sapi
112	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 185	32	0.9	75251	2	AC018562	Homo sapi
113	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 186	32	0.9	75251	2	AC018562	Homo sapi
114	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 187	32	0.9	75251	2	AC018562	Homo sapi
115	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 188	32	0.9	75251	2	AC018562	Homo sapi
116	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 189	32	0.9	75251	2	AC018562	Homo sapi
117	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 190	32	0.9	75251	2	AC018562	Homo sapi
118	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 191	32	0.9	75251	2	AC018562	Homo sapi
119	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 192	32	0.9	75251	2	AC018562	Homo sapi
120	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 193	32	0.9	75251	2	AC018562	Homo sapi
121	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 194	32	0.9	75251	2	AC018562	Homo sapi
122	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 195	32	0.9	75251	2	AC018562	Homo sapi
123	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 196	32	0.9	75251	2	AC018562	Homo sapi
124	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 197	32	0.9	75251	2	AC018562	Homo sapi
125	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 198	32	0.9	75251	2	AC018562	Homo sapi
126	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 199	32	0.9	75251	2	AC018562	Homo sapi
127	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 200	32	0.9	75251	2	AC018562	Homo sapi
128	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 201	32	0.9	75251	2	AC018562	Homo sapi
129	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 202	32	0.9	75251	2	AC018562	Homo sapi
130	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 203	32	0.9	75251	2	AC018562	Homo sapi
131	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 204	32	0.9	75251	2	AC018562	Homo sapi
132	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 205	32	0.9	75251	2	AC018562	Homo sapi
133	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 206	32	0.9	75251	2	AC018562	Homo sapi
134	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 207	32	0.9	75251	2	AC018562	Homo sapi
135	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 208	32	0.9	75251	2	AC018562	Homo sapi
136	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 209	32	0.9	75251	2	AC018562	Homo sapi
137	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 210	32	0.9	75251	2	AC018562	Homo sapi
138	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 211	32	0.9	75251	2	AC018562	Homo sapi

c 212	32	0.9 108908	3	PFMA13P8	AL034560 Plaemodiu	c 285	32	0.9 154176	2	AC118829	Rattus no
c 213	32	0.9 108979	9	AC090041	AC090041 Homo sapi	c 286	32	0.9 154364	9	AC091893	Homo sapi
c 214	32	0.9 109200	2	AC099349	AC099349 Rattus no	c 287	32	0.9 154690	2	AC007208	Drosophil
c 215	32	0.9 109465	9	AL158821	AL158821 Human DNA	c 288	32	0.9 155151	9	AL137143	Human DNA
c 216	32	0.9 110000	2	AC113004_1	Continuation (2 of	c 289	32	0.9 155220	2	AC122947	Rattus no
c 217	32	0.9 110000	2	PFMA14P1_1	Continuation (2 of	c 290	32	0.9 155560	2	AC119601	Rattus no
c 218	32	0.9 110000	2	TBCHRIA_06	Continuation (7 of	c 291	32	0.9 155580	9	AC024597	Homo sapi
c 219	32	0.9 110085	8	AP004578	AP004578 Lotus jap	c 292	32	0.9 155580	9	AC024597	Homo sapi
c 220	32	0.9 111104	9	AC117389	AC117389 Homo sapi	c 293	32	0.9 155580	9	AC024946	Homo sapi
c 221	32	0.9 111182	2	AC128602	AC128602 Rattus no	c 294	32	0.9 155580	9	AC024946	Homo sapi
c 222	32	0.9 113031	9	AL445672	AL445672 Human DNA	c 295	32	0.9 155592	2	AC118866	Rattus no
c 223	32	0.9 115109	9	AC107216	AC107216 Homo sapi	c 296	32	0.9 155676	2	AC044780	Homo sapi
c 224	32	0.9 115928	9	AC037475	AC037475 Homo sapi	c 297	32	0.9 155676	2	AC044780	Homo sapi
c 225	32	0.9 116541	2	AC097016	AC097016 Rattus no	c 298	32	0.9 156060	2	AC004153	Plaemodiu
c 226	32	0.9 116696	3	PFMA13P3	Z98547 Plaemodiu	c 299	32	0.9 156357	9	AC011456	Homo sapi
c 227	32	0.9 117453	3	AE003670	AE003670 Drosophil	c 300	32	0.9 156874	2	AC098039	Rattus no
c 228	32	0.9 118131	9	AC074132	AC074132 Homo sapi	c 301	32	0.9 156947	9	AL359435	Human DNA
c 229	32	0.9 119385	5	AL645782	AL645782 Zebrafish	c 302	32	0.9 158174	8	AP003414	Oryza sat
c 230	32	0.9 120846	9	AL365232	AL365232 Human DNA	c 303	32	0.9 158293	9	AC004746	Homo sapi
c 231	32	0.9 121621	2	AC131559	AC131559 Rattus no	c 304	32	0.9 159176	2	AC098283	Rattus no
c 232	32	0.9 121822	9	AC118456	AC118456 Homo sapi	c 305	32	0.9 159338	9	AC016761	Homo sapi
c 233	32	0.9 121941	5	AL596022	AL596022 Zebrafish	c 306	32	0.9 159722	9	AC011293	Homo sapi
c 234	32	0.9 125411	8	ATF8L15	AL392174 Arabidops	c 307	32	0.9 159761	8	AP003921	Oryza sat
c 235	32	0.9 125497	2	AC128455	AC128455 Rattus no	c 308	32	0.9 160678	2	AC097200	Rattus no
c 236	32	0.9 127007	10	AL627432	AL627432 Mouse DNA	c 309	32	0.9 160693	9	AC124043	Homo sapi
c 237	32	0.9 127295	2	AL772298	AL772298 Danio rer	c 310	32	0.9 161125	2	AC128771	Rattus no
c 238	32	0.9 127714	9	AL590677	AL590677 Human DNA	c 311	32	0.9 161896	2	AC113862	Rattus no
c 239	32	0.9 127816	2	AC103042	AC103042 Rattus no	c 312	32	0.9 161911	2	AC021497	Homo sapi
c 240	32	0.9 127982	2	AC104473	AC104473 Oryza sat	c 313	32	0.9 161951	2	CNS07YPU	Oryza sat
c 241	32	0.9 128071	2	AC094497	AC094497 Rattus no	c 314	32	0.9 162025	6	AX112387	Sequence
c 242	32	0.9 128411	5	AC107365	AC107365 Danio rer	c 315	32	0.9 162025	6	AX112388	Sequence
c 243	32	0.9 128918	2	AL358945	AL358945 Homo sapi	c 316	32	0.9 162025	6	AX360260	Sequence
c 244	32	0.9 131098	9	AC010607	AC010607 Homo sapi	c 317	32	0.9 162025	6	AX360261	Sequence
c 245	32	0.9 131811	9	AC068305	AC068305 Homo sapi	c 318	32	0.9 162025	6	AX360264	Sequence
c 246	32	0.9 132224	2	AC102898	AC102898 Mus muscu	c 319	32	0.9 162025	6	AX360265	Sequence
c 247	32	0.9 132688	8	AC099733	AC099733 Oryza sat	c 320	32	0.9 162025	9	AC005730	Homo sapi
c 248	32	0.9 134687	9	AL445259	AL445259 Human DNA	c 321	32	0.9 162101	8	AC027661	Oryza sat
c 249	32	0.9 134743	9	HUAC002300	AC002300 Homo sapi	c 322	32	0.9 163115	3	AC010661	Drosophil
c 250	32	0.9 135398	2	AC130452	AC130452 Homo sapi	c 323	32	0.9 163188	2	AC126074	Rattus no
c 251	32	0.9 135760	2	AC118530	AC118530 Rattus no	c 324	32	0.9 163229	2	AP004651	Oryza sat
c 252	32	0.9 136448	2	AC012231	AC012231 Homo sapi	c 325	32	0.9 163384	9	AC009180	Homo sapi
c 253	32	0.9 136805	2	AC117958	AC117958 Rattus no	c 326	32	0.9 163387	2	AC130912	Rattus no
c 254	32	0.9 137568	8	AC093178	AC093178 Oryza sat	c 327	32	0.9 163466	2	AC106980	Rattus no
c 255	32	0.9 138003	2	AC018346	AC018346 Homo sapi	c 328	32	0.9 164991	9	AC092023	Homo sapi
c 256	32	0.9 138020	9	AC108043	AC108043 Homo sapi	c 329	32	0.9 165062	2	AC098324	Rattus no
c 257	32	0.9 138947	2	AC131011	AC131011 Homo sapi	c 330	32	0.9 165618	9	AL442636	Human DNA
c 258	32	0.9 141430	8	AC069329	AC069329 Genomic S	c 331	32	0.9 166277	2	AC109794	Bos tauru
c 259	32	0.9 141529	2	AC025330	AC025330 Homo sapi	c 332	32	0.9 167072	2	AC060780	Homo sapi
c 260	32	0.9 141534	2	AP003685	AP003685 Oryza sat	c 333	32	0.9 167114	2	AP004685	Oryza sat
c 261	32	0.9 141825	9	AL355358	AL355358 Human DNA	c 334	32	0.9 167503	2	AC129344	Rattus no
c 262	32	0.9 141927	2	AL645926	AL645926 Danio rer	c 335	32	0.9 167968	2	AC109799	Bos tauru
c 263	32	0.9 141927	2	AL645926	AL645926 Danio rer	c 336	32	0.9 168080	2	AC073172	Homo sapi
c 264	32	0.9 144249	2	AC011262	AC011262 Homo sapi	c 337	32	0.9 168310	2	AC010775	Homo sapi
c 265	32	0.9 144249	2	AC011262	AC011262 Homo sapi	c 338	32	0.9 169845	2	AP004784	Oryza sat
c 266	32	0.9 144713	2	AC128020	AC128020 Rattus no	c 339	32	0.9 169879	2	AC073144	Homo sapi
c 267	32	0.9 144859	9	AC104997	AC104997 Homo sapi	c 340	32	0.9 170026	2	AC013627	Homo sapi
c 268	32	0.9 146403	9	AC027067	AC027067 Homo sapi	c 341	32	0.9 170227	2	AC093816	Homo sapi
c 269	32	0.9 148271	9	AL392046	AL392046 Human DNA	c 342	32	0.9 170466	2	AC129242	Rattus no
c 270	32	0.9 149255	9	AC009262	AC009262 Homo sapi	c 343	32	0.9 171162	2	AC096402	Rattus no
c 271	32	0.9 149291	10	AC116328	AC116328 Mus muscu	c 344	32	0.9 171426	2	AC097183	Mus muscu
c 272	32	0.9 149548	9	AC099066	AC099066 Homo sapi	c 345	32	0.9 171462	2	AC117832	Homo sapi
c 273	32	0.9 149704	9	AL138955	AL138955 Human DNA	c 346	32	0.9 171954	2	AC040957	Homo sapi
c 274	32	0.9 150162	9	AC026722	AC026722 Homo sapi	c 347	32	0.9 172784	9	AC024918	Homo sapi
c 275	32	0.9 150328	2	AP004460	AP004460 Oryza sat	c 348	32	0.9 172800	2	AL356597	Homo sapi
c 276	32	0.9 150573	2	AC097473	AC097473 Homo sapi	c 349	32	0.9 173053	2	AC118097	Rattus no
c 277	32	0.9 151191	2	AC117952	AC117952 Rattus no	c 350	32	0.9 173404	2	AC096147	Rattus no
c 278	32	0.9 151367	9	AC025750	AC025750 Homo sapi	c 351	32	0.9 173434	2	AL365496	Human DNA
c 279	32	0.9 151533	8	AC090873	AC090873 Oryza sat	c 352	32	0.9 173728	9	AL365496	Human DNA
c 280	32	0.9 151696	9	AF240629	AF240629 Homo sapi	c 353	32	0.9 174711	2	AC104512	Drosophil
c 281	32	0.9 152354	2	AC120598	AC120598 Homo sapi	c 354	32	0.9 174874	10	AC123054	Mus muscu
c 282	32	0.9 152631	9	AC117432	AC117432 Homo sapi	c 355	32	0.9 175111	2	AC101999	Mus muscu
c 283	32	0.9 152794	9	AL139376	AL139376 Human DNA	c 356	32	0.9 175179	2	AC095321	Rattus no
c 284	32	0.9 153339	9	AC007350	AC007350 Homo sapi	c 357	32	0.9 176019	2	AC124492	Mus muscu

358	32	0.9	176106	2	AC096415	AC096415 Rattus no	431	32	0.9	206030	9	AC021439	Homo sapi
359	32	0.9	176388	2	AC025273	AC025273 Homo sapi	432	32	0.9	206590	9	AC026951	Homo sapi
360	32	0.9	176409	2	AC097955	AC097955 Rattus no	c 433	32	0.9	206633	2	AC109275	Mus muscu
361	32	0.9	176437	2	AC110463	AC110463 Rattus no	c 434	32	0.9	206915	10	AL663081	Mouse DNA
362	32	0.9	177034	9	AP002840	AP002840 Homo sapi	435	32	0.9	207804	2	AC011714	Homo sapi
363	32	0.9	177089	9	AC008277	AC008277 Homo sapi	436	32	0.9	208083	2	AC009649	Homo sapi
364	32	0.9	178091	2	AC126702	AC126702 Rattus no	437	32	0.9	208657	2	AC046179	Homo sapi
365	32	0.9	178273	2	AC005308	AC005308 Plasmodiu	438	32	0.9	209636	2	AL732412	Mus muscu
366	32	0.9	178384	2	AL591026	AL591026 Homo sapi	439	32	0.9	210620	2	AC094500	Rattus no
367	32	0.9	178482	2	AC119832	AC119832 Mus muscu	440	32	0.9	210636	9	AC006443	Homo sapi
368	32	0.9	178764	2	AC126507	AC126507 Rattus no	441	32	0.9	211046	2	AC115784	Mus muscu
369	32	0.9	179332	2	AC068754	AC068754 Homo sapi	c 442	32	0.9	211607	2	AC094844	Rattus no
370	32	0.9	179429	2	AC114933	AC114933 Homo sapi	443	32	0.9	212479	2	AC125200	Mus muscu
371	32	0.9	179685	2	AC110477	AC110477 Rattus no	444	32	0.9	212827	9	AC009412	Homo sapi
372	32	0.9	179757	9	AC006960	AC006960 Homo sapi	445	32	0.9	213743	2	AL359918	Homo sapi
373	32	0.9	179788	2	AC009690	AC009690 Rattus no	c 446	32	0.9	215516	2	AC024694	Mus muscu
374	32	0.9	179788	2	AC009690	AC009690 Rattus no	447	32	0.9	216599	2	AC087379	Homo sapi
375	32	0.9	179899	2	AL645822	AL645822 Danio rer	448	32	0.9	216800	10	AL589744	Mouse DNA
376	32	0.9	180159	2	AC110652	AC110652 Rattus no	c 449	32	0.9	216800	10	AL589744	Mouse DNA
377	32	0.9	180277	2	AC104270	AC104270 Oryza sat	450	32	0.9	217263	2	AC108831	Mus muscu
378	32	0.9	180278	9	AC092343	AC092343 Homo sapi	451	32	0.9	217454	2	AL592070	Mus muscu
379	32	0.9	180320	2	AC123135	AC123135 Rattus no	c 452	32	0.9	218900	2	AC122502	Mus muscu
380	32	0.9	180440	2	AC113570	AC113570 Canis fam	453	32	0.9	219912	2	AC020855	Mus muscu
381	32	0.9	180583	9	CNS01DW8	AL136501 Human chr	454	32	0.9	220035	2	AC122047	Mus muscu
382	32	0.9	180603	2	AC110400	AC110400 Rattus no	c 455	32	0.9	220936	2	AC113162	Rattus no
383	32	0.9	181168	2	AC103469	AC103469 Rattus no	456	32	0.9	221250	2	AC122337	Mus muscu
384	32	0.9	182223	3	AC023674	AC023674 Drosophil	457	32	0.9	222512	2	AC124497	Mus muscu
c 385	32	0.9	182978	30	AC067824	AC067824 Homo sapi	458	32	0.9	225481	2	AC122393	Mus muscu
386	32	0.9	183105	3	AC104606	AC104606 Drosophil	459	32	0.9	225569	2	AC097963	Rattus no
387	32	0.9	183228	2	AC097076	AC097076 Rattus no	460	32	0.9	225611	2	AC129605	Mus muscu
388	32	0.9	183273	9	AC093898	AC093898 Homo sapi	c 461	32	0.9	227184	2	AC009868	Homo sapi
389	32	0.9	183342	9	AC087490	AC087490 Homo sapi	462	32	0.9	228094	2	AC124736	Mus muscu
c 390	32	0.9	184178	2	AC126586	AC126586 Rattus no	463	32	0.9	228404	2	AC095672	Rattus no
391	32	0.9	184677	2	AL831760	AL831760 Mus muscu	464	32	0.9	231618	2	AC124356	Mus muscu
392	32	0.9	184894	2	AC102582	AC102582 Mus muscu	c 465	32	0.9	231618	2	AC124356	Mus muscu
393	32	0.9	184909	2	AL844863	AL844863 Mus muscu	c 466	32	0.9	231938	2	AC079025	Mus muscu
394	32	0.9	185116	9	AC005823	AC005823 Homo sapi	c 467	32	0.9	233117	2	AL844512	Danio rer
395	32	0.9	185155	2	AL807760	AL807760 Mus muscu	468	32	0.9	236121	2	AC126796	Mus muscu
396	32	0.9	185596	2	AC127921	AC127921 Rattus no	469	32	0.9	238554	2	AC020965	Mus muscu
c 397	32	0.9	185596	2	AC127921	AC127921 Rattus no	470	32	0.9	240438	2	AC125142	Mus muscu
c 398	32	0.9	185711	2	AC107087	AC107087 Rattus no	471	32	0.9	242835	2	AC079243	Mus muscu
c 399	32	0.9	185857	2	AC129281	AC129281 Rattus no	472	32	0.9	242913	2	AC129210	Mus muscu
c 400	32	0.9	186457	9	AC068359	AC068359 Homo sapi	473	32	0.9	243915	2	AC115291	Mus muscu
c 401	32	0.9	187088	2	AC101852	AC101852 Mus muscu	c 474	32	0.9	249088	2	AL831726	Danio rer
c 402	32	0.9	187142	2	AC018598	AC018598 Homo sapi	c 475	32	0.9	253576	2	AC103320	Rattus no
c 403	32	0.9	187473	2	AC122043	AC122043 Mus muscu	476	32	0.9	271134	2	AC124402	Mus muscu
c 404	32	0.9	187837	2	AC130991	AC130991 Rattus no	c 477	32	0.9	276831	2	AC126690	Mus muscu
c 405	32	0.9	188357	9	AL159996	AL159996 Human DNA	478	32	0.9	285272	3	AE003441	Drosophil
c 406	32	0.9	193281	2	AC124558	AC124558 Homo sapi	c 479	32	0.9	293431	2	PFMAL13P4	Plasmodiu
c 407	32	0.9	189979	2	AC118037	AC118037 Mus muscu	c 480	32	0.9	310779	2	AC005140	Plasmodiu
c 408	32	0.9	189994	2	AC113784	AC113784 Rattus no	481	32	0.9	318221	2	PFMAL13P3	Plasmodiu
c 409	32	0.9	190624	2	AC026892	AC026892 Homo sapi	482	32	0.9	333530	2	AC087242	Homo sapi
c 410	32	0.9	190734	2	AC120283	AC120283 Rattus no	483	32	0.9	340000	9	AP001679	Homo sapi
c 411	32	0.9	190937	9	AP000957	AP000957 Homo sapi	c 484	32	0.9	340000	9	HS21C002	Homo sapi
c 412	32	0.9	191267	2	AC129189	AC129189 Mus muscu	c 485	31	0.9	150	11	G38001	G38001 C1M39 Plasm
c 413	32	0.9	191420	2	AL672221	AL672221 Mus muscu	486	31	0.9	194	11	G42718	G42718 C3M86 Plasm
c 414	32	0.9	192518	2	HSBA539A6	HSBA539A6 Homo sapi	c 487	31	0.9	226	8	AY018186	Oryza sat
c 415	32	0.9	193214	2	AC129424	AC129424 Rattus no	c 488	31	0.9	1090	5	AF316124	Kinostern
c 416	32	0.9	193503	2	CNS08C94	AL732381 Oryza sat	c 489	31	0.9	1094	5	AF316125	Kinostern
c 417	32	0.9	194076	2	AC131241	AC131241 Mus muscu	c 490	31	0.9	3148	3	AF323928	Plasmodiu
c 418	32	0.9	194612	9	AL357354	AL357354 Human DNA	491	31	0.9	4012	3	PPACAM	M59770 P.falci
c 419	32	0.9	195434	9	AC090744	AC090744 Homo sapi	492	31	0.9	4060	5	XLNRI	X34081 X.laevis
c 420	32	0.9	195434	9	AC090744	AC090744 Homo sapi	493	31	0.9	4060	5	XLNRI	X34156 X.laevis
c 421	32	0.9	196628	2	AL772388	AL772388 Danio rer	c 494	31	0.9	12029	3	AE001395	Plasmodiu
c 422	32	0.9	196877	8	AC063947	AC063947 Homo sapi	c 495	31	0.9	12029	3	AE001395	Plasmodiu
c 423	32	0.9	197975	8	ATCHRIV2	AL161472 Arabidops	c 496	31	0.9	15861	3	AE001413	Plasmodiu
c 424	32	0.9	199551	2	AC006281	AC006281 Plasmodiu	c 497	31	0.9	15903	2	AC115612	Dictyoste
c 425	32	0.9	199609	9	AC009432	AC009432 Homo sapi	c 498	31	0.9	29246	8	AP004947	Lotus jap
c 426	32	0.9	199639	2	AL805905	AL805905 Danio rer	c 499	31	0.9	41112	9	AL590323	Human DNA
c 427	32	0.9	200501	10	AL596086	AL596086 Mouse DNA	c 500	31	0.9	44704	9	AL672167	Rattus no
c 428	32	0.9	202921	2	AC117602	AC117602 Mus muscu	c 501	31	0.9	47519	2	AC110100	Human DNA
c 429	32	0.9	204185	2	AL844521	AL844521 Danio rer	502	31	0.9	61273	2	AC120141	Mus muscu
c 430	32	0.9	204782	2	AC011168	AC011168 Homo sapi	503	31	0.9	62263	2	AC100239	Mus muscu

504	31	0.9	63239	2	AC094243	AC094243 Rattus no	577	31	0.9	164867	9	AC103864	AC103864 Homo sapi
c 505	31	0.9	67331	2	AC067920	AC067920 Homo sapi	c 578	31	0.9	166219	9	AC003084	AC003084 Human BAC
c 506	31	0.9	68105	2	HSJ974111	AL050339 Human DNA	c 579	31	0.9	166796	2	AC126437	AC126437 Mus muscu
c 507	31	0.9	71990	2	AC116160	AC116160 Homo sapi	c 580	31	0.9	167564	2	AF267170	AF267170 Homo sapi
c 508	31	0.9	73260	5	AL606809	AL606809 Zebrafish	c 581	31	0.9	168056	2	AC099254	AC099254 Rattus no
c 509	31	0.9	74562	2	HS22502	295124 Human DNA s	c 582	31	0.9	168223	2	AC019020	AC019020 Homo sapi
c 510	31	0.9	76985	2	AC112544	AC112544 Rattus no	c 583	31	0.9	168672	2	AC027102	AC027102 Homo sapi
c 511	31	0.9	77953	9	AC108031	AC108031 Homo sapi	c 584	31	0.9	169401	2	AC069056	AC069056 Homo sapi
c 512	31	0.9	80578	2	PFMAL13P9	AL096783 Plasmodiu	c 585	31	0.9	169514	9	AC064869	AC064869 Homo sapi
c 513	31	0.9	8518	2	PFMAL13PA	AL109815 Plasmodiu	c 586	31	0.9	169536	2	AC016496	AC016496 Homo sapi
c 514	31	0.9	84730	2	AC074054	AC074054 Oryza sat	c 587	31	0.9	170588	9	CNS01RHF	AL161747 Human chr
c 515	31	0.9	84838	2	AC111501	AC111501 Rattus no	c 588	31	0.9	170608	2	AC096172	AC096172 Rattus no
c 516	31	0.9	86384	9	AC116172	AC116172 Homo sapi	c 589	31	0.9	170731	2	AC111988	AC111988 Rattus no
c 517	31	0.9	88818	2	AC097812	AC097812 Rattus no	c 590	31	0.9	170965	9	AB017654	AB017654 Homo sapi
c 518	31	0.9	92985	9	AL157378	AL157378 Human DNA	c 591	31	0.9	170996	2	AL592432	AL592432 Homo sapi
c 519	31	0.9	93173	2	AC094918	AC094918 Rattus no	c 592	31	0.9	171623	2	AC107829	AC107829 Mus muscu
c 520	31	0.9	94384	9	AC011718	AC011718 Homo sapi	c 593	31	0.9	171781	2	AC027510	AC027510 Homo sapi
c 521	31	0.9	95472	2	AC068387	AC068387 Homo sapi	c 594	31	0.9	172402	2	AC115411	AC115411 Rattus no
c 522	31	0.9	95845	8	AF411807	AF411807 Lycopersi	c 595	31	0.9	172405	9	AC053523	AC053523 Homo sapi
c 523	31	0.9	97759	2	AC097789	AC097789 Rattus no	c 596	31	0.9	173349	9	AC010600	AC010600 Homo sapi
c 524	31	0.9	100132	9	AC114813	AC114813 Homo sapi	c 597	31	0.9	173450	2	AC127901	AC127901 Homo sapi
c 525	31	0.9	100785	9	AP000617	AP000617 Homo sapi	c 598	31	0.9	173639	10	AL606921	AL606921 Mouse DNA
c 526	31	0.9	103097	9	AL445464	AL445464 Human DNA	c 599	31	0.9	174151	2	AC011182	AC011182 Homo sapi
c 527	31	0.9	103836	9	AC079791	AC079791 Homo sapi	c 600	31	0.9	174765	2	AC073103	AC073103 Homo sapi
c 528	31	0.9	106642	9	AL662781	AL662781 Homo sapi	c 601	31	0.9	175645	9	AC073114	AC073114 Homo sapi
c 529	31	0.9	109465	9	AL158821	AL158821 Human DNA	c 602	31	0.9	175647	2	AC110565	AC110565 Mus muscu
c 530	31	0.9	110000	2	AC092450	Continuation (4 of	c 603	31	0.9	176784	2	AC099347	AC099347 Rattus no
c 531	31	0.9	110000	2	PFMAL13P2_1	Continuation (2 of	c 604	31	0.9	176979	8	AP001168	AP001168 Oryza sat
c 532	31	0.9	110098	9	AL358976	AL358976 Human DNA	c 605	31	0.9	177034	9	AP002840	AP002840 Homo sapi
c 533	31	0.9	113596	2	AC026438	AC026438 Homo sapi	c 606	31	0.9	177670	2	AC101716	AC101716 Mus muscu
c 534	31	0.9	114467	9	AP000462	AP000462 Homo sapi	c 607	31	0.9	178534	2	AC027203	AC027203 Homo sapi
c 535	31	0.9	114965	9	AC108306	AC108306 Rattus no	c 608	31	0.9	179576	2	AC114702	AC114702 Rattus no
c 536	31	0.9	117296	9	AC092865	AC092865 Homo sapi	c 609	31	0.9	180650	9	AC109474	AC109474 Homo sapi
c 537	31	0.9	120138	2	AC024624	AC024624 Mus muscu	c 610	31	0.9	180708	9	AL590725	AL590725 Human DNA
c 538	31	0.9	120450	9	AC093393	AC093393 Rattus no	c 611	31	0.9	181265	2	AC105526	AC105526 Rattus no
c 539	31	0.9	128802	2	AC123139	AC123139 Rattus no	c 612	31	0.9	181492	2	AC099587	AC099587 Mus muscu
c 540	31	0.9	129422	9	AL589677	AL589677 Human DNA	c 613	31	0.9	181614	2	AC115744	AC115744 Mus muscu
c 541	31	0.9	131296	9	AC105104	AC105104 Homo sapi	c 614	31	0.9	181774	2	AL844152	AL844152 Danio rer
c 542	31	0.9	133651	9	AC092791	AC092791 Homo sapi	c 615	31	0.9	181829	9	AC023425	AC023425 Homo sapi
c 543	31	0.9	135932	8	AC079736	AC079736 Oryza sat	c 616	31	0.9	182529	2	AC064832	AC064832 Homo sapi
c 544	31	0.9	136687	9	AL662857	AL662857 Human DNA	c 617	31	0.9	183178	2	AC121981	AC121981 Mus muscu
c 545	31	0.9	137463	2	AC107474	AC107474 Rattus no	c 618	31	0.9	183291	2	AC106101	AC106101 Rattus no
c 546	31	0.9	140044	8	AC084406	AC084406 Oryza sat	c 619	31	0.9	184671	2	AC112648	AC112648 Homo sapi
c 547	31	0.9	140363	10	AC104097	AC104097 Mus muscu	c 620	31	0.9	187045	2	AC073253	AC073253 Homo sapi
c 548	31	0.9	141386	2	AC119454	AC119454 Rattus no	c 621	31	0.9	188068	2	AC109085	AC109085 Rattus no
c 549	31	0.9	143614	2	AC025147	AC025147 Homo sapi	c 622	31	0.9	188212	2	AC111688	AC111688 Rattus no
c 550	31	0.9	143717	2	AC083933	AC083933 Homo sapi	c 623	31	0.9	188392	2	AC095573	AC095573 Rattus no
c 551	31	0.9	145220	2	AC095447	AC095447 Rattus no	c 624	31	0.9	188636	9	HUAC002287	AC002287 Homo sapi
c 552	31	0.9	145510	8	AC074355	AC074355 Oryza sat	c 625	31	0.9	188807	2	AC036199	AC036199 Homo sapi
c 553	31	0.9	145625	2	AC131010	AC131010 Homo sapi	c 626	31	0.9	188876	2	AC119852	AC119852 Mus muscu
c 554	31	0.9	146403	2	AC027067	AC027067 Homo sapi	c 627	31	0.9	189015	2	AC090560	AC090560 Homo sapi
c 555	31	0.9	150669	2	AC112836	AC112836 Rattus no	c 628	31	0.9	189486	9	AC008733	AC008733 Homo sapi
c 556	31	0.9	151311	2	AP004885	AP004885 Oryza sat	c 629	31	0.9	189829	2	AC094664	AC094664 Rattus no
c 557	31	0.9	151675	9	AP000470	AP000470 Homo sapi	c 630	31	0.9	190549	10	AL591512	AL591512 Mouse DNA
c 558	31	0.9	151720	2	AC122663	AC122663 Rattus no	c 631	31	0.9	191136	2	AC098997	AC098997 Rattus no
c 559	31	0.9	151878	9	AC093820	AC093820 Homo sapi	c 632	31	0.9	191265	2	AC130450	AC130450 Homo sapi
c 560	31	0.9	152409	2	PFMAL1P1	AL031744 Plasmodiu	c 633	31	0.9	191434	9	AC087477	AC087477 Homo sapi
c 561	31	0.9	153472	9	AB020868	AB020868 Homo sapi	c 634	31	0.9	191967	2	AC021962	AC021962 Homo sapi
c 562	31	0.9	154984	9	AC019246	AC019246 Homo sapi	c 635	31	0.9	192581	2	PFMAL13P1	AL049180 Plasmodiu
c 563	31	0.9	155220	2	AC122947	AC122947 Rattus no	c 636	31	0.9	192929	2	AC005505	AC005505 Plasmodiu
c 564	31	0.9	158060	2	AC004153	AC004153 Plasmodiu	c 637	31	0.9	193157	2	AC073853	AC073853 Homo sapi
c 565	31	0.9	158422	2	AC016102	AC016102 Homo sapi	c 638	31	0.9	193916	2	AC123184	AC123184 Rattus no
c 566	31	0.9	157756	2	AP001075	AP001075 Homo sapi	c 639	31	0.9	194076	2	AC131241	AC131241 Mus muscu
c 567	31	0.9	158700	2	AC097633	AC097633 Homo sapi	c 640	31	0.9	194181	2	AC018886	AC018886 Homo sapi
c 568	31	0.9	159349	9	AC097633	AC097633 Homo sapi	c 641	31	0.9	196431	2	CNS01DUS	AL133162 Homo sapi
c 569	31	0.9	160242	9	AP002778	AP002778 Homo sapi	c 642	31	0.9	196055	2	AC021333	AC021333 Homo sapi
c 570	31	0.9	160253	2	AC021157	AC021157 Homo sapi	c 643	31	0.9	198130	2	AC122464	AC122464 Mus muscu
c 571	31	0.9	161678	2	AC009337	AC009337 Homo sapi	c 644	31	0.9	198821	2	AC123036	AC123036 Mus muscu
c 572	31	0.9	162475	2	AC126737	AC126737 Rattus no	c 645	31	0.9	199434	10	AL669956	AL669956 Mouse DNA
c 573	31	0.9	162743	2	CNS08CAI	AL831805 Oryza sat	c 646	31	0.9	199639	2	AL805905	AL805905 Danio rer
c 574	31	0.9	163122	2	AC117930	AC117930 Papilio cyn	c 647	31	0.9	200761	10	AC122140	AC122140 Mus muscu
c 575	31	0.9	163309	9	AP005434	AP005434 Homo sapi	c 648	31	0.9	200806	2	AC127265	AC127265 Mus muscu
c 576	31	0.9	164216	9	AC093578	AC093578 Homo sapi	c 649	31	0.9	201106	2	AC110375	AC110375 Mus muscu

c 650	31	0.9	201838	2	AC124508	AC124508 Mus muscu	c 723	30	0.9	99186	2	AL732580	Danio rer
c 651	31	0.9	203470	2	AC118155	AC118155 Rattus no	c 724	30	0.9	100000	9	AP000150	Homo sapi
c 652	31	0.9	204652	2	PFMAL13P6	AL049183 Plasmodiu	c 725	30	0.9	100871	5	AL591170	Zebrafish
c 653	31	0.9	204652	2	PFMAL13P6	AL049183 Plasmodiu	c 726	30	0.9	101965	2	AC097915	Rattus no
c 654	31	0.9	209508	2	AC111912	AC111912 Rattus no	c 727	30	0.9	102579	9	AC002375	Homo sapi
c 655	31	0.9	209507	2	AC111912	AC111912 Rattus no	c 728	30	0.9	103566	9	AC003087	Homo sapi
c 656	31	0.9	212827	9	AC009412	AC009412 Mus muscu	c 729	30	0.9	104992	2	AC005504	Plasmodiu
c 657	31	0.9	213070	10	AL691427	AL691427 Homo sapi	c 730	30	0.9	106360	2	CNS08C96	AC1732331 Oryza sat
c 658	31	0.9	213991	2	AC119579	AC119579 Rattus no	c 731	30	0.9	110000	2	AC125124_3	Continuation (4 of
c 659	31	0.9	217263	2	AC108831	AC108831 Mus muscu	c 732	30	0.9	110000	2	AC125124_3	Continuation (4 of
c 660	31	0.9	217374	2	AC106531	AC106531 Rattus no	c 733	30	0.9	110000	2	AL357131	Homo sapi
c 661	31	0.9	219346	10	AC098740	AC098740 Mus muscu	c 734	30	0.9	110000	2	PFMAL4P1_0	AL034557 Plasmodiu
c 662	31	0.9	219346	10	AC098740	AC098740 Mus muscu	c 735	30	0.9	110174	9	D83253	Homo sapien
c 663	31	0.9	219582	10	AL625764	AL625764 Mouse DNA	c 736	30	0.9	113880	3	PFMAL13P4	AL008970 Plasmodiu
c 664	31	0.9	222481	2	AC122393	AC122393 Mus muscu	c 737	30	0.9	114226	2	AC004710	Plasmodiu
c 665	31	0.9	222734	2	AC091445	AC091445 Rattus no	c 738	30	0.9	114226	2	AC004710	Plasmodiu
c 666	31	0.9	228094	2	AC124736	AC124736 Mus muscu	c 739	30	0.9	114809	2	AC083823	Homo sapi
c 667	31	0.9	229420	2	AL772373	AL772373 Danio rer	c 740	30	0.9	115565	2	OSIG00046	AL732352 Oryza sat
c 668	31	0.9	231772	2	AC125217	AC125217 Mus muscu	c 741	30	0.9	116147	2	AC097254	Rattus no
c 669	31	0.9	234112	2	PFMAL4P2	AL035475 Plasmodiu	c 742	30	0.9	116788	9	AC007247	Homo sapi
c 670	31	0.9	238890	2	AL591542	AL591542 Mus muscu	c 743	30	0.9	116969	9	AL450423	Human DNA
c 671	31	0.9	253305	3	PFMAL13P7	AL034559 Plasmodiu	c 744	30	0.9	120450	9	AC093393	Homo sapi
c 672	31	0.9	293431	2	PFMAL13P4	AL049181 Plasmodiu	c 745	30	0.9	122032	9	AL513187	Human DNA
c 673	31	0.9	340000	9	AP001689	AP001689 Homo sapi	c 746	30	0.9	122969	9	AC098862	Homo sapi
c 674	31	0.9	347342	2	AL831721	AL831721 Danio rer	c 747	30	0.9	123204	10	AL672005	AL672005 Mouse DNA
c 675	30	0.9	226	8	AY020725	AY020725 Oryza sat	c 748	30	0.9	123233	2	AC084100	Homo sapi
c 676	30	0.9	400	11	GI6237	GI6237 human SRS S	c 749	30	0.9	124010	9	HS340G1	Human DNA s
c 677	30	0.9	694	4	BTMSAT16	X71509 B.taurus mi	c 750	30	0.9	126736	2	AC044788	Homo sapi
c 678	30	0.9	2085	3	PFTH10RED	X87095 P.falciiparu	c 751	30	0.9	128500	9	AC069426	Homo sapi
c 679	30	0.9	6012	6	AX344487	AX344487 Sequence	c 752	30	0.9	129517	2	AC016400	Homo sapi
c 680	30	0.9	6012	6	AX348896	AX348896 Sequence	c 753	30	0.9	131004	2	AC084184	Homo sapi
c 681	30	0.9	6552	6	AX251432	AX251432 Sequence	c 754	30	0.9	134856	2	AC098220	Rattus no
c 682	30	0.9	8451	6	AX339147	AX339147 Sequence	c 755	30	0.9	135378	9	AL390060	Human DNA
c 683	30	0.9	8451	6	AX345361	AX345361 Sequence	c 756	30	0.9	135736	9	AL391645	Human DNA
c 684	30	0.9	8451	6	AX348369	AX348369 Sequence	c 757	30	0.9	138176	2	AC117887	Rattus no
c 685	30	0.9	8561	6	AX281215	AX281215 Sequence	c 758	30	0.9	142318	2	AC121392	Rattus no
c 686	30	0.9	8961	6	AX323814	AX323814 Sequence	c 759	30	0.9	142994	2	CNS08C7P	AL731740 Oryza sat
c 687	30	0.9	12029	3	AE001381	AE001381 Plasmodiu	c 760	30	0.9	143534	9	AC113380	Homo sapi
c 688	30	0.9	12029	3	AE001427	AE001427 Plasmodiu	c 761	30	0.9	143701	2	AC022853	Homo sapi
c 689	30	0.9	12404	3	AE001424	AE001424 Plasmodiu	c 762	30	0.9	144138	9	AC011196	Homo sapi
c 690	30	0.9	13951	3	AE001406	AE001406 Plasmodiu	c 763	30	0.9	144162	2	AC008434	Homo sapi
c 691	30	0.9	14005	3	AE001409	AE001409 Plasmodiu	c 764	30	0.9	144406	2	AC008396	Homo sapi
c 692	30	0.9	16422	3	AE001421	AE001421 Plasmodiu	c 765	30	0.9	147009	2	AC084179	Homo sapi
c 693	30	0.9	17470	3	AE001402	AE001402 Plasmodiu	c 766	30	0.9	148295	9	AC090510	Homo sapi
c 694	30	0.9	28670	9	AC104621	AC104621 Homo sapi	c 767	30	0.9	148757	2	AC130885	Homo sapi
c 695	30	0.9	40100	2	AC130558	AC130558 Rattus no	c 768	30	0.9	148807	9	AC007028	Homo sapi
c 696	30	0.9	40668	9	AC003112	AC003112 Human DNA	c 769	30	0.9	148872	2	AC073168	Homo sapi
c 697	30	0.9	47844	9	AC008998	AC008998 Homo sapi	c 770	30	0.9	148876	9	AC011455	Homo sapi
c 698	30	0.9	54940	9	AL596211	AL596211 Human DNA	c 771	30	0.9	149218	2	AC023997	Homo sapi
c 699	30	0.9	58346	2	AC100546	AC100546 Mus muscu	c 772	30	0.9	149366	2	AC127223	Mus muscu
c 700	30	0.9	62043	9	AL161893	AL161893 Human DNA	c 773	30	0.9	149869	9	AC006026	Homo sapi
c 701	30	0.9	64386	2	AC104222	AC104222 Mus muscu	c 774	30	0.9	150573	9	AC097473	Homo sapi
c 702	30	0.9	66448	9	AC091286	AC091286 Homo sapi	c 775	30	0.9	151324	9	AC098936	Homo sapi
c 703	30	0.9	66448	9	AC091286	AC091286 Homo sapi	c 776	30	0.9	151745	2	AC102069	Mus muscu
c 704	30	0.9	69324	2	AL117589	AL117589 Mus muscu	c 777	30	0.9	152039	9	AC097489	Homo sapi
c 705	30	0.9	70788	2	AL353144	AL353144 Homo sapi	c 778	30	0.9	152345	9	AP000009	Homo sapi
c 706	30	0.9	74126	9	AC055825	AC055825 Homo sapi	c 779	30	0.9	152409	2	PFMAL1P1	AL031744 Plasmodiu
c 707	30	0.9	78866	9	AL358452	AL358452 Human DNA	c 780	30	0.9	154386	2	AC016314	Homo sapi
c 708	30	0.9	80518	2	PFMAL13P3	AL109815 Plasmodiu	c 781	30	0.9	154530	9	AL160151	Human DNA
c 709	30	0.9	81851	9	HSDJ719K3	AL109931 Human DNA	c 782	30	0.9	155421	2	AC109554	Rattus no
c 710	30	0.9	83110	2	PFMAL13P8	AL109814 Plasmodiu	c 783	30	0.9	155523	2	AC025367	Homo sapi
c 711	30	0.9	83351	8	AC101657	AC101657 Genomic s	c 784	30	0.9	155523	2	AC128023	Rattus no
c 712	30	0.9	85691	9	AP001429	AP001429 Homo sapi	c 785	30	0.9	156547	9	AL359435	Human DNA
c 713	30	0.9	85974	2	AC021283	AC021283 Homo sapi	c 786	30	0.9	157665	10	AC069018	Mus muscu
c 714	30	0.9	88037	2	PFMAL13P8	AL096782 Plasmodiu	c 787	30	0.9	158335	2	AC130857	Rattus no
c 715	30	0.9	90050	9	HSJ136A11	AL121962 Human DNA	c 788	30	0.9	159288	2	AP005533	Oryza sat
c 716	30	0.9	92501	2	AC107549	AC107549 Rattus no	c 789	30	0.9	160135	9	AL590427	Human DNA
c 717	30	0.9	95560	2	AC103136	AC103136 Rattus no	c 790	30	0.9	160324	9	AC079117	Homo sapi
c 718	30	0.9	97083	9	AF130249	AF130249 Homo sapi	c 791	30	0.9	160519	2	AC128328	Rattus no
c 719	30	0.9	97898	9	AL353613	AL353613 Human DNA	c 792	30	0.9	160519	2	AC128328	Rattus no
c 720	30	0.9	98341	9	AC074024	AC074024 Homo sapi	c 793	30	0.9	160562	2	AC098172	Rattus no
c 721	30	0.9	98734	2	PFMAL1P2	AL031745 Plasmodiu	c 794	30	0.9	160707	2	AC044899	Homo sapi
c 722	30	0.9	99145	2	AC112379	AC112379 Rattus no	c 795	30	0.9	161067	2	AL607133	Homo sapi

C 796	30	0.9	161083	2	AC129224	AC129224	Oryza sat	C 869	30	0.9	190624	2	AC026892	AC026892	Homo sapi
C 797	30	0.9	161876	2	AC073634	AC073634	Homo sapi	C 870	30	0.9	190848	9	AC113416	AC113416	Homo sapi
C 798	30	0.9	162549	9	AC090802	AC090802	Homo sapi	C 871	30	0.9	191027	2	AC022271	AC022271	Homo sapi
C 799	30	0.9	162803	2	AC032000	AC032000	Homo sapi	C 872	30	0.9	191136	2	AC098997	AC098997	Rattus no
C 800	30	0.9	163361	2	AC128954	AC128954	Rattus no	C 873	30	0.9	191161	2	AC107539	AC107539	Rattus no
C 801	30	0.9	163521	10	AC121966	AC121966	Mus muscu	C 874	30	0.9	191241	2	AC116461	AC116461	Mus muscu
C 802	30	0.9	164118	2	AL732629	AL732629	Danio rer	C 875	30	0.9	195634	2	AC013464	AC013464	Homo sapi
C 803	30	0.9	164217	9	AC093264	AC093264	Homo sapi	C 876	30	0.9	196490	2	AC005507	AC005507	Plasmodi
C 804	30	0.9	164339	3	PFMAL3P6	PFMAL3P6		C 877	30	0.9	196490	2	AC005507	AC005507	Plasmodi
C 805	30	0.9	164399	3	PFMAL3P6	PFMAL3P6		C 878	30	0.9	196946	2	AC067934	AC067934	Homo sapi
C 806	30	0.9	164399	3	PFMAL3P6	PFMAL3P6		C 879	30	0.9	196966	2	AC031975	AC031975	Homo sapi
C 807	30	0.9	165010	9	HSDJ339B4	HSDJ339B4		C 880	30	0.9	196999	2	AL772173	AL772173	Mus muscu
C 808	30	0.9	165425	2	AC120888	AC120888	Oryza sat	C 881	30	0.9	197778	9	AF130358	AF130358	Homo sapi
C 809	30	0.9	166395	5	AL627383	AL627383	Zebratfish	C 882	30	0.9	197915	9	AC005725	AC005725	Homo sapi
C 810	30	0.9	166459	2	AC073374	AC073374	Homo sapi	C 883	30	0.9	198480	2	AC025077	AC025077	Homo sapi
C 811	30	0.9	166572	2	AC091102	AC091102	Homo sapi	C 884	30	0.9	198952	10	AL773600	AL773600	Mouse DNA
C 812	30	0.9	166796	2	AC126437	AC126437	Mus muscu	C 885	30	0.9	199610	2	AC109243	AC109243	Mus muscu
C 813	30	0.9	167087	2	AF004001	AF004001	Oryza sat	C 886	30	0.9	199610	2	AC109243	AC109243	Mus muscu
C 814	30	0.9	167346	9	AC096640	AC096640	Homo sapi	C 887	30	0.9	200966	10	AL596108	AL596108	Mouse DNA
C 815	30	0.9	167409	2	AC073374	AC073374	Homo sapi	C 888	30	0.9	202563	9	AC021192	AC021192	Homo sapi
C 816	30	0.9	168008	2	AC027488	AC027488	Homo sapi	C 889	30	0.9	204254	2	AC087783	AC087783	Homo sapi
C 817	30	0.9	168008	2	AC027488	AC027488	Homo sapi	C 890	30	0.9	204358	2	AC111121	AC111121	Mus muscu
C 818	30	0.9	168062	30	AC022292	AC022292	Homo sapi	C 891	30	0.9	204480	2	AC019083	AC019083	Homo sapi
C 819	30	0.9	168506	9	AC007404	AC007404	Homo sapi	C 892	30	0.9	205429	2	AC005506	AC005506	Plasmodi
C 820	30	0.9	168662	2	AC022241	AC022241	Homo sapi	C 893	30	0.9	206214	2	AC095934	AC095934	Rattus no
C 821	30	0.9	169546	2	AC004157	AC004157	Plasmodi	C 894	30	0.9	210233	2	AC104431	AC104431	Homo sapi
C 822	30	0.9	169869	2	AC005867	AC005867	Homo sapi	C 895	30	0.9	210282	9	AP001274	AP001274	Homo sapi
C 823	30	0.9	170512	2	AC021806	AC021806	Homo sapi	C 896	30	0.9	211325	2	AP002757	AP002757	Homo sapi
C 824	30	0.9	170789	2	AC106198	AC106198	Rattus no	C 897	30	0.9	215891	2	AL732451	AL732451	Mus muscu
C 825	30	0.9	171026	9	AL590416	AL590416	Human DNA	C 898	30	0.9	220633	9	HU091321	HU091321	Human Chrom
C 826	30	0.9	171152	2	AC101183	AC101183	Mus muscu	C 899	30	0.9	222572	10	AL691519	AL691519	Mouse DNA
C 827	30	0.9	171578	2	AC011791	AC011791	Homo sapi	C 900	30	0.9	223280	2	AC130456	AC130456	Homo sapi
C 828	30	0.9	172180	9	AC109494	AC109494	Homo sapi	C 901	30	0.9	224236	2	AL806518	AL806518	Mus muscu
C 829	30	0.9	172248	2	AC124336	AC124336	Mus muscu	C 902	30	0.9	224717	2	AC106281	AC106281	Rattus no
C 830	30	0.9	172433	2	AC118973	AC118973	Rattus no	C 903	30	0.9	225208	2	AC015561	AC015561	Homo sapi
C 831	30	0.9	172747	9	AL359835	AL359835	Human DNA	C 904	30	0.9	226616	2	AC022235	AC022235	Mus muscu
C 832	30	0.9	172758	2	AC117918	AC117918	Rattus no	C 905	30	0.9	228502	2	AC111540	AC111540	Rattus no
C 833	30	0.9	173415	9	AL591890	AL591890	Human DNA	C 906	30	0.9	228502	2	AC111540	AC111540	Rattus no
C 834	30	0.9	173532	2	AC040890	AC040890	Homo sapi	C 907	30	0.9	229518	2	AC069058	AC069058	Homo sapi
C 835	30	0.9	173696	2	AC111981	AC111981	Rattus no	C 908	30	0.9	231129	2	AC094132	AC094132	Rattus no
C 836	30	0.9	174402	9	AC016991	AC016991	Homo sapi	C 909	30	0.9	234515	2	AL805943	AL805943	Mus muscu
C 837	30	0.9	176634	2	AC118163	AC118163	Homo sapi	C 910	30	0.9	234960	2	AC115675	AC115675	Rattus no
C 838	30	0.9	177076	2	AC092949	AC092949	Homo sapi	C 911	30	0.9	235150	2	AC073776	AC073776	Mus muscu
C 839	30	0.9	177127	2	AC026287	AC026287	Homo sapi	C 912	30	0.9	244075	2	AC110157	AC110157	Mus muscu
C 840	30	0.9	177519	9	AC068702	AC068702	Homo sapi	C 913	30	0.9	245802	2	AC006279	AC006279	Plasmodi
C 841	30	0.9	178116	2	AC073491	AC073491	Homo sapi	C 914	30	0.9	253576	2	AC103320	AC103320	Rattus no
C 842	30	0.9	178328	2	AC092547	AC092547	Homo sapi	C 915	30	0.9	256172	2	AC005139	AC005139	Plasmodi
C 843	30	0.9	178480	2	AC125834	AC125834	Rattus no	C 916	30	0.9	291641	2	AC092893	AC092893	Homo sapi
C 844	30	0.9	178524	9	AC006427	AC006427	Homo sapi	C 917	30	0.9	306130	2	AC110996	AC110996	Homo sapi
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* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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RESULT 3
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DEFINITION complete cds.
ACCESSION AF123656
VERSION AF123656.1 GI:4572469
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1515)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1515)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer Institute, 2338 10th street, Philadelphia, PA 19107, USA
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Query Match 21.8%; Score 757; DB 9; Length 1515;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Homo sapiens clone T8D145M4 FEZ1 (FEZ1) mRNA, alternatively
spliced, complete cds.
ACCESSION AF123655

AF123655.1 GI:4572467
Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1614)
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
99199287
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2 (bases 1 to 1614)
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2338 10th street, Philadelphia, PA 19107, USA
Location/Qualifiers
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Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 776 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCCTGTGCTGCCACCGTCCAGG 835
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AF123658 1722 bp mRNA linear PRI 07-APR-1999
LOCUS Homo sapiens clone G3612 FEZ1 (FEZ1) mRNA, alternatively spliced,
DEFINITION complete cds.
ACCESSION AF123658
VERSION AF123658.1 GI:4572473
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1722)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1722)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
DIRECT SUBMISSION
TITLE Immunology/Microbiology, Kimmel Cancer
JOURNAL Submitted (27-JAN-1999)
INSTITUTE Location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1556 CGCGCTGGAGAGACCCAGTGGAGGTG 1583
Db 1125 CGCGCTGGAGAGACCCAGTGGAGGTG 1152

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LOCUS Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.
DEFINITION AF123659
ACCESSION AF123659
VERSION AF123659.1 GI:4572475
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5492)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 5492)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
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TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2338 10th street, Philadelphia, PA 19107, USA
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1376 CRAAGCTCAAGCAGCGCTCGCAGAGAGCAGCGCGCGCAGCAGCTCTCGACCTGCAGGT 1435
DB 1056 CAAGCTCAAGCAGCGCTCGCAGAGAGCAGCGCGCGCAGCAGCTCTCGACCTGCAGGT 1115
QY 1436 ACTGCAGCTTCAGCAGGAGAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCTTCATGAAGGA 1495
DB 1116 ACTGCAGCTTCAGCAGGAGAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCTTCATGAAGGA 1175
QY 1496 GCAGGACCTCTCGAGACCAAGCTCAGGTCTTACGAGAGGAGAGCAGCTTCGGCCC 1555
DB 1176 GCAGGACCTCTCGAGACCAAGCTCAGGTCTTACGAGAGGAGAGCAGCTTCGGCCC 1235
QY 1556 CGGCTGAGGAGACCAAGCTGGGAGGTG 1583
DB 1236 CGGCTGAGGAGACCAAGCTGGGAGGTG 1263
RESULT 8
AF123654 Homo sapiens clone E264162 FEZ1 (FEZ1) mRNA linear PRI 07-APR-1999
LOCUS complete cds.
DEFINITION AF123654
ACCESSION AF123654.1 GI:4572465
VERSION
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 633)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 633)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2338 10th street, Philadelphia, PA 19107, USA
FEATURES Location/Qualifiers
source 1..633
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8p22"
1..633
/gene="FEZ1"
1..633
/gene="FEZ1"
/note="alternatively spliced"
/codon_start=1
/product="FEZ1"
/protein_id="AAD23835.1"
/db_xref="GI:4572466"
gene
CDS
BASE COUNT 136 a 217 c 175 g 105 t
ORIGIN
Query Match 6.2%; Score 214; DB 9; Length 633;
Best Local Similarity 100.0%; Pred. No. 7.9e-109;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 776 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCTGTGCTGCCACCGTTCAGG 835

```

Db 345 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCTGTGCTGCCACCGTCCAGG 404
Qy 836 AGCCATCTGTCACCTCTCTCCCGGAGAGTGCAGCCAGCAGCTGCACCCCGCCCTCCAGA 895
Db 405 AGCCATCTGTCACCTCTCTCCCGGAGAGTGCAGCCAGCAGCTGCACCCCGCCCTCCAGA 464
Qy 896 CAAGCCCAAGAGAGAGAGTGAAGCTGGCTGTGCTCTGGGCGGTGTGAGACTCCGG 955
Db 465 CAAGCCCAAGAGAGAGAGTGAAGCTGGCTGTGCTCTGGGCGGTGTGAGACTCCGG 524
Qy 956 CCGGAATCCATGTCAGCTGCCAGCTGCCACACACAGC 989
Db 525 CCGGAATCCATGTCAGCTGCCAGCTGCCACACACAGC 558

RESULT 9
AC093002
LOCUS AC093002 70707 bp DNA linear PRI 07-MAR-2002
DEFINITION Homo sapiens 3q BAC RP11-490H13 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
ACCESSION AC093002
VERSION AC093002.4 GI:18873802
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 70707)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.B., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Halle,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulsegh,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,
Nickerson,E., Nwokenwo,S., Ogih,M., Okwuonu,G., Oragunye,N.,
Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
Pickens,R., Primus,E., Pu.L.L., Quiles,M., Ren,Y., Rives,M.,
Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
Scott,G., Shen,H., Shooshkari,N., Sisson,I., Sodergren,E.,
Sonaikhe,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,
Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S.,
Warren,R., Washington,C., Watlington,S., Williams,G.,
Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 70707)

```

AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

Worley, K.C.
Direct Submission
Submitted (09-AUG-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 70707)
Worley, K.C.
Direct Submission
Submitted (23-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 70707)
Worley, K.C.
Direct Submission
Submitted (26-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 70707)
Worley, K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Feb 23, 2002 this sequence version replaced gi:17646866.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
source	1..70707 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3"
repeat_region	/clone="RP11-490H13" complement(609..913) /rpt_family="AluSc"
repeat_region	1193..1236 /rpt_family="(TA)n"
repeat_region	1649..1918

TITLE JOURNAL REFERENCE

RESULT 13

AC021439/c
 LOCUS AC021439
 DEFINITION Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.
 AC021439
 VERSION AC021439.9 GI:21206407
 HTG.
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 206030)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 15, clone RP11-484P15

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 206030)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F.,
 Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
 DeArillano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
 Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
 Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
 Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G., Locke,K.,
 Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
 McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
 Norman,C.H., O'Connor,T., O'Donnell,P., Olivart,T.M., Peterson,K.,
 Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
 Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
 Zimmer,A. and Zody,M.

Direct Submission

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 206030)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
 Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
 Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
 Cook,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Fero,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
 Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lakocque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
 Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
 Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Pollara,V., Raymond,C., Ratta,R., Rieback,M., Riley,R., Rise,C.,
 Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
 Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
 Theodore,J., Topham,K., Travers,M., Travis,N., Triggilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (25-MAY-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 25, 2002 this sequence version replaced gi:14994160.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WDR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L5100

Center clone name: 484_P15

FEATURES

source

Location/Qualifiers

1..206030
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="15"
 /map="15"
 /clone="RP11-484P15"
 /clone_lib="RPCI-11 Human Male BAC"
 19..189
 /rpt_family="MLTIE"
 complement(277..375)
 /rpt_family="L1PA10"
 430..881
 /rpt_family="LTR38B"
 complement(2539..2833)
 /rpt_family="AluY"
 complement(2925..4060)
 /rpt_family="PRIMA41-int"
 complement(4063..5234)
 /rpt_family="L1PA11"
 5270..5706
 /rpt_family="L1MC2"
 5715..5939
 /rpt_family="L1MC2"
 6014..6341
 /rpt_family="AluY"
 6346..6590
 /rpt_family="L1MD3"
 6624..6795
 /rpt_family="Tigger4(Zombi)"
 6801..6855
 /rpt_family="MER51A"
 6881..7201
 /rpt_family="MER51A"
 7202..7798
 /rpt_family="MER51A-int"
 7960..8138
 /rpt_family="MER51A-int"
 8362..8482
 /rpt_family="MER51B-int"
 8484..8843
 /rpt_family="MER51B"
 complement(8854..9606)
 /rpt_family="Tigger3(Golem)"
 9607..9910
 /rpt_family="AluSq"
 9926..10062
 /rpt_family="Tigger4(Zombi)"
 10101..10134
 /rpt_family="AT-rich"
 10165..10262
 /rpt_family="MER83"
 10269..10646
 /rpt_family="MER83"
 10858..11701
 /rpt_family="MER83-int"
 11720..12258
 /rpt_family="MER83-int"
 12318..12613
 /rpt_family="MER4-int"
 12624..12754
 /rpt_family="MER4-int"
 12755..13055
 /rpt_family="AluY"
 13056..13720
 /rpt_family="MER4-int"
 13756..15037
 /rpt_family="MER4-int"
 15322..15675

repeat_region

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```

Center project name: L23473
Center clone name: 171_P_5
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 225162 bases at least Q40
Consensus quality: 226535 bases at least Q30
Consensus quality: 227117 bases at least Q20
Insert size: 225000; agarose-fp
Insert size: 227484; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; agarose-fp
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 301: contig of 301 bp in length
* 302 401: gap of 100 bp
* 402 5831: contig of 5430 bp in length
* 5832 5931: gap of 100 bp
* 5932 173029: contig of 167098 bp in length
* 173030 173129: gap of 100 bp
* 173130 210061: contig of 36932 bp in length
* 210062 210161: gap of 100 bp
* 210162 227884: contig of 17723 bp in length.
*
FEATURES
    source
        1. .227884
        /organism="Mus musculus"
        /db_xref="taxon:10090"
        /clone="RP23-171P5"
        /clone_lib="RPCI-23 Female Mouse BAC"
        1. .301
        /note="assembly_fragment"
        clone end: SP6
        vector side: left"
        402. .5831
        /note="assembly_fragment"
        5932. .173029
        /note="assembly_fragment"
        173130. .210061
        /note="assembly_fragment"
        210162. .227884
        /note="assembly_fragment"
        clone end: T7
        vector side: right"
BASE COUNT 65784 a 48825 c 49902 g 62967 t 402 others
ORIGIN
Query Match 1.1%; Score 38; DB 2; Length 227884;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 807 GCCTTCAAGCTGTGCTGCCAGGTCAGGACCATCT 844
|||||
Db 84402 GCCTTCAAGCTGTGCTGCCAGGTCAGGACCATCT 84439

RESULT 15
AC099416/c AC099416 263546 bp DNA linear HTG 23-MAY-2002
LOCUS Mus musculus chromosome UNK clone RP23-122M11, WORKING DRAFT
DEFINITION SEQUENCE, 8 unordered pieces.
ACCESSION AC099416
VERSION AC099416.2 GI:21105058
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus.

```

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 263546)

AUTHORS

McPherson, J.D. and Waterston, R.H.

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 263546)

AUTHORS

McPherson, J.D. and Waterston, R.H.

JOURNAL

Submitted (14-NOV-2001) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE

3 (bases 1 to 263546)

AUTHORS

McPherson, J.D. and Waterston, R.H.

JOURNAL

Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT

On May 23, 2002 this sequence version replaced gi:16924178.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

Contact: submissions@watson.wustl.edu

----- Project Information -----

Center project name: M BAO122M11

----- Summary Statistics -----

Sequencing vector: M13; 32%

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 278310 bases at least Q40

Consensus quality: 282938 bases at least Q30

Consensus quality: 286149 bases at least Q20

Insert size: 250000; agarose-fp

Insert size: 387570; sum-of-contigs

Quality coverage: 25.74 in Q20 bases; agarose-fp

Quality coverage: 16.86 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1204: contig of 1204 bp in length

* 1205 1304: gap of unknown length

* 1305 2524: contig of 1220 bp in length

* 2525 2624: gap of unknown length

* 2625 4136: contig of 1512 bp in length

* 4137 4236: gap of unknown length

* 4237 16434: contig of 12198 bp in length

* 16435 16534: gap of unknown length

* 16535 32106: contig of 15572 bp in length

* 32107 32206: gap of unknown length

* 32207 140224: contig of 108018 bp in length

* 140225 140324: gap of unknown length

* 140325 262693: contig of 122369 bp in length

* 262694 262793: gap of unknown length

* 262794 263546: contig of 753 bp in length.

* Location/Qualifiers

1. .263546

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="UNK"

/clone="RP23-122M11"

1. .1204

/note="assembly_name:Contig127"

1305. .2524

* misc_feature

* misc_feature

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2625..4136
misc_feature /note="assembly_name:Contig360"
4237..16434
misc_feature /note="assembly_name:Contig396"
16535..32106
misc_feature /note="assembly_name:Contig397"
32207..140224
misc_feature /note="assembly_name:Contig398"
140325..262693
misc_feature /note="assembly_name:Contig399"
262794..263546
misc_feature /note="assembly_name:Contig154"
BASE COUNT 76628 a 56149 c 55623 g 74436 t 710 others
ORIGIN
Query Match 1.1%; Score 38; DB 2; Length 263546;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 807 GCCTCAAGCCTGTGCTGCCACGGTCAGGAGCCATCCT 844
Db 250484 GCCTCAAGCCTGTGCTGCCACGGTCAGGAGCCATCCT 250447
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Search completed: June 17, 2003, 03:55:22
Job time : 6462.51 secs

Accession No.	Score	Query Match	Length	DB	ID	Description
1	3473	100.0	9048	21	AA064507	Nucleotide
2	1677	48.3	2411	22	AA330637	DNA encoding
3	1677	48.3	2411	22	AA528699	Genomic sequence
4	757	21.8	1512	21	AA064513	Nucleotide
5	757	21.8	1614	21	AA064512	Nucleotide
6	757	21.8	1692	21	AA064514	Nucleotide
7	757	21.8	1722	21	AA064515	Nucleotide
8	757	21.8	1791	21	AA064508	cDNA sequence
9	757	21.8	5492	21	AA064509	cDNA sequence

229	25	0.7	1503900	22	AAK96733	Human neutregulin-1	302	24	0.7	17792	22	AAK36099	Human cardiovascular
230	24	0.7	125	21	AAC25418	Human secreted pro	303	24	0.7	17809	23	ABK42246	Genomic sequence #
231	24	0.7	426	22	AAC36828	Human cardiovascular	304	24	0.7	18357	24	ABQ67083	Human angiogenesis
232	24	0.7	487	21	AAC68735	Human TSC39 cDNA f	305	24	0.7	32221	22	AAK39766	Genomic sequence #
233	24	0.7	504	24	ABO17474	Oligonucleotide fo	306	24	0.7	32221	22	AAK90119	Human digestive sy
234	24	0.7	504	24	ABO17475	Oligonucleotide fo	307	24	0.7	34769	22	AAK46774	Tumour suppressor
235	24	0.7	505	23	ABV58881	Human prostate exp	308	24	0.7	40324	24	ABQ67149	Human angiogenesis
236	24	0.7	633	13	AAQ20841	Pfs16 gene. Plasm	309	24	0.7	42573	23	ABQ28622	Drosophila melanog
237	24	0.7	789	12	AAQ10792	Bovine vascular en	310	24	0.7	49999	24	AAK23902	Human LOBO homolog
238	24	0.7	789	14	AAQ44255	Partial bovine VEG	311	24	0.7	50000	24	ABL56201	AmEPV genome fragm
239	24	0.7	829	12	AAQ10796	Bovine vascular en	312	24	0.7	58708	22	AAK64739	Human immune/haema
240	24	0.7	961	12	AAQ10791	Bovine vascular en	313	24	0.7	103929	21	AAK22287	BAC containing rep
241	24	0.7	961	14	AAQ44259	Bovine VEGF-164 co	314	24	0.7	113515	24	ABL34175	Human immune syste
242	24	0.7	1543	11	AAQ06600	Clone lambda.vegf.	315	24	0.7	237326	19	AAK57903	Hereditary haemoch
243	24	0.7	1547	21	AAC68736	Human TSC39 cDNA.	316	23	0.7	23	21	AAK64525	PCR primer G20 use
244	24	0.7	1560	24	ABK48976	Physics-based gene	317	23	0.7	23	21	AAK64527	PCR primer G32 use
245	24	0.7	1698	21	AAA81571	N meningitidis pa	318	23	0.7	23	21	AAK64541	Nucleotide sequenc
246	24	0.7	2141	21	AAZ50203	Petunia hybrida ne	319	23	0.7	151	22	AAK64541	Soybean 318013 reg
247	24	0.7	2141	21	AAZ35496	Petunia nectary-sp	320	23	0.7	236	22	AAK93306	Plasmodium falcipa
248	24	0.7	2459	23	ABL26096	Drosophila melanog	321	23	0.7	238	22	AAK161524	Soybean 240017 reg
249	24	0.7	2461	23	ABL13728	Drosophila melanog	322	23	0.7	269	22	AAK161702	Soybean 318013 reg
250	24	0.7	2500	23	ABL28394	Drosophila melanog	323	23	0.7	286	24	ABN96424	Gene #2922 used to
251	24	0.7	2780	23	ABL27136	Drosophila melanog	324	23	0.7	300	20	AAK213456	Human gene express
252	24	0.7	2948	24	ABL19697	Mouse ischaemic co	325	23	0.7	377	22	AAK181403	Human polynucleoti
253	24	0.7	3054	24	ABK36165	cDNA sequence #556	326	23	0.7	453	22	AAK933193	Human polynucleoti
254	24	0.7	3175	23	ABL02810	Drosophila melanog	327	23	0.7	470	22	AAK93301	Plasmodium falcipa
255	24	0.7	4578	22	AAS27741	DNA encoding novel	328	23	0.7	472	21	AAK28226	Human secreted pro
256	24	0.7	4578	22	AAS27742	DNA encoding novel	329	23	0.7	480	24	ABK62665	Rat sequence diffe
257	24	0.7	4684	23	ABL18548	Drosophila melanog	330	23	0.7	509	22	ABK61512	Human foetal liver
258	24	0.7	5005	23	ABL28704	Drosophila melanog	331	23	0.7	509	22	ABA29232	Probe #7698 for ge
259	24	0.7	5204	24	ABL32900	Human immune syste	332	23	0.7	509	22	AAK09812	Human brain expres
260	24	0.7	5457	24	ABL33130	Human immune syste	333	23	0.7	509	22	AAK35706	Human bone marrow
261	24	0.7	5457	23	ABL33131	Human immune syste	334	23	0.7	509	22	AAK141421	Probe #10107 used
262	24	0.7	5497	23	ABL04596	Drosophila melanog	335	23	0.7	509	24	ABSO9980	Human genome-deriv
263	24	0.7	5557	24	ABL33546	Human immune syste	336	23	0.7	543	22	ABA21513	Human nervous syst
264	24	0.7	5814	24	ABL33560	Human immune syste	337	23	0.7	543	22	ABA21514	Human nervous syst
265	24	0.7	5956	24	ABL70325	Chemically treated	338	23	0.7	543	22	ABA21515	Human nervous syst
266	24	0.7	5956	24	AAS61272	Human gene regulat	339	23	0.7	582	22	AAK93310	Plasmodium falcipa
267	24	0.7	5956	24	ABK31368	Signal transductio	340	23	0.7	582	22	AAK93310	Plasmodium falcipa
268	24	0.7	5989	22	AAS46515	Tumour suppressor	341	23	0.7	703	22	AAK87363	Human developmenta
269	24	0.7	5995	22	AAS46515	Tumour suppressor	342	23	0.7	742	22	AAK07077	Human cDNA clone (
270	24	0.7	6103	24	ABL34171	Human immune syste	343	23	0.7	809	22	AAK29793	S cerevisiae apopt
271	24	0.7	6103	24	ABL34171	Signal transductio	344	23	0.7	821	20	AAK16428	Human gene express
272	24	0.7	6454	23	ABK31513	Drosophila melanog	345	23	0.7	824	24	ABN89109	Human prostate spe
273	24	0.7	6853	22	AAK87155	Human immune/haema	346	23	0.7	844	22	AAK03515	Human cDNA clone (
274	24	0.7	7862	24	ABL34054	Human immune syste	347	23	0.7	944	22	AAH33445	Human colon cancer
275	24	0.7	7913	22	AAS46311	Tumour suppressor	348	23	0.7	1501	22	AAH13748	Human cDNA sequenc
276	24	0.7	7913	24	ABL70531	Chemically treated	349	23	0.7	1514	24	ABK34631	Human cDNA for nov
277	24	0.7	7913	24	AAS61128	Human gene regulat	350	23	0.7	1560	24	ABK48976	Physics-based gene
278	24	0.7	7913	24	ABL31216	Signal transductio	351	23	0.7	1636	22	ABA19549	Human nervous syst
279	24	0.7	7928	24	ABL70123	Chemically treated	352	23	0.7	1636	22	AAI99154	Human excretory re
280	24	0.7	7928	24	ABL32094	Human immune syste	353	23	0.7	1636	22	AAK32848	Human genomic DNA
281	24	0.7	7928	24	AAS61055	Human gene regulat	354	23	0.7	1636	22	AAK63504	Human kidney relat
282	24	0.7	7928	24	ABK31168	Signal transductio	355	23	0.7	1731	24	ABL64393	Stomach cancer rel
283	24	0.7	8237	22	AAS46801	Tumour suppressor	356	23	0.7	1764	24	ABK48066	cDNA encoding conl
284	24	0.7	8447	24	ABN80093	Human chemically m	357	23	0.7	1829	7	AAK60863	Sequence encoding
285	24	0.7	10483	22	AAK90686	Human immune/haema	358	23	0.7	1843	22	AAK74307	Human H11 coding s
286	24	0.7	10619	22	AAS45296	Chemically pretrea	359	23	0.7	1843	22	AAK74328	Human H11 coding s
287	24	0.7	10619	24	ABL92192	Chemically treated	360	23	0.7	1966	21	AAK77664	Human cancer assoc
288	24	0.7	10619	24	ABL49303	Human polynucleoti	361	23	0.7	2093	22	AAH15345	Human cDNA sequenc
289	24	0.7	10619	24	ABL32070	Human immune syste	362	23	0.7	2273	20	AAK27465	Human ovarian tumo
290	24	0.7	10619	24	ABK28127	DNA transcription	363	23	0.7	2562	23	ABL13566	Drosophila melanog
291	24	0.7	12202	23	ABL02770	Drosophila melanog	364	23	0.7	2707	23	ABK43641	DNA encoding novel
292	24	0.7	12202	23	ABL21186	Drosophila melanog	365	23	0.7	2780	23	ABL271136	Drosophila melanog
293	24	0.7	15037	22	AAI99283	Human excretory re	366	23	0.7	2780	22	AAH18583	Human cDNA sequenc
294	24	0.7	15037	22	AAI99283	Human kidney relat	367	23	0.7	3237	22	AAH18583	Ocean pout DNA seq
295	24	0.7	15548	24	ABL63633	Human immune syste	368	23	0.7	3350	13	AAK29361	Drosophila melanog
296	24	0.7	16258	24	ABL70376	Chemically treated	369	23	0.7	3391	22	ABL01932	Drosophila melanog
297	24	0.7	16258	24	ABK40038	Human chemically p	370	23	0.7	3730	22	ABA19745	Human nervous syst
298	24	0.7	16258	24	ABN80068	Human chemically m	371	23	0.7	3975	13	AAK81157	Malaria-specific g
299	24	0.7	16602	24	ABL32726	Human immune syste	372	23	0.7	3975	9	AAK22959	SERP gene. Plasm
300	24	0.7	17239	22	AAS36826	Human cardiovascular	373	23	0.7	3997	24	ABL99812	Human secretory po
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C 376	23	0.7	4858	24	ABK33961	Human DNA for stag	C 449	23	0.7	31718	22	AAL06416	Human reproductive
C 377	23	0.7	5037	24	ABN59798	Novel human coding	450	23	0.7	31718	22	AAK73104	Human immune/haema
C 378	23	0.7	5218	24	ABL33266	Human immune syste	451	23	0.7	31718	22	AAK73120	Human immune/haema
C 379	23	0.7	5586	24	AAS63356	Chemically pretrea	C 452	23	0.7	31718	22	AAK87442	Human immune/haema
C 380	23	0.7	5591	23	ABL05500	Drosophila melanog	C 453	23	0.7	31718	22	AAK87443	Human immune/haema
C 381	23	0.7	5795	24	ABN80222	Human chemically m	454	23	0.7	31718	22	AAK87573	Human immune/haema
C 382	23	0.7	5795	24	ABL33768	Human immune syste	455	23	0.7	31718	22	AAK87592	Human immune/haema
C 383	23	0.7	5818	22	AAS46635	Tumour suppressor	C 456	23	0.7	31718	22	AAK90359	Human digestive sy
C 384	23	0.7	5908	22	AAS45386	Chemically pretrea	C 457	23	0.7	31718	22	AAK90360	Human digestive sy
C 385	23	0.7	5908	22	AAS61216	Human gene regulat	C 458	23	0.7	32192	22	ABA17963	Human nervous syst
C 386	23	0.7	5908	24	ABK28231	DNA transcription	C 459	23	0.7	42573	23	ABL28622	Drosophila melanog
C 387	23	0.7	5930	24	ABL32517	Human immune syste	C 460	23	0.7	44211	22	AAK85974	Human immune/haema
C 388	23	0.7	5995	22	AAS46720	Tumour suppressor	461	23	0.7	56153	22	AAS46794	Tumour suppressor
C 389	23	0.7	6025	22	AAS45338	Chemically pretrea	462	23	0.7	149671	24	ABK84797	Human cDNA differe
C 390	23	0.7	6048	24	ABQ67001	Human angiogenesis	463	23	0.7	335913	22	AAI61371	Soybean 240017 reg
C 391	23	0.7	6065	24	ABL32505	Human immune syste	464	23	0.7	335913	22	AAI61372	Soybean 240017 reg
C 392	23	0.7	6124	11	AAQ03568	Sequence encoding	465	23	0.7	513445	22	AAI61373	Soybean 318013 reg
C 393	23	0.7	6124	24	ABK15042	Plasmodium gene fo	C 466	22	0.6	22	21	AAA64524	PCR primer G17 use
C 394	23	0.7	6145	24	ABL32973	Human immune syste	C 467	22	0.6	22	21	AAA64528	PCR primer IntBCR
C 395	23	0.7	6155	24	ABK28361	DNA transcription	C 468	22	0.6	22	21	AAL32385	Human SNP oligonuc
C 396	23	0.7	6168	22	AAK85162	Human immune/haema	C 469	22	0.6	100	21	AAI19497	Human secreted pro
C 397	23	0.7	6170	22	AAK85163	Human immune/haema	C 470	22	0.6	177	22	AAH93314	Plasmodium falci
C 398	23	0.7	6216	24	ABL70139	Chemically treated	471	22	0.6	200	24	ABL86078	Human ovarian canc
C 399	23	0.7	6216	24	ABK39932	Human chemically p	472	22	0.6	209	22	AAH93323	Plasmodium falci
C 400	23	0.7	6306	22	AAK85746	Human immune/haema	C 473	22	0.6	218	22	AAH93315	Plasmodium falci
C 401	23	0.7	6430	24	ABN80122	Human chemically m	474	22	0.6	250	21	AAF21208	Human low adenosin
C 402	23	0.7	7109	22	ABAI19555	Human nervous syst	475	22	0.6	250	21	AAA35086	Human adenosine re
C 403	23	0.7	7109	22	AAI19157	Human excretory re	476	22	0.6	256	21	AAH32079	Plant microsatelli
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C 408	23	0.7	7570	23	ABL06842	Drosophila melanog	C 481	22	0.6	348	23	ABV34186	Human prostate exp
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C 410	23	0.7	8085	24	ABK33986	Human DNA for stag	C 483	22	0.6	375	23	ABV13065	Human prostate exp
C 411	23	0.7	8210	24	ABK32506	Human prostate spe	C 484	22	0.6	386	22	AAI89642	Human polynucleoti
C 412	23	0.7	8310	20	AAZ29911	CDNA encoding a SC	C 485	22	0.6	402	21	AAH70130	Plasmodium falci
C 413	23	0.7	8588	22	AAS45469	Chemically pretrea	C 486	22	0.6	409	22	AAI87008	Human polynucleoti
C 414	23	0.7	8588	24	ABK28325	DNA transcription	C 487	22	0.6	410	24	ABH79733	Human ovarian canc
C 415	23	0.7	8693	24	ABL32808	Human immune syste	C 488	22	0.6	412	22	AAH93300	Plasmodium falci
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C 417	23	0.7	8842	24	ABL33448	Human immune syste	C 490	22	0.6	426	21	AAH32069	Plant microsatelli
C 418	23	0.7	8842	24	AAS83334	Human immune syste	C 491	22	0.6	427	22	AAK62516	Human immune/haema
C 419	23	0.7	8896	24	ABN80327	Chemically pretrea	C 492	22	0.6	431	21	AAH32052	Plant microsatelli
C 420	23	0.7	8920	15	AAQ62924	Carbamoyl-phosphat	C 493	22	0.6	479	21	AAH32052	Arabidopsis thalia
C 421	23	0.7	9402	22	AAS46672	Tumour suppressor	C 494	22	0.6	479	21	AAH32052	Arabidopsis thalia
C 422	23	0.7	9566	22	ABA20411	Human nervous syst	C 495	22	0.6	495	24	ABN64967	Plasmodium falci
C 423	23	0.7	9566	22	AAI37121	Human musculocele	C 496	22	0.6	496	24	ABL86815	Human cancer relat
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C 425	23	0.7	9840	22	AAK67429	Human immune/haema	C 498	22	0.6	516	22	AAH11579	Human cDNA clone (
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C 429	23	0.7	11394	24	ABK28221	DNA transcription	C 502	22	0.6	549	21	AAQ95306	Cat flea head and
C 430	23	0.7	11662	24	ABL33901	Human immune syste	C 503	22	0.6	553	21	AAQ79990	Cat flea head and
C 431	23	0.7	12069	24	ABK39931	Human chemically p	C 504	22	0.6	553	21	AAQ79990	Human secreted pro
C 432	23	0.7	13774	22	AAK83209	Human immune/haema	C 505	22	0.6	565	22	AAK82704	Human immune/haema
C 433	23	0.7	15548	24	ABL34154	Human immune syste	C 506	22	0.6	565	22	AAK82705	Human immune/haema
C 434	23	0.7	16299	22	AAK71100	Human immune/haema	C 507	22	0.6	637	22	ABQ07877	Human polynucleoti
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C 436	23	0.7	18647	21	AAF21059	Human low adenosin	C 509	22	0.6	637	24	ABQ24141	Oligonucleotide fo
C 437	23	0.7	18648	21	AAAS4937	Human adenosine re	C 510	22	0.6	642	21	ABQ24141	Oligonucleotide fo
C 438	23	0.7	18648	24	ABL65840	Lung cancer relate	C 511	22	0.6	649	24	ABQ57268	Oligonucleotide fo
C 439	23	0.7	18648	24	ABL69114	Kidney cancer rela	C 512	22	0.6	649	24	ABQ52679	Oligonucleotide fo
C 440	23	0.7	21537	24	ABL33998	Human immune syste	C 513	22	0.6	670	21	AAQ32632	Arabidopsis thalia
C 441	23	0.7	21748	23	ABL02520	Drosophila melanog	C 514	22	0.6	710	24	ABQ20510	Oligonucleotide fo
C 442	23	0.7	24102	22	AAK74877	Human immune/haema	C 515	22	0.6	710	24	ABQ20510	Oligonucleotide fo
C 443	23	0.7	25012	22	ABAI5431	Human nervous syst	C 516	22	0.6	750	14	AAQ35214	Rat synaptophysin
C 444	23	0.7	25955	22	ABAI9852	Human nervous syst	C 517	22	0.6	819	24	ABK35901	cDNA sequence #292
C 445	23	0.7	28149	22	ABAI7961	Human nervous syst	C 518	22	0.6	936	24	ABQ48606	Oligonucleotide fo
C 446	23	0.7	31718	22	AAS39915	Genomic sequence #	C 519	22	0.6	936	24	ABQ48607	Oligonucleotide fo
C 447	23	0.7	31718	22	AAS39916	Genomic sequence #	C 520	22	0.6	937	19	AAV52661	Human native hepat

c 521	22	0.6	954	14	AAQ46148	NKG2. Tropaeolum	c 594	22	0.6	6129	24	ABK31237	Signal transductio
c 522	22	0.6	1006	24	ABN74683	Bovine embryonic g	595	22	0.6	6149	24	AA663306	Chemically pretrea
c 523	22	0.6	1167	22	AAAD17481	Rat glucose-depend	596	22	0.6	6239	24	ABL333776	Human immune syste
c 524	22	0.6	1297	20	AA568827	X. laevis pRNDkk-1	597	22	0.6	6239	24	ABK28297	DNA transcription
c 525	22	0.6	1361	24	AAJ38827	Human PSNA CDNA #7	c 598	22	0.6	6253	24	ABK83716	Human cDNA differe
c 526	22	0.6	1409	21	AAZ97090	Human secreted pro	c 599	22	0.6	6254	24	ABL33620	Human immune syste
c 527	22	0.6	1545	24	ABQ67136	Human angiogenesis	c 600	22	0.6	6261	22	AA466643	Tumour suppressor
c 528	22	0.6	1614	23	ABL25018	Drosophila melanog	c 602	22	0.6	6261	22	AA466644	Tumour suppressor
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c 534	22	0.6	2226	23	ABL24114	Drosophila melanog	c 606	22	0.6	6261	22	ABK31161	Signal transductio
c 535	22	0.6	2334	22	AAI58874	Human polynucleoti	c 607	22	0.6	6298	24	ABL32434	Human immune syste
c 536	22	0.6	2349	22	AAH41951	Putative human CLA	c 608	22	0.6	6298	24	ABL32434	Human immune syste
c 537	22	0.6	2441	23	ABL10994	Drosophila melanog	c 609	22	0.6	6436	24	ABL33693	Human immune syste
c 538	22	0.6	2451	20	AAV82439	Vascular endotheli	c 610	22	0.6	6436	24	ABL33693	Human immune syste
c 539	22	0.6	2567	20	AAZ52889	Human prostate tum	c 611	22	0.6	6436	24	ABL33693	Human immune syste
c 540	22	0.6	2582	22	AAH16248	Human prostate sequ	c 612	22	0.6	6588	23	ABU24492	Human immune syste
c 541	22	0.6	2634	16	AAQ87841	Human neuronal cal	c 613	22	0.6	6588	23	ABU24492	Human immune syste
c 542	22	0.6	2634	21	AAQ87841	Human neuronal cal	c 614	22	0.6	6615	24	ABQ67035	Drosophila melanog
c 543	22	0.6	2642	22	AAH14538	Human calcium chan	c 615	22	0.6	6615	24	ABQ67035	Drosophila melanog
c 544	22	0.6	2704	24	ABK88007	Human cDNA sequenc	c 616	22	0.6	6775	24	ABO67159	Human angiogenesis
c 545	22	0.6	2712	16	AAQ87836	CDNA encoding huma	c 617	22	0.6	6831	24	ABL33486	Human immune syste
c 546	22	0.6	2712	21	AAQ87836	Human neuronal cal	c 618	22	0.6	6831	24	ABL33486	Human immune syste
c 547	22	0.6	2760	22	AAQ87836	Human calcium chan	c 619	22	0.6	6852	24	ABL70311	Chemically treated
c 548	22	0.6	2772	22	AAZ52679	Human breast cance	c 620	22	0.6	6852	24	AA661249	Human gene regulat
c 549	22	0.6	2772	22	AAZ52679	Human cDNA encodin	c 621	22	0.6	6988	24	ABL34440	Human immune syste
c 550	22	0.6	2970	16	AAQ87835	Human neuronal cal	c 622	22	0.6	7070	24	ABN80054	Human chemically m
c 551	22	0.6	2975	21	AAQ87835	Human calcium chan	c 623	22	0.6	7109	22	ABN80054	Human chemically m
c 552	22	0.6	2993	19	AAV15529	Human lymphoid-spe	c 624	22	0.6	7109	22	ABN80054	Human chemically m
c 553	22	0.6	2993	24	ABK84329	Human cDNA differe	c 625	22	0.6	7109	22	AAI99157	Human excretory re
c 554	22	0.6	3001	21	AAH51775	Drosophila melanog	c 626	22	0.6	7109	22	AAI99157	Human excretory re
c 555	22	0.6	3022	24	ABQ54722	Chromosome 13q31-q	c 627	22	0.6	7238	24	AAI63507	Human kidney relat
c 556	22	0.6	3129	22	ABQ54722	Human ovarian anti	c 628	22	0.6	7346	22	AAI63507	Human kidney relat
c 557	22	0.6	3230	23	ABL24328	Human nervous syst	c 629	22	0.6	7346	22	AAI63507	Human kidney relat
c 558	22	0.6	3240	19	AAV15530	Drosophila melanog	c 630	22	0.6	7346	22	AAI63507	Human kidney relat
c 559	22	0.6	3471	14	AAQ46673	Human lymphoid-spe	c 631	22	0.6	7593	23	AAI63507	Human kidney relat
c 560	22	0.6	3720	24	ABK17123	P mySB CDNA clone.	c 632	22	0.6	7635	23	ABL11336	Drosophila melanog
c 561	22	0.6	3741	22	AAQ91367	Eucalyptus grandis	c 633	22	0.6	7635	23	ABL11336	Drosophila melanog
c 562	22	0.6	3742	22	AAQ91367	Peroxidase Swpa2 c	c 634	22	0.6	7635	23	ABL11336	Drosophila melanog
c 563	22	0.6	3957	22	ABA06411	Peroxidase Swpa2 c	c 635	22	0.6	7903	22	AAI63507	Human immune syste
c 564	22	0.6	4282	23	AAI41898	Human cDNA SEQ ID	c 636	22	0.6	7903	22	AAI63507	Human immune syste
c 565	22	0.6	4809	23	ABL07632	Human GA733-2 gene	c 637	22	0.6	8087	24	ABL32742	Human immune syste
c 566	22	0.6	4936	23	ABL30286	Drosophila melanog	c 638	22	0.6	8087	24	ABL32742	Human immune syste
c 567	22	0.6	5040	24	ABL34405	Drosophila melanog	c 639	22	0.6	8319	22	AAI63507	Human immune syste
c 568	22	0.6	5152	22	AAQ70178	Human immune syste	c 640	22	0.6	8413	24	ABL70519	Human immune syste
c 569	22	0.6	5170	22	AAQ70178	Human immune/haema	c 641	22	0.6	8413	24	ABL70519	Human immune syste
c 570	22	0.6	5179	24	ABL33997	Human reproductive	c 642	22	0.6	8577	24	ABL333787	Human metastasis a
c 571	22	0.6	5179	24	ABL33997	Human immune syste	c 643	22	0.6	8577	24	ABL333787	Human metastasis a
c 572	22	0.6	5413	23	AA466694	DNA transcription	c 644	22	0.6	8753	24	ABL92271	Chemically treated
c 573	22	0.6	5413	23	AA466694	Tumour suppressor	c 645	22	0.6	8998	22	ABL333707	Human immune syste
c 574	22	0.6	5426	22	ABAL6522	Drosophila melanog	c 646	22	0.6	9021	22	AA466694	Tumour suppressor
c 575	22	0.6	5525	24	ABK33929	Human nervous syst	c 647	22	0.6	9789	17	AA466694	Tumour suppressor
c 576	22	0.6	5525	24	ABK33929	Human nervous syst	c 648	22	0.6	9789	17	AA466694	Tumour suppressor
c 577	22	0.6	5546	24	ABK34004	Human DNA for stag	c 649	22	0.6	9965	24	ABL34443	Human immune syste
c 578	22	0.6	5546	24	ABK34004	Human immune syste	c 650	22	0.6	9965	24	ABL34443	Human immune syste
c 579	22	0.6	5632	24	ABL32436	Human immune syste	c 651	22	0.6	10023	19	AAV52731	Human hepatocyte n
c 580	22	0.6	5815	24	ABL70586	Chemically treated	c 652	22	0.6	10132	24	ABL54372	Chemically treated
c 581	22	0.6	5834	22	AA545429	Chemically treated	c 653	22	0.6	10132	24	ABL54372	Chemically treated
c 582	22	0.6	5923	22	AAQ90320	Pea auxin-induced	c 654	22	0.6	10140	22	AAH49201	Human immune syste
c 583	22	0.6	5951	24	ABL33005	Human immune syste	c 655	22	0.6	10329	24	ABL34122	Human immune syste
c 584	22	0.6	6031	22	AA466622	Tumour suppressor	c 656	22	0.6	10425	22	ABA17962	Human nervous syst
c 585	22	0.6	6059	24	ABL33480	Human immune syste	c 657	22	0.6	10736	22	AAK80161	Human immune/haema
c 586	22	0.6	6063	24	ABL32748	Human immune syste	c 658	22	0.6	10736	22	AAK80161	Human immune/haema
c 587	22	0.6	6120	24	ABN80277	Human chemically m	c 659	22	0.6	10762	24	ABL92232	Chemically treated
c 588	22	0.6	6120	24	ABL70462	Chemically treated	c 660	22	0.6	11046	22	ABK31537	Signal transductio
c 589	22	0.6	6120	24	AA611429	Human gene regulat	c 661	22	0.6	11735	24	AA611429	Chemically pretrea
c 590	22	0.6	6120	24	ABK31489	Signal transductio	c 662	22	0.6	11735	24	AA611429	Chemically pretrea
c 591	22	0.6	6128	24	ABQ67040	Human angiogenesis	c 663	22	0.6	11836	22	AA453395	DNA transcription
c 592	22	0.6	6129	24	AA611550	Human gene regulat	c 664	22	0.6	11836	24	AA453395	DNA transcription
c 593	22	0.6	6129	24	AA611550	Human gene regulat	c 665	22	0.6	11836	24	AA453395	DNA transcription
c 594	22	0.6	6129	24	AA611550	Human gene regulat	c 666	22	0.6	11934	22	AAK82197	Human immune/haema

c 667	22	0.6	12010	23	ABL06138	Drosophila melanog	c 740	22	0.6	66804	24	ABK87050	Human transporter
c 668	22	0.6	12620	22	ABA16691	Human nervous syst	c 741	22	0.6	68356	22	AAK67283	Human immune/haema
c 669	22	0.6	13158	22	AAK68742	Human immune/haema	c 742	22	0.6	68356	22	AAK83312	Human immune/haema
c 670	22	0.6	13573	24	ABL33869	Human immune syste	c 743	22	0.6	68940	20	AAK57351	Human chromosome 6
c 671	22	0.6	13830	22	AAO202659	Tomato chromosome	c 744	22	0.6	73334	24	ABL92319	Chemically treated
c 672	22	0.6	14253	24	ABL33495	Human immune syste	c 745	22	0.6	73334	24	ABL34125	Human immune syste
c 673	22	0.6	14426	22	AAK71817	Human immune/haema	c 746	22	0.6	81369	21	AAA97997	Human T gene DNA
c 674	22	0.6	14426	22	AAK73115	Human immune/haema	c 747	22	0.6	84539	24	ABL64158	Stomach cancer rel
c 675	22	0.6	14426	22	AAK87586	Human immune/haema	c 748	22	0.6	107820	22	AAI16230	Human ATP-binding
c 676	22	0.6	14426	22	AAI162924	Human genomic DNA	c 749	22	0.6	109906	24	ABK94411	DNA encoding endot
c 677	22	0.6	14448	22	AAK71815	Human immune/haema	c 750	22	0.6	112460	24	ABK83567	Human cDNA differe
c 678	22	0.6	14448	22	AAK73111	Human immune/haema	c 751	22	0.6	126512	24	ABN83429	Human transporter
c 679	22	0.6	14448	22	AAK87580	Human immune/haema	c 752	22	0.6	127197	24	AAI161370	Soybean 51S002 reg
c 680	22	0.6	14448	22	AAI162922	Human genomic DNA	c 753	22	0.6	154465	24	AAD28763	Human AKAP allelic
c 681	22	0.6	14451	22	AAK71818	Human immune/haema	c 754	22	0.6	158245	24	AAD28762	Human AKAP allelic
c 682	22	0.6	14451	22	AAK73116	Human immune/haema	c 755	22	0.6	161425	22	AAH02340	Human AKAP10 gene
c 683	22	0.6	14451	22	AAK87587	Human immune/haema	c 756	22	0.6	162025	24	AAH02339	Human AKAP10 gene
c 684	22	0.6	14451	22	AAI162925	Human genomic DNA	c 757	22	0.6	162025	24	AAH02339	Human AKAP allelic
c 685	22	0.6	14537	22	AAK86355	Tumour suppressor	c 758	22	0.6	162025	24	AAH02339	Human AKAP allelic
c 686	22	0.6	15201	22	AAK83176	Human immune/haema	c 759	22	0.6	183999	22	AAH02339	Human AKAP allelic
c 687	22	0.6	15364	22	AAK83152	Human immune/haema	c 760	22	0.6	222930	24	ABK84349	Human cDNA differe
c 688	22	0.6	15743	24	ABK28396	DNA transcription	c 761	22	0.6	319608	21	AAH51601	Human chromosome 1
c 689	22	0.6	15772	22	AAK83220	Human immune/haema	c 762	22	0.6	319608	22	AAH51601	Human chromosome 1
c 690	22	0.6	15811	23	ABL12090	Drosophila melanog	c 763	22	0.6	1503900	22	AAK95240	Human neurotrophin-1
c 691	22	0.6	16037	22	AAK78529	Human immune/haema	c 764	22	0.6	1503900	22	AAK95240	Human neurotrophin-1
c 692	22	0.6	16037	24	ABK59947	Human secreted pro	c 765	21	0.6	21	21	AAK64523	PCR primer Int. ABF
c 693	22	0.6	16107	22	AAK78528	Human immune/haema	c 766	21	0.6	21	21	AAK64523	PCR primer G21. use
c 694	22	0.6	16107	22	AAK69948	Human secreted pro	c 767	21	0.6	31	16	AAQ79634	Primer 603 to ampl
c 695	22	0.6	16235	22	AAK86192	Human immune/haema	c 768	21	0.6	32	22	AAH54052	hFIX gene AE3, age
c 696	22	0.6	18110	24	ABK15357	Human interleukin	c 769	21	0.6	41	22	AAH54056	hFIX gene AE3, age
c 697	22	0.6	18281	22	ABL32963	Human immune syste	c 770	21	0.6	50	22	AAH32385	Human SNP oligonuc
c 698	22	0.6	18340	22	AAI19368	Mammalian interleu	c 771	21	0.6	51	22	AAH32384	Human SNP oligonuc
c 699	22	0.6	18488	22	AAK83173	Human immune/haema	c 772	21	0.6	51	22	AAH76309	Human silent SNP c
c 700	22	0.6	18663	22	AAK75859	Human immune/haema	c 773	21	0.6	79	21	AAH23093	Human secreted pro
c 701	22	0.6	19191	22	AAK67485	Human immune/haema	c 774	21	0.6	101	22	AAH54059	hFIX gene AE3, age
c 702	22	0.6	20300	24	ABK47337	Genomic nucleotide	c 775	21	0.6	102	22	AAH54085	hFIX gene AE3, el
c 703	22	0.6	20829	23	ABL14502	Drosophila melanog	c 776	21	0.6	106	24	ABL81741	Human ovarian canc
c 704	22	0.6	21621	22	AAK74867	Human immune/haema	c 777	21	0.6	123	22	AAH54118	hFIX gene AE3, ag
c 705	22	0.6	23457	22	AAK74866	Human immune/haema	c 778	21	0.6	124	22	AAH54117	hFIX gene AE3, ag
c 706	22	0.6	23544	22	AAH05829	Human reproductive	c 779	21	0.6	125	22	AAH54116	hFIX gene AE3, ag
c 707	22	0.6	23544	23	ABL98393	Human testicular a	c 780	21	0.6	126	22	AAH54115	hFIX gene AE3, ag
c 708	22	0.6	23670	24	ABA97077	Tomato Hero gene c	c 781	21	0.6	127	22	AAH54114	hFIX gene AE3, ag
c 709	22	0.6	23683	24	ABL70482	Chemically treated	c 782	21	0.6	128	22	AAH54113	hFIX gene AE3, ag
c 710	22	0.6	23683	24	ABL34623	Human metastasis a	c 783	21	0.6	129	22	AAH54112	hFIX gene AE3, ag
c 711	22	0.6	24161	22	AAK80711	Human immune/haema	c 784	21	0.6	130	22	AAH54111	hFIX gene AE3, ag
c 712	22	0.6	25378	22	AAK80709	Human immune/haema	c 785	21	0.6	131	22	AAH54110	hFIX gene AE3, ag
c 713	22	0.6	26997	22	AAH46748	Tumour suppressor	c 786	21	0.6	132	22	AAH54109	hFIX gene AE3, ag
c 714	22	0.6	27689	24	AAH19494	Arabidopsis RPM8 c	c 787	21	0.6	133	22	AAH54108	hFIX gene AE3, ag
c 715	22	0.6	28136	22	AAK69755	Human immune/haema	c 788	21	0.6	134	22	AAH54107	hFIX gene AE3, ag
c 716	22	0.6	28149	22	ABA17961	Human nervous syst	c 789	21	0.6	134	22	AAH54138	hFIX gene AE3, ag
c 717	22	0.6	31405	22	AAK67293	Human immune/haema	c 790	21	0.6	135	22	AAH54106	hFIX gene AE3, ag
c 718	22	0.6	31405	22	AAK74865	Human immune/haema	c 791	21	0.6	135	22	AAH54137	hFIX gene AE3, ag
c 719	22	0.6	31405	22	AAK83153	Human immune/haema	c 792	21	0.6	136	22	AAH54105	hFIX gene AE3, ag
c 720	22	0.6	32192	22	ABA17963	Human nervous syst	c 793	21	0.6	136	22	AAH54136	hFIX gene AE3, ag
c 721	22	0.6	32193	22	AAH27848	DNA encoding novel	c 794	21	0.6	137	22	AAH66832	Human immune/haema
c 722	22	0.6	32248	22	ABA20412	Human nervous syst	c 795	21	0.6	137	22	AAH66592	Human immune/haema
c 723	22	0.6	32248	22	AAH37122	Human musculoskele	c 796	21	0.6	137	22	AAH87285	Human immune/haema
c 724	22	0.6	32248	22	AAH26795	Human genomic DNA	c 797	21	0.6	137	22	AAH54104	hFIX gene AE3, ag
c 725	22	0.6	33942	22	AAK80281	Human immune/haema	c 798	21	0.6	137	22	AAH54135	hFIX gene AE3, ag
c 726	22	0.6	33942	22	AAK862174	Human immune/haema	c 799	21	0.6	138	22	AAH54103	hFIX gene AE3, ag
c 727	22	0.6	34769	22	AAH62774	Tumour suppressor	c 800	21	0.6	138	22	AAH54134	hFIX gene AE3, ag
c 728	22	0.6	38186	20	AAH232028	Human METHI relate	c 801	21	0.6	139	22	AAH54102	hFIX gene AE3, ag
c 729	22	0.6	38186	21	AAH232028	Human METHI relate	c 802	21	0.6	139	22	AAH54133	hFIX gene AE3, ag
c 730	22	0.6	41783	21	AAH21221	Human low adenosin	c 803	21	0.6	140	22	AAH54101	hFIX gene AE3, ag
c 731	22	0.6	41783	21	AAH35099	Human adenosine re	c 804	21	0.6	140	22	AAH54132	hFIX gene AE3, ag
c 732	22	0.6	41477	24	ABK84481	Human cDNA differe	c 805	21	0.6	141	22	AAH54100	hFIX gene AE3, ag
c 733	22	0.6	47108	24	ABK31511	Signal transductio	c 806	21	0.6	141	22	AAH54131	hFIX gene AE3, ag
c 734	22	0.6	49634	24	ABL68647	Kidney cancer rela	c 807	21	0.6	142	22	AAH54099	hFIX gene AE3, ag
c 735	22	0.6	53522	24	AAH30228	Human PKD1 gene.	c 808	21	0.6	142	22	AAH54130	hFIX gene AE3, ag
c 736	22	0.6	53526	17	AAH94101	Human PKD1 gene.	c 809	21	0.6	143	22	AAH54098	hFIX gene AE3, ag
c 737	22	0.6	53577	19	AAH18551	Human polycystic k	c 810	21	0.6	143	22	AAH54129	hFIX gene AE3, ag
c 738	22	0.6	53577	19	AAH94108	Human PKD1 locus b	c 811	21	0.6	144	22	AAH54097	hFIX gene AE3, ag
c 739	22	0.6	65057	23	ABL03490	Drosophila melanog	c 812	21	0.6	144	22	AAH54128	hFIX gene AE3, ag

813	21	0.6	145	22	AAF54096	hFIX gene AE3'' ag	c 886	21	0.6	404	23	ABV18543	Human prostate exp
814	21	0.6	145	22	AAF54127	hFIX gene AE3'' ag	c 887	21	0.6	408	23	ABV04866	Human prostate exp
815	21	0.6	146	22	AAF54095	hFIX gene AE3'' ag	c 888	21	0.6	409	23	AAI89061	Human polynucleoti
816	21	0.6	146	22	AAF54126	hFIX gene AE3'' ag	c 889	21	0.6	409	23	ABV10144	Human prostate exp
817	21	0.6	147	22	AAF54094	hFIX gene AE3'' ag	c 890	21	0.6	410	23	ABL79733	Human ovarian can
818	21	0.6	147	22	AAF54125	hFIX gene AE3'' ag	c 891	21	0.6	412	23	ABV32285	Human prostate exp
819	21	0.6	148	22	AAF54093	hFIX gene AE3'' ag	c 892	21	0.6	413	22	AAK58934	Human immune/haema
820	21	0.6	148	22	AAF54124	hFIX gene AE3'' ag	c 893	21	0.6	414	22	ABV31230	Human prostate exp
821	21	0.6	149	22	AAF54092	hFIX gene AE3'' ag	c 894	21	0.6	416	22	AAK96685	Human neuregulin g
822	21	0.6	149	22	AAF54123	hFIX gene AE3'' ag	c 895	21	0.6	416	22	AAK98178	Human polynucleoti
823	21	0.6	150	22	AAF54091	hFIX gene AE3'' ag	c 896	21	0.6	416	22	AAI91938	Human prostate exp
824	21	0.6	150	22	AAF54122	hFIX gene AE3'' ag	c 897	21	0.6	416	23	ABV05771	Human prostate exp
825	21	0.6	151	22	AAF54090	hFIX gene AE3'' ag	c 898	21	0.6	416	23	ABV35141	Human prostate exp
826	21	0.6	151	22	AAF54121	hFIX gene AE3'' ag	c 899	21	0.6	416	23	ABV43983	Human polynucleoti
827	21	0.6	152	22	AAF54089	hFIX gene AE3'' ag	c 900	21	0.6	420	22	AAI87096	Human prostate exp
828	21	0.6	152	22	AAF54120	hFIX gene AE3'' ag	c 901	21	0.6	422	23	ABV51084	Human prostate exp
829	21	0.6	153	22	AAF54088	hFIX gene AE3'' ag	c 902	21	0.6	423	22	AAI89138	Human polynucleoti
830	21	0.6	153	22	AAF54119	hFIX gene AE3'' ag	c 903	21	0.6	424	22	AAI84041	Human polynucleoti
831	21	0.6	154	22	AAF54087	hFIX gene AE3'' ag	c 904	21	0.6	426	23	ABV10058	Human prostate exp
832	21	0.6	160	22	AAI61473	Soybean 240017 reg	c 905	21	0.6	427	21	AAA28561	Human PC-1 gene in
833	21	0.6	170	21	AAI61548	Human secreted pro	c 906	21	0.6	428	22	AAK66386	Human immune/haema
834	21	0.6	188	22	AAI61667	Soybean 318013 reg	c 907	21	0.6	430	22	AAI17775	Human breast cance
835	21	0.6	193	22	AAK67054	Human immune/haema	c 908	21	0.6	436	22	AAI10700	Human breast cance
836	21	0.6	193	22	AAK67055	Human immune/haema	c 909	21	0.6	441	21	AAO18834	Human secreted pro
837	21	0.6	213	19	AAV16134	Microsatellite mar	c 910	21	0.6	443	22	AAI83572	Human polynucleoti
838	21	0.6	227	22	AAI61521	Soybean 240017 reg	c 911	21	0.6	448	23	ABV31316	Human prostate exp
839	21	0.6	239	22	AAI04403	Human reproductive	c 912	21	0.6	448	23	ABV40285	Human prostate exp
840	21	0.6	239	22	AAI26703	Human genomic DNA	c 913	21	0.6	449	22	AAK32417	Human bone marrow
841	21	0.6	240	22	AAI91712	Human polynucleoti	c 914	21	0.6	449	23	AAK32417	Human prostate exp
842	21	0.6	244	22	AAI61525	Soybean 240017 reg	c 915	21	0.6	449	24	ABS07201	Human genome-deriv
843	21	0.6	247	21	AAI55332	Human secreted pro	c 916	21	0.6	460	23	ABV43326	Human prostate exp
844	21	0.6	252	24	ABL68431	Kidney cancer rela	c 917	21	0.6	462	23	ABV43353	Human prostate exp
845	21	0.6	268	21	AAA43676	Human secreted exp	c 918	21	0.6	463	23	ABV40335	Human prostate exp
846	21	0.6	269	22	AAH93299	Plasmodium falcipa	c 919	21	0.6	469	23	ABV59953	Human prostate exp
847	21	0.6	271	21	AAI04521	Human secreted pro	c 920	21	0.6	480	16	AAQ81474	HMG2 promoter II.
848	21	0.6	277	21	AAI91712	Human secreted pro	c 921	21	0.6	480	16	AAQ81474	HMG2 promoter II.
849	21	0.6	296	23	ABV59802	Human prostate exp	c 922	21	0.6	484	23	ABV15018	Human prostate exp
850	21	0.6	299	22	ABAI2005	Human nervous syst	c 923	21	0.6	485	22	AAI16193	Human breast cance
851	21	0.6	299	22	AAK64933	Human immune/haema	c 924	21	0.6	487	23	AAK90446	DNA encoding novel
852	21	0.6	299	22	AAK70243	Human immune/haema	c 925	21	0.6	488	23	AAI16178	Human breast cance
853	21	0.6	299	22	AAK70244	Human immune/haema	c 926	21	0.6	492	23	ABV22727	Human prostate exp
854	21	0.6	304	23	AAK57335	cDNA #11 encoding	c 927	21	0.6	492	23	ABV22727	Human prostate exp
855	21	0.6	305	22	AAK68337	Human immune/haema	c 928	21	0.6	496	24	ABL86815	Human ovarian can
856	21	0.6	308	23	ABV59784	Human prostate exp	c 929	21	0.6	500	23	ABV39099	Human prostate exp
857	21	0.6	312	21	AAI31477	Human secreted pro	c 930	21	0.6	502	22	AAH11854	Human cDNA clone (
858	21	0.6	313	22	AAK77064	Human immune/haema	c 931	21	0.6	505	22	AAI12818	Human breast cance
859	21	0.6	315	21	AAK57237	Human breast cance	c 932	21	0.6	515	22	AAH09732	Human cDNA clone (
860	21	0.6	315	22	AAK66554	Human immune/haema	c 933	21	0.6	517	24	ABN62972	Human cancer relat
861	21	0.6	317	23	ABV60229	Human prostate exp	c 934	21	0.6	526	23	ABV32217	Human prostate exp
862	21	0.6	326	21	AAI04522	Human secreted pro	c 935	21	0.6	526	23	ABV41148	Human prostate exp
863	21	0.6	334	22	AAI83597	Human polynucleoti	c 936	21	0.6	530	23	ABV01902	Human prostate exp
864	21	0.6	339	22	AAK62643	Human immune/haema	c 937	21	0.6	530	24	ABN64214	Human cancer relat
865	21	0.6	343	23	ABV61438	Human prostate exp	c 938	21	0.6	532	22	AAK65304	Human immune/haema
866	21	0.6	344	22	AAH933307	Plasmodium falcipa	c 939	21	0.6	547	24	ABQ14986	Oligonucleotide fo
867	21	0.6	346	21	AAI30200	Human secreted pro	c 940	21	0.6	547	24	ABQ14987	Oligonucleotide fo
868	21	0.6	356	22	AAI37451	Novel human diagno	c 941	21	0.6	550	21	AAK94842	Cat flea hindgut a
869	21	0.6	360	21	AAI18637	Human secreted pro	c 942	21	0.6	552	22	AAK88826	Human digestive sy
870	21	0.6	373	24	ABL64614	Stomach cancer rel	c 943	21	0.6	553	21	AAK79930	Human secreted pro
871	21	0.6	375	22	AAK78393	Human immune/haema	c 944	21	0.6	561	21	AAK69740	Human ovarian carc.
872	21	0.6	375	22	AAK78396	Human immune/haema	c 945	21	0.6	561	24	ABN72634	Ovarian carcinoma
873	21	0.6	375	22	AAK67264	Novel human polynu	c 946	21	0.6	562	24	ABN60958	Human cancer relat
874	21	0.6	380	22	AAI80226	Human polynucleoti	c 947	21	0.6	563	22	AAH10207	Human cDNA clone (
875	21	0.6	383	22	AAI19639	Human breast cance	c 948	21	0.6	570	22	AAH13416	Human cDNA clone (
876	21	0.6	388	24	ABL81123	Human ovarian can	c 949	21	0.6	572	20	AAV88520	EST clone GM153
877	21	0.6	389	22	AAI99402	Human excretory re	c 950	21	0.6	572	22	AAH09154	Human cDNA clone (
878	21	0.6	389	22	AAI32245	Human polynucleoti	c 951	21	0.6	575	22	AAK80944	Human immune/haema
879	21	0.6	389	22	AAI63752	Human kidney relat	c 952	21	0.6	575	23	ABK42954	Genomic sequence #
880	21	0.6	393	22	AAI16171	Human breast cance	c 953	21	0.6	579	24	ABN63192	Human cancer relat
881	21	0.6	393	22	AAI191857	Human polynucleoti	c 954	21	0.6	580	22	AAK64801	Human immune/haema
882	21	0.6	394	22	AAI38091	Novel human diagno	c 955	21	0.6	582	24	ABQ36542	Oligonucleotide fo
883	21	0.6	395	22	AAI83016	Human polynucleoti	c 956	21	0.6	582	24	ABQ36543	Oligonucleotide fo
884	21	0.6	400	22	AAI81313	Human polynucleoti	c 957	21	0.6	583	22	AAH10034	Human cDNA clone (
885	21	0.6	401	22	AAI80907	Human polynucleoti	c 958	21	0.6	589	23	ABV58556	Human prostate exp

959	21	0.6	592	22	ABA62687	Human foetal liver
960	21	0.6	592	22	ABA29991	Probe #8457 for ge
961	21	0.6	592	22	AAK11065	Human brain expres
962	21	0.6	592	22	AAK36891	Human bone marrow
963	21	0.6	592	22	AAI17741	Probe #7674 for ge
964	21	0.6	592	22	AAI42689	Probe #11375 used
965	21	0.6	601	23	ABV52214	Human prostate exp
966	21	0.6	608	23	ABV41216	Human prostate exp
967	21	0.6	610	23	ABV50324	Human prostate exp
968	21	0.6	610	23	ABV50324	Human prostate exp
969	21	0.6	612	22	AAI25036	Human breast cance
970	21	0.6	615	23	ABV14940	Human prostate exp
971	21	0.6	615	23	ABK42536	Genomic sequence #
972	21	0.6	616	22	AAH87648	Peppermint plant o
973	21	0.6	624	22	AAK74618	Human immune/haema
974	21	0.6	624	22	AAK74619	Human immune/haema
975	21	0.6	624	22	AAK74620	Human immune/haema
976	21	0.6	624	23	ABV39025	Human prostate exp
977	21	0.6	624	23	ABV44812	Human prostate exp
978	21	0.6	624	23	ABV44885	Human prostate exp
979	21	0.6	625	21	AAZ80509	Human colon cancer
980	21	0.6	626	23	ABV48170	Human prostate exp
981	21	0.6	627	22	AAI42591	Human breast cance
982	21	0.6	627	22	AAK59153	Human immune/haema
983	21	0.6	637	22	AAK07877	Human secreted pro
984	21	0.6	654	22	AAI37107	Human musculoskele
985	21	0.6	662	24	ABQ14046	Oligonucleotide fo
986	21	0.6	662	24	ABQ14047	Oligonucleotide fo
987	21	0.6	672	22	AAI36427	Human musculoskele
988	21	0.6	699	22	ABA21522	Human nervous syst
989	21	0.6	700	22	AAH92455	Human inflammatory
990	21	0.6	700	22	AAH92911	Human inflammatory
991	21	0.6	709	24	ABQ31714	Oligonucleotide fo
992	21	0.6	709	24	ABQ31715	Oligonucleotide fo
993	21	0.6	715	23	ABV11139	Human prostate exp
994	21	0.6	735	22	AAI21464	Human breast cance
995	21	0.6	739	22	AAI28421	Genomic sequence #
996	21	0.6	739	22	AAI28422	Genomic sequence #
997	21	0.6	739	23	ABV18384	Human prostate exp
998	21	0.6	749	21	AAI46565	Zea mays DNA fragm
999	21	0.6	749	21	AAI46565	Zea mays DNA fragm
C1000	21	0.6	757	22	AAI96793	Human neuroblastom

ALIGNMENTS

RESULT 1
AAA64507
ID AAA64507 standard; DNA; 9048 BP.
XX
AC AAA64507;
XX
DT
XX
XX
02-JAN-2001 (first entry)
DE Nucleotide sequence comprising the human FEZ1 gene.
XX
XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
KW tumorigenesis; tumour survival; metastasis; ss..
XX
OS Homo sapiens.
XX
XX WO200050565-A2.
PN
XX
XX
PD
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US04950.
XX
XX 25-FEB-1999; 99US-0121537.
XX

PA
XX
PI Croce CM, Ishii H;
XX WPI; 2000-558396/51.
XX
XX
PT New polynucleotide homologous with a portion of one strand of the human
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
PT cancer -
XX
XX Claim 2; Fig 5A; 255pp; English.
XX
XX The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour
XX suppressor gene located at chromosome location 8p22. Decreased or no
XX expression of FEZ1 is detected in a variety of cancer cells. Expression
XX of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts
XX with tubulin, with microtubules, and with protein Efi-gamma.
XX Post-translational phosphorylation and dephosphorylation modulates the
XX effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are
XX useful for inducing cells to proliferate. Compounds which modulate FEZ1
XX association with tubulin are useful for alleviating tubulin hyper- or
XX hypo- polymerisation disorders, such as those associated with aberrant
XX initiation of mitosis, modulation of the initiation and rate of cell
XX proliferation and cell growth, modulation of cell shape, cell rigidity,
XX cell motility, rate and stage of cellular DNA replication, intracellular
XX distribution of organelles, metastatic potential of cell and cellular
XX transformation from a non-cancerous to cancerous phenotype. Compounds
XX which modulate FEZ1 binding and phosphorylation are also useful for
XX alleviating a disorder, such as tumorigenesis, tumour survival, growth
XX and metastasis.
SQ Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;

Query Match 100.0%; Score 3473; DB 21; Length 9048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCTGCCCTGGGGGCATCTTGAATACAGCTGGAGCTTTGTCTCATCATTTACACAGA 60
Db 871 AGCTGCCCTGGGGGCATCTTGAATACAGCTGGAGCTTTGTCTCATCATTTACACAGA 930
Qy 61 CTAGGGCAAGAGAGGCCCGCAGGCACTGAGAAATCAGCCCTCACACAGCTCAAGCCCTCG 120
Db 931 CTAGGGCAAGAGAGGCCCGCAGGCACTGAGAAATCAGCCCTCACACAGCTCAAGCCCTCG 990
Qy 121 TGGTCCACAGTGGGACACTGAAATCAATTTCTTATTCAGTCTCTGCCCCCTTGGCCT 180
Db 991 TGGTCCACAGTGGGACACTGAAATCAATTTCTTATTCAGTCTCTGCCCCCTTGGCCT 1050
Qy 181 GGGGAAATGAATCCCGGCTTTGATTTACTAGGAAAGAGCCTCTTATTTGTCATAGAGC 240
Db 1051 GGGGAAATGAATCCCGGCTTTGATTTACTAGGAAAGAGCCTCTTATTTGTCATAGAGC 1110
Qy 241 ATTCAGCTTTTCAAATTAAGGGCTTGTAACTGTGAAGCACTCTACAGGAAATTAAC 300
Db 1111 ATTCAGCTTTTCAAATTAAGGGCTTGTAACTGTGAAGCACTCTACAGGAAATTAAC 1170
Qy 301 AGTTTTAAAGAGATCGTGAATTTGGAGTGAGCCTCCCAACCTCTGAAGGAGCCAGTTC 360
Db 1171 AGTTTTAAAGAGATCGTGAATTTGGAGTGAGCCTCCCAACCTCTGAAGGAGCCAGTTC 1230
Qy 361 CGTGTCTTGTCTCAGGCTTAATGGAAGAGAGCAGTGAACAGAGAAAGAGGATGGACCTAA 420
Db 1231 CGTGTCTTGTCTCAGGCTTAATGGAAGAGAGCAGTGAACAGAGAAAGAGGATGGACCTAA 1290
Qy 421 AGAGGGACAGCAAGCTCGGCCAGCCTGATGCCCTTAATTTGCCCCACACAGAGACCTAGAG 480
Db 1291 AGAGGGACAGCAAGCTCGGCCAGCCTGATGCCCTTAATTTGCCCCACACAGAGACCTAGAG 1350
Qy 481 CAGGAGCTCAAGATGATGTTATTCACCTCGGGAGGCTGGGCAAGCTGGTGGCAGGTT 540
Db 1351 CAGGAGCTCAAGATGATGTTATTCACCTCGGGAGGCTGGGCAAGCTGGTGGCAGGTT 1410

Qy	541	GCTATTTTCATAGAACAAAGTGCCCAAGTCGCACATTAGGGTTTTTCCCTCTCTAAGAGAGAT	600
Db	1411	GCTATTTTCATAGAACAAAGTGCCCAAGTCGCACATTAGGGTTTTTCCCTCTCTAAGAGAGAT	1470
Qy	601	GACATTCAGCTGCTTTCAAAGCAACAGCAGCAGGTCTGCTGAGACAATTTGACCAAGAGGGGT	660
Db	1471	GACATTCAGCTGCTTTCAAAGCAACAGCAGCAGGTCTGCTGAGACAATTTGACCAAGAGGGGT	1530
Qy	661	GCTCGTGCGCTCAGAGAGGCCAGACTGGCTCAAGGTCGGCACGCGTGCCTTTCCTCTACAGGGCT	720
Db	1531	GCTCGTGCGCTCAGAGAGGCCAGACTGGCTCAAGGTCGGCACGCGTGCCTTTCCTCTACAGGGCT	1590
Qy	721	GGGTGCAATCGCGCGCAGGGGAGGCATGAGTCAACGCGGTCTCTTTTCCTCTACAGGGCT	780
Db	1591	GGGTGCAATCGCGCGCAGGGGAGGCATGAGTCAACGCGGTCTCTTTTCCTCTACAGGGCT	1650
Qy	781	CCGAGAAAGGGTGCAGTGAGGCCACAGCCTTCAAGCCTGTGCTGCCACGCGTCAGGAGGCCA	840
Db	1651	CCGAGAAAGGGTGCAGTGAGGCCACAGCCTTCAAGCCTGTGCTGCCACGCGTCAGGAGGCCA	1710
Qy	841	TCCTGCACTCTCTCCCGGAGAGTGCCAGCCACCAAGCTGCACCCCGCCCTTCCAGACAAGC	900
Db	1711	TCCTGCACTCTCTCCCGGAGAGTGCCAGCCACCAAGCTGCACCCCGCCCTTCCAGACAAGC	1770
Qy	901	CCAAGGACGAGAGCTGAAGCTGGCTGTGCTCTGGGGCGCTGTGACATCTCGCGCCGGA	960
Db	1771	CCAAGGACGAGAGCTGAAGCTGGCTGTGCTCTGGGGCGCTGTGACATCTCGCGCCGGA	1830
Qy	961	ACTCCATGTCAGGCTCCCCACACAGCAGCAGCAGCAGCTACCACTGGAGCCCGCTGG	1020
Db	1831	ACTCCATGTCAGGCTCCCCACACAGCAGCAGCAGCAGCTACCACTGGAGCCCGCTGG	1890
Qy	1021	TCACACCGCTGGGACCCACAAAGCCGTTTTGGGGGCTCCGCCCAACAATCACCCAGGGCA	1080
Db	1891	TCACACCGCTGGGACCCACAAAGCCGTTTTGGGGGCTCCGCCCAACAATCACCCAGGGCA	1950
Qy	1081	TCGTCCTCAGGACAGCAACATGATAGCCTGAAGGCTCTGTCTTCTCCGACGGAGGTA	1140
Db	1951	TCGTCCTCAGGACAGCAACATGATAGCCTGAAGGCTCTGTCTTCTCCGACGGAGGTA	2010
Qy	1141	GCAAGCTGGGCCACTCCGAAACAGGACAGAGGGCCCTCGTGTGTCGCTCCCCCATCT	1200
Db	2011	GCAAGCTGGGCCACTCCGAAACAGGACAGAGGGCCCTCGTGTGTCGCTCCCCCATCT	2070
Qy	1201	CCACGGACGAGTGACGATCCAGAGCTGGAAACAGAAAGCTGTTGGAGAGGAGGGGCGCCC	1260
Db	2071	CCACGGACGAGTGACGATCCAGAGCTGGAAACAGAAAGCTGTTGGAGAGGAGGGGCGCCC	2130
Qy	1261	TCCAGAAAGCTCAGCGCAGCTTTGAGAGAGGAGTTCCTCTCAGCCTGGCCTACGAGG	1320
Db	2131	TCCAGAAAGCTCAGCGCAGCTTTGAGAGAGGAGTTCCTCTCAGCCTGGCCTACGAGG	2190
Qy	1321	AGCGGCGCGCGCTGCAGGACGAGCTGAGGGCCCGGAGCCCAAGGCGGCAACAAGC	1380
Db	2191	AGCGGCGCGCGCTGCAGGACGAGCTGAGGGCCCGGAGCCCAAGGCGGCAACAAGC	2250
Qy	1381	TCAAGCAGGCTCTCAGAAAGACGCGCGCAGCAGAGTCTTGCTGCACTTCAGAGTACTGC	1440
Db	2251	TCAAGCAGGCTCTCAGAAAGACGCGCGCAGCAGAGTCTTGCTGCACTTCAGAGTACTGC	2310
Qy	1441	AGCTTCAGCAGGAGAACGCGCAGCTCCGCGAGGAGCTTCGAGAGCCTCATGAAGGAGCAGG	1500
Db	2311	AGCTTCAGCAGGAGAACGCGCAGCTCCGCGAGGAGCTTCGAGAGCCTCATGAAGGAGCAGG	2370
Qy	1501	ACCTGCTGGAGACCAAGCTCAGTCTTACGAGAGGGAGAAAGACAGGCTTCGGCCCCCGCGC	1560
Db	2371	ACCTGCTGGAGACCAAGCTCAGTCTTACGAGAGGGAGAAAGACAGGCTTCGGCCCCCGCGC	2430
Qy	1561	TGAGGAGACCCAGTGGGAGGTGAGGCCACACAGGGCTCATGGTTGGGTGCTCAGCGG	1620
Db	2431	TGAGGAGACCCAGTGGGAGGTGAGGCCACACAGGGCTCATGGTTGGGTGCTCAGCGG	2490
Qy	1621	TTTGGGCCCAAGTACCCCCCTCTCTCTCTGGTGTGGCCAAATAGCGTGCAAACACAGACCG	1680

DB	2491	 TTTTGGCCCAAGTACCCCCCTCTCCTTGGTGTCGCCAATAGCGTGAACAACACAGACCG	2550
QY	1681	CGCAGGCAAGCGGGCTTAATTGCTGGCTTTATCACCCAAAGAAGGGCTCCCTCGCAAAC	1740
DB	2551	CGCAGGCAAGCGGGCTTAATTGCTGGCTTTATCCCAAAGAAGGGCTCCCTCGCAAAC	2610
QY	1741	CATGTTGGGGATGACTTACATCTGAGCTTCCTCTGTGTCCTCCACCATCACCTCATGGC	1800
DB	2611	CATGTTGGGGATGCACTTACATCTGAGCTTCCTCTGTGTCCTCCACCATCACCTCATGGC	2670
QY	1801	TCCTAGATTTTCAGTTTCCCAAGTGAGCCATAAATCATGAGCGCGGAAGCCAGATGACCA	1860
DB	2671	TCCTAGATTTTCAGTTTCCCAAGTGAGCCATAAATCATGAGCGCGGAAGCCAGATGACCA	2730
QY	1861	AGGCCACAGCAGGCTGTGGCTGACCTCCCTCCATCAGCTCCACGAGGCTCAGAAGAA	1920
DB	2731	AGGCCACAGCAGGCTGTGGCTGACCTCCCTCCATCAGCTCCACGAGGCTCAGAAGAA	2790
QY	1921	GAAACAAGCCGTGCTGATTTCAGGCGGGGCCAGGGCCCCAAGAGAGACACAGAAATGCATTT	1980
DB	2791	GAAACAAGCCGTGCTGATTTCAGGCGGGGCCAGGGCCCCAAGAGAGACACAGAAATGCATTT	2850
QY	1981	GTTCCTTTTGAGGAGGAGACTGCACCACTAGTAAAGAGGGAACCTATTTGGTGGCAGGTTT	2040
DB	2851	GTTCCTTTTGAGGAGGAGACTGCACCACTAGTAAAGAGGGAACCTATTTGGTGGCAGGTTT	2910
QY	2041	CAGTGATGGAAGTGGCCACTCCTTGCTGAAGTGTAAAGTGGAACTCTATTTGGTAGCTG	2100
DB	2911	CAGTGATGGAAGTGGCCACTCCTTGCTGAAGTGTAAAGTGGAACTCTATTTGGTAGCTG	2970
QY	2101	AGATGGAACCTTAGGAGAGGAAGTAAAGAGTCCCCCACTCACACTTACACACTCACAC	2160
DB	2971	AGATGGAACCTTAGGAGAGGAAGTAAAGAGTCCCCCACTCACACTTACACACTCACAC	3030
QY	2161	ACACTCACTCACCCGGTCAACGTGGAAATGAGGCATCTGTACTGACCGTGTGGAGAA	2220
DB	3031	ACACTCACTCACCCGGTCAACGTGGAAATGAGGCATCTGTACTGACCGTGTGGAGAA	3090
QY	2221	CCCCATAACCTCTGCATCTATTAGTGGGAAGCAGCTTTTCTACACAGCCTGGTGTCTG	2280
DB	3091	CCCCATAACCTCTGCATCTATTAGTGGGAAGCAGCTTTTCTACACAGCCTGGTGTCTG	3150
QY	2281	GATGACTCATGGAGTTCAAGCCCATCGTTGAGGCTCTTTACATGCTCGCACCCAGCTGG	2340
DB	3151	GATGACTCATGGAGTTCAAGCCCATCGTTGAGGCTCTTTACATGCTCGCACCCAGCTGG	3210
QY	2341	TCTGTCCAAGTGTGCTCCTCACCCCGAGTTTCAGAGTCCAAAATCTAGTCTACACGCAAC	2400
DB	3211	TCTGTCCAAGTGTGCTCCTCACCCCGAGTTTCAGAGTCCAAAATCTAGTCTACACGCAAC	3270
QY	2401	CCCTGGGTATGCAAGTCAACAACCAAGTGGTTTAACCTTGCCCACTGCTGGGAGCTGTAT	2460
DB	3271	CCCTGGGTATGCAAGTCAACAACCAAGTGGTTTAACCTTGCCCACTGCTGGGAGCTGTAT	3330
QY	2461	CACCCCATTTAACACCAATGGTATTGGTGTGAGCCTGATTTCTGTGTCATCGATG	2520
DB	3331	CACCCCATTTAACACCAATGGTATTGGTGTGAGCCTGATTTCTGTGTCATCGATG	3390
QY	2521	TTTATGCCACATCCTCTGACCTCACCCCTGCATGCAACCGAGCCCTCCTCTCTCTGTCT	2580
DB	3391	TTTATGCCACATCCTCTGACCTCACCCCTGCATGCAACCGAGCCCTCCTCTCTCTGTCT	3450
QY	2581	ACTGGAGTAAAGACTACCTCAAAAATCTACTGTGTACCGAGTACTAGTATCATGCTGG	2640
DB	3451	ACTGGAGTAAAGACTACCTCAAAAATCTACTGTGTACCGAGTACTAGTATCATGCTGG	3510
QY	2641	CTTGGATGACGCCCAATCCACATCTGTCAACACGAGGAATCAATTTCTCTCTCTTCC	2700
DB	3511	CTTGGATGACGCCCAATCCACATCTGTCAACACGAGGAATCAATTTCTCTCTCTTCC	3570
QY	2701	TCTTCTTCTCTATTTTCCACCCCTATCCCCCATCAAAATTTGGGCCAAGAGCAATGATGA	2760

Db 3571 TCCTCTTCTCTATTTCCACCCCTATCCCATCAAAAATTTGGCCAGAGCAATGATGA 3630
Qy 2761 AAACCGAAGCCACAGGTTAGACCCATGTGTCTCTGGATCTTGGCCATCTGGGTCATGGG 2820
Db 3631 AAACCGAAGCCACAGGTTAGACCCATGTGTCTCTGGATCTTGGCCATCTGGGTCATGGG 3690
Qy 2821 AGACCAAGGCCAGTCTGGCTGAATCTTAAGAGTGAATGAAGTCCAGAGCATGTGGCTCTA 2880
Db 3691 AGACCAAGGCCAGTCTGGCTGAATCTTAAGAGTGAATGAAGTCCAGAGCATGTGGCTCTA 3750
Qy 2881 CAGAAATGATTTCTTGGAACTAGCTGGAGCCACCTTTCACATTTCTTTACAGTAGAAA 2940
Db 3751 CAGAAATGATTTCTTGGAACTAGCTGGAGCCACCTTTCACATTTCTTTACAGTAGAAA 3810
Qy 2941 TTTCCCTTGGCCCTCAGTGAACACTGCAAGTCTCTGGAGAAATCCGACCTACCCAGG 3000
Db 3811 TTTCCCTTGGCCCTCAGTGAACACTGCAAGTCTCTGGAGAAATCCGACCTACCCAGG 3870
Qy 3001 ATGGTGTCTTGGACCAAGAAATTTTCATTCGAAGCCCAACCTGTATTTCATCCACGAGG 3060
Db 3871 ATGGTGTCTTGGACCAAGAAATTTTCATTCGAAGCCCAACCTGTATTTCATCCACGAGG 3930
Qy 3061 GAGTGACACAGTCTAGTGGTGGAGGATGGCTGGCTTTGAACCTCAGCTTGACCACTTAT 3120
Db 3931 GAGTGACACAGTCTAGTGGTGGAGGATGGCTGGCTTTGAACCTCAGCTTGACCACTTAT 3990
Qy 3121 GATCAGGTGATTTGAATACATTAAGCATGGTGGCAATGGGTATAGTAACTGT 3180
Db 3991 GATCAGGTGATTTGAATACATTAAGCATGGTGGCAATGGGTATAGTAACTGT 4050
Qy 3181 TGGGATCAAACTCTACTCTTATCTTATATTTATATATATATATATATATATATATAT 3240
Db 4051 TGGGATCAAACTCTACTCTTATCTTATATTTATATATATATATATATATATATATAT 4110
Qy 3241 ATATATTAGCCCTCAGGCTGTGTCACTTCCACAGCTGTTTGTATCAATCAACCTCTGTGC 3300
Db 4111 ATATATTAGCCCTCAGGCTGTGTCACTTCCACAGCTGTTTGTATCAATCAACCTCTGTGC 4170
Qy 3301 CTCAGTTTCATGATTAATTTAGGACTACTATAGTACCTACTTCACTCGGTTGTAAAG 3360
Db 4171 CTCAGTTTCATGATTAATTTAGGACTACTATAGTACCTACTTCACTCGGTTGTAAAG 4230
Qy 3361 GAATAGATGAGCAAAATGATGGCTTGGCACTTATAACACTACAAATATTATTAGTGAAGT 3420
Db 4231 GAATAGATGAGCAAAATGATGGCTTGGCACTTATAACACTACAAATATTATTAGTGAAGT 4290
Qy 3421 ATGTTTATAATAATATCTTCTGTGTGGCTAGGCGTGTGGCTCAGCCTGCA 3473
Db 4291 ATGTTTATAATAATATCTTCTGTGTGGCTAGGCGTGTGGCTCAGCCTGCA 4343

RESULT 2
ID AAS30637
XX AAS30637 standard; DNA; 2411 BP.
AC AAS30637;
XX 21-NOV-2001 (first entry)
XX DNA encoding novel lung cancer antigen, Seq ID No 89.
KW Human; lung cancer; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neotropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; autoimmune disease; rheumatoid arthritis; neoplasm;
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; skin aging;
KW ocular disorder; wound healing; organ transplantation; ds.
XX Homo sapiens.
OS
XX WO200155300-A2.
PN
XX

PD 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01238.
XX 31-JAN-2000; 2000US-0179065.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-465565/50.
DR Isolated nucleic acid molecule encoding a lung cancer antigen is used
XX in preventing, treating or ameliorating a medical condition
PT Disclosure; SEQ ID No 89; 475pp; English.
PS The invention relates to novel isolated lung cancer antigen
XX polynucleotides (I) and polypeptides (II). (I) and (II) are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are
CC also used in diagnosing a pathological condition or susceptibility to a
CC pathological condition, in particular, lung cancer. The antibodies to
CC (II) can also be used in alleviating symptoms associated with the
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. AAS30580-AAS30685 represent novel human lung cancer antigen
CC coding sequences, PCR primers and related sequences of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at: ffp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2411 BP; 558 A; 681 C; 733 G; 439 T; 0 other;
Query Match 48.3%; Score 1677; DB 22; Length 2411;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 AGCTGCGCCCTGGGGGCATCTTTGAATACAGCTGGAGTTTGTGCATCATTACCAGAGA 60
Db 531 AGCTGCGCCCTGGGGGCATCTTTGAATACAGCTGGAGTTTGTGCATCATTACCAGAGA 590
Qy 61 CTAGGGCAAGAGAGGCCCGCAGCACTGAGAAATCCAGCCCTCACACAGCTCAAGCCCTCG 120
Db 591 TTAGGGCAAGAGAGGCCCGCAGCACTGAGAAATCCAGCCCTCACACAGCTCAAGCCCTCG 650
Qy 121 TGGCTCCACAGTGGGACACTGAAATCAATTTTCTTATTCAGTCTCTGCCCCCTTGGCCT 180
Db 651 TGGCTCCACAGTGGGACACTGAAATCAATTTTCTTATTCAGTCTCTGCCCCCTTGGCCT 710
Qy 181 GGGGAAATGAATCCCGGCTTTTGAATTTACTAGGAAGAGCCCTTTATGTTTGCATAGAGC 240
Db 711 GGGGAAATGAATCCCGGCTTTTGAATTTACTAGGAAGAGCCCTTTATGTTTGCATAGAGC 770
Qy 241 ATTACAGCTTTTCAAAATTAAGGGGCTTGTAACTGTGAAGCACTCTACAGGAAAATTAC 300
Db 771 ATTACAGCTTTTCAAAATTAAGGGGCTTGTAACTGTGAAGCACTCTACAGGAAAATTAC 830
Qy 301 AGTTTAAAAAGGATCGTGAATTTGGAGTGGAGCTCCCAACCCCTGTAGGAGGCCAGTGC 360
Db 831 AGTTTAAAAAGGATCGTGAATTTGGAGTGGAGCTCCCAACCCCTGTAGGAGGCCAGTGC 890
Qy 361 CGTGTCTCTTGTCCAGGCTTAAATCGAAGAGGCACTGAACAGGAAGAGGATGACCTTAA 420

Query Match		48.3%;	Score 1677;	DB 22;	Length 2411;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1877;		Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	AGCTGCGCGCTGGGGCATCTTTGTAATACAGAGCTGGAGTTTGTCTATCATTTACCAGAGA	60		
Db	531	AGCTGCGCGCTGGGGCATCTTTGTAATACAGAGCTGGAGTTTGTCTATCATTTACCAGAGA	590		
Qy	61	CTAGGGCAAGAGAGGCCCGCCAGGCACTGAGAAATTCAGAGCCCTCACACCAGCTCAAGCCCTCG	120		
Db	591	TTAGGGCAAGAGAGGCCCGCCAGGCACTGAGAAATTCAGAGCCCTCACACCAGCTCAAGCCCTCG	650		
Qy	121	TGCGTCCACAGTGGACACATGAAATCAATTTTCTATTCAGTCTCTGCCCCCTTGCCCT	180		
Db	651	TGCGTCCACAGTGGACACATGAAATCAATTTTCTATTCAGTCTCTGCCCCCTTGCCCT	710		
Qy	181	GGGGAATGAATCCCGCGCTTTGATTTACTAGGAAGAGCCCTCTATGTTTGCATAGAGC	240		
Db	711	GGGGAATGAATCCCGCGCTTTGATTTACTAGGAAGAGCCCTCTATGTTTGCATAGAGC	770		
Qy	241	ATTCAGCTTTTCAAAATTAAGGGCTTGTAAACTGTGAAGCACTCTACACAGGAAATTAAC	300		
Db	771	ATTCAGCTTTTCAAAATTAAGGGCTTGTAAACTGTGAAGCACTCTACACAGGAAATTAAC	830		
Qy	301	AGTTTTAAAGAGTCTGTGATTTTGGAGTGAAGCTTCCCAACCTGTAAAGGAGGCCAGGTC	360		
Db	831	AGTTTTAAAGAGTCTGTGATTTTGGAGTGAAGCTTCCCAACCTGTAAAGGAGGCCAGGTC	890		
Qy	361	CGTGCTCTGCTCCAGGCTTAATGGAAGAGGAGTGAACAGAGAGAGGATGACACTTAA	420		
Db	891	CGTGCTCTGCTCCAGGCTTAATGGAAGAGGAGTGAACAGAGAGAGGATGACACTTAA	950		
Qy	421	AGAGGACAGCAAGCTCGGCCAGCTGATGCCCTAACTTGGCCACACAGAGAGCTAGAG	480		
Db	951	AGAGGACAGCAAGCTCGGCCAGCTGATGCCCTAACTTGGCCACACAGAGAGCTAGAG	1010		
Qy	481	CAGGAGCCTCAAGATGTTATTTATCACCTCGGGAGGCTGGGGCAAGCTGGTGAGGCTT	540		
Db	1011	CAGGAGCCTCAAGATGTTATTTATCACCTCGGGAGGCTGGGGCAAGCTGGTGAGGCTT	1070		
Qy	541	GCTATTTATAGAACAAAGTCCCAAGTCGCGCATTAGGGTTTTCCTCTCAAGAGAGAT	600		
Db	1071	GCTATTTATAGAACAAAGTCCCAAGTCGCGCATTAGGGTTTTCCTCTCAAGAGAGAT	1130		
Qy	601	GACATTACGCTGCTTCAAGCAACAGGCAAGTCTGCTGAGACAAATTGACCAAGAGGGGT	660		
Db	1131	GACATTACGCTGCTTCAAGCAACAGGCAAGTCTGCTGAGACAAATTGACCAAGAGGGGT	1190		
Qy	661	GCTGCTGCGCTCAGAGAGCCAGACTGGCTCAAGGTGCGCACGCGTGCCTGGGGAGGGA	720		
Db	1191	GCTGCTGCGCTCAGAGAGCCAGACTGGCTCAAGGTGCGCACGCGTGCCTGGGGAGGGA	1250		
Qy	721	GGGTGCAATGCGCGCAGAGGAGGAGTGAAGTCAAGCGGCTCTTCTCTACAGGCT	780		
Db	1251	GGGTGCAATGCGCGCAGAGGAGGAGTGAAGTCAAGCGGCTCTTCTCTACAGGCT	1310		
Qy	781	CCGAGAGGGTGCAGTGAAGGCCACAGCTTCAAGCTGTGCTGCCAGGTCAGAGGCCA	840		
Db	1311	CCGAGAGGGTGCAGTGAAGGCCACAGCTTCAAGCTGTGCTGCCAGGTCAGAGGCCA	1370		
Qy	841	TCCTGCACTCTCTCCCGGAGAGTGCAGGCCACAGCTGCACCCCGCCCTCCAGCAAGC	900		
Db	1371	TCCTGCACTCTCTCCCGGAGAGTGCAGGCCACAGCTGCACCCCGCCCTCCAGCAAGC	1430		
Qy	901	CCAGGAGCAGAGTGAAGCTTGGCTGTGCTCTGGGGCGCTGTACAGCTCCCGCCGGA	960		
Db	1431	CCAGGAGCAGAGTGAAGCTTGGCTGTGCTCTGGGGCGCTGTACAGCTCCCGCCGGA	1490		
Qy	961	ACTCCATGTCAGGCTGCCACACACAGCAGCAGCAGCAGTACAGCTGACCCGCTGG	1020		
Db	1491	ACTCCATGTCAGGCTGCCACACACAGCAGCAGCAGCAGTACAGCTGACCCGCTGG	1550		

Qy	1021	TCACACCCGCTGGGACCCACAAAGCCGTTTTTGGGGCTCCGCCCAACAAATCACCCAGGGCA	1080
Db	1551	TCACACCCGCTGGGACCCACAAAGCCGTTTTTGGGGCTCCGCCCAACAAATCACCCAGGGCA	1610
Qy	1081	TCGTCCTCCAGGACAGCAACATGATGACCTTGAAGGCTCTGTCTCTTCTCCACCGAGGTA	1140
Db	1611	TCGTCCTCCAGGACAGCAACATGATGACCTTGAAGGCTCTGTCTCTTCTCCACCGAGGTA	1670
Qy	1141	GCAAGCTGGGCGCACTCGAAACAAAGGACAGAAAGGCGCCCTCGTGTCTCGCTCCCCCATCT	1200
Db	1671	GCAAGCTGGGCGCACTCGAAACAAAGGACAGAAAGGCGCCCTCGTGTCTCGCTCCCCCATCT	1730
Qy	1201	CCACGAGCAGAGTCAGAGCATCCAGAGCTGGAACAGAAAGCTTTGGAGAGGAGGCGGCC	1260
Db	1731	CCACGAGCAGAGTCAGAGCATCCAGAGCTGGAACAGAAAGCTTTGGAGAGGAGGCGGCC	1790
Qy	1261	TCCAGAGCTGCAGCGCAGCTTTTGGAGAGAGGAGCTTGCTCCAGCTGCGCTACGAGG	1320
Db	1791	TCCAGAGCTGCAGCGCAGCTTTTGGAGAGAGGAGCTTGCTCCAGCTGCGCTACGAGG	1850
Qy	1321	AGCGCGCGCGCGCTGCAGGAGCAGCTTGAAGGCGCCGAGGCCCAAGGCGGCAACAAGC	1380
Db	1851	AGCGCGCGCGCGCTGCAGGAGCAGCTTGAAGGCGCCGAGGCCCAAGGCGGCAACAAGC	1910
Qy	1381	TCAAGCAGGCTTCGCAAGAGAGCCAGCGCGCAGCAGGCTCTGCACCTGCAGGTACTGC	1440
Db	1911	TCAAGCAGGCTTCGCAAGAGAGCCAGCGCGCAGCAGGCTCTGCACCTGCAGGTACTGC	1970
Qy	1441	AGCTTCAGCAGGAGAAAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCTCATGAAGAGCAGG	1500
Db	1971	AGCTTCAGCAGGAGAAAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCTCATGAAGAGCAGG	2030
Qy	1501	ACCTGCTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGAACAGCTTCCGGCCCCCGGC	1560
Db	2031	ACCTGCTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGAACAGCTTCCGGCCCCCGGC	2090
Qy	1561	TGGAGGAGACCCAGTGGAGGTGAGGCCACACAGGGCTCATGGGTTTGGGTGGTCAAGCG	1620
Db	2091	TGGAGGAGACCCAGTGGAGGTGAGGCCACACAGGGCTCATGGGTTTGGGTGGTCAAGCG	2150
Qy	1621	TTTGGCGCAGTACCCCGCTCTCTCTGCTGCTGGCCCAATAGCGTGCMAACACAGACCG	1680
Db	2151	TTTGGCGCAGTACCCCGCTCTCTCTGCTGCTGGCCCAATAGCGTGCMAACACAGACCG	2210
Qy	1681	CGCAGGCAAGCGGGCTTAATGCTGCTTATCACCACCAAGAGAGGCTCCCTGCAAAAC	1740
Db	2211	CGCAGGCAAGCGGGCTTAATGCTGCTTATCACCACCAAGAGAGGCTCCCTGCAAAAC	2270
Qy	1741	CATGTTGGGGATCGACTTACATCTGAGCTTCTCTCTGCTCCCAACCATCACCTCATGGC	1800
Db	2271	CATGTTGGGGATCGACTTACATCTGAGCTTCTCTCTGCTCCCAACCATCACCTCATGGC	2330
Qy	1801	TCCTAGATTTTCAAGTTTCCCAAGTGAAGCATTAATATCATGAAGCGGAGAGCCAGATGACCA	1860
Db	2331	TCCTAGATTTTCAAGTTTCCCAAGTGAAGCATTAATATCATGAAGCGGAGAGCCAGATGACCA	2390
Qy	1861	AGSCCCAGCCAGGCTGTGGGC	1881
Db	2391	AGSCCCAGCCAGGCTGTGGGC	2411

RESULT 4

AAA64513
ID AAA64513 standard; cDNA; 1512 BP.

XX AAA64513;

XX AC AC

DT 02-JAN-2001 (first entry)

XX Nucleotide sequence of truncated FEZ1 transcript D14.

DE Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;

XX tumour proliferation; tubulin; microtubule; protein BF1-gamma;

KW

KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
 XX tumorigenesis; tumour survival; metastasis; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 1..1512
 FT /*tag= a
 FT /product= "truncated FEZ1"

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Iehii H;

XX WPI; 2000-558396/51.

XX P-PSDB; AAB08720.

XX New polynucleotide homologous with a portion of one strand of the human
 PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
 PT cancer -

XX Disclosure; Fig 5F; 255pp; English.

XX The present sequence encodes a truncated human FEZ1 polypeptide. The
 CC encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour
 CC suppressor gene, located at chromosome location 8p22. Decreased
 CC or no expression of FEZ1 is detected in a variety of cancer cells.
 CC Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
 CC also interacts with tubulin, with microtubules, and with protein
 CC EPI-gamma. Post-translational phosphorylation and dephosphorylation
 CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
 CC expression are useful for inducing cells to proliferate. Compounds
 CC which modulate FEZ1 association with tubulin are useful for alleviating
 CC tubulin hyper- or hypo- polymerisation disorders, such as those
 CC associated with aberrant initiation of mitosis, modulation of the
 CC initiation and rate of cell proliferation and cell growth, modulation of
 CC cell shape, cell rigidity, cell motility, rate and stage of cellular
 CC DNA replication, intracellular distribution of organelles, metastatic
 CC potential of cell and cellular transformation from a non-cancerous to
 CC cancerous phenotype. Compounds which modulate FEZ1 binding and
 CC phosphorylation are also useful for alleviating a disorder, such as
 CC tumorigenesis, tumour survival, growth and metastasis.

XX Sequence 1512 BP; 335 A; 483 C; 481 G; 213 T; 0 other;

Query Match 21.8%; Score 757; DB 21; Length 1512;
 Best Local Similarity 99.9%; Pred No. 0;
 Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 776 GGGCTCCGAGAGGGTGCAGTGCAGGCCACACAGCCTTCAAGCCTGTGCTGCCACCGTCAAG 835
 Db |
 345 GGGCTCCGAGAGGGTGCAGTGCAGGCCACACAGCCTTCAAGCCTGTGCTGCCACCGTCAAG 404
 QY 836 AGCCATCTGCNCTCTCTCCCGGAGAGTGCAGGCCACACAGCTGCACCCCGCCCTCCAGA 895
 Db |
 405 AGCCATCTGCNCTCTCTCCCGGAGAGTGCAGGCCACACAGCTGCACCCCGCCCTCCAGA 464
 QY 896 CAAGCCCAAGGAGAGGAGTGAAGCCTGGCCTGTGCTCTGGGGCGCTGTGCAGACTCCGG 955
 Db |
 465 CAAGCCCAAGGAGAGGAGTGAAGCCTGGCCTGTGCTCTGGGGCGCTGTGCAGACTCCGG 524
 QY 956 CGGGAATCCATGTCCAGCCTGCCACACACAGCAGCAGCAGCAGCTACCAAGCTGGACCC 1015
 Db |
 525 CGGGAATCCATGTCCAGCCTGCCACACACAGCAGCAGCAGCAGCTACCAAGCTGGACCC 584

QY 1016 GCTGGTCAACCGTGGAGCCGACACAGCCGTTTTGGGGGCTCCGCCACACATCACC 1075
 Db |
 585 GCTGGTCAACCGTGGAGCCGACACAGCCGTTTTGGGGGCTCCGCCACACATCACC 644
 QY 1076 GGGCATCGTCTCTCAGGACAGCAACATGATGAGCCTGAAGGCTCTGTCTCTCCGACGG 1135
 Db |
 645 GGGCATCGTCTCTCAGGACAGCAACATGATGAGCCTGAAGGCTCTGTCTCTCCGACGG 704
 QY 1136 AGGTAGCAAGCTGGGCCACTTCGAACAAGGACAGCAAGGGCCCTCTGTGTCTCCCTCCC 1195
 Db |
 705 AGGTAGCAAGCTGGGCCACTTCGAACAAGGACAGCAAGGGCCCTCTGTGTCTCCCTCCC 764
 QY 1196 CATCTCCACGGAGAGTGCAGCATCCAGAGCTGGACAGAGCTGTGGAGAGGGAGGG 1255
 Db |
 765 CATCTCCACGGAGAGTGCAGCATCCAGAGCTGGACAGAGCTGTGGAGAGGGAGGG 824
 QY 1256 CGCCCTCCAGAAGCTGCAGCGCAGCTTTGAGGAGAGAGAGCTTGCCTCCAGCCTGGCCTA 1315
 Db |
 825 CGCCCTCCAGAAGCTGCAGCGCAGCTTTGAGGAGAGAGAGCTTGCCTCCAGCCTGGCCTA 884
 QY 1316 CGAGGAGCGCGCGCGCTTCGAGGGACAGAGCTGGAGGGCCCGAGGCCCAAGCGCGCAA 1375
 Db |
 885 CGAGGAGCGCGCGCGCTTCGAGGGACAGAGCTGGAGGGCCCGAGGCCCAAGCGCGCAA 944
 QY 1376 CAAGCTCAAGCAGCGCTTCGAGAGAGAGCGCGCGCAGCAGCTCTGCACCTGCAGGT 1435
 Db |
 945 CAAGCTCAAGCAGCGCTTCGAGAGAGAGCGCGCGCAGCAGGTCTCTGCACCTGCAGGT 1004
 QY 1436 ACTGCAGCTTCAGCAGGAGAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCCTCATGAAGGA 1495
 Db |
 1005 ACTGCAGCTTCAGCAGGAGAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCCTCATGAAGGA 1064
 QY 1496 GCAGGACCTCTGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACCAAGCTTCGGGCC 1555
 Db |
 1065 GCAGGACCTCTGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACCAAGCTTCGGGCC 1124
 QY 1556 CGCGCTGGAGGAGACCCAGTGGGAGGTG 1583
 Db |
 1125 CGCGCTGGAGGAGACCCAGTGGGAGGTG 1152

RESULT 5

AAA64512
 ID AAA64512 standard; cDNA; 1614 BP.

XX AAA64512;

XX AC
 DT 02-JAN-2001 (first entry)

XX DE Nucleotide sequence of truncated FEZ1 transcript T8D145M4.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
 KW tumour proliferation; tubulin; microtubule; protein EPI-gamma;
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
 KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 1..633

XX FT /*tag= a
 XX FT /product= "truncated FEZ1"

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

CC	BFL-gamma. Post-translational phosphorylation and dephosphorylation modulates the effect of the FE21 protein. Inhibitors of FE21 gene expression are useful for inducing cells to proliferate. Compounds which modulate FE21 association with tubulin are useful for alleviating tubulin hyper- or hypo- polymerisation disorders, such as those associated with aberrant initiation of mitosis, modulation of the initiation and rate of cell proliferation and cell growth, modulation of cell shape, cell rigidity, cell motility, rate and stage of cellular DNA replication, intracellular distribution of organelles, metastatic potential of cell and cellular transformation from a non-cancerous to cancerous phenotype. Compounds which modulate FE21 binding and phosphorylation are also useful for alleviating a disorder, such as tumorigenesis, tumour survival, growth and metastasis.	CC	XX	SQ
Sequence 1692 BP; 380 A; 523 C; 553 G; 236 T; 0 other;				
Query Match	21.8%; Score 757; DB 21; Length 1692;			
Best Local Similarity	99.9%; Pred. No. 0;			
Matches 807; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
QY	776	GGGCTCGAGAAGGGTGCAGTGGAGGCCACAGCCTTCAAGCCCTGTGCTGCCACGGTCAGG	835	
DB	345	GGGCTTCGAGAAGGGTGCAGTGGAGGCCACAGCCTTCAAGCCCTGTGCTGCCACGGTCAGG	404	
QY	836	AGGCATCTCTCACTCTCTCCCGGAGAGTGCAGCACAGCTGCACCCGCCCTCCAGA	895	
DB	405	AGCCATCTTGCATCTCTCTCCCGGAGAGTGCAGCACAGCTGCACCCGCCCTCCAGA	464	
QY	896	CAAGCCCAAGGAGGAGGAGCTGAAGCCTTGGCCTGTGCTCTGGGGCGCTGTCAAGCTCCGG	955	
DB	465	CAAGCCCAAGGAGGAGGAGCTGAAGCCTTGGCCTGTGCTCTGGGGCGCTGTCAAGCTCCGG	524	
QY	956	CCGGAACTCTCATGTGCAGCTGCCACACAGCAGCAGCAGCAGCTTACCAGCTGGACCC	1015	
DB	525	CCGGAACTCTCATGTGCAGCTGCCACACAGCAGCAGCAGCAGCTTACCAGCTGGACCC	584	
QY	1016	GCTGGTTCACACCCGTGGGACCCACAAGCCCGTTTTGGGGGCTCGGCCACAACATCACCCA	1075	
DB	585	GCTGGTTCACACCCGTGGGACCCACAAGCCCGTTTTGGGGGCTCGGCCACAACATCACCCA	644	
QY	1076	GGGATGCTCTTCAGAGACAGCAATATGAGCTGAAGGCTCTGTCTTCTCCGACGG	1135	
DB	645	GGGATGCTCTTCAGAGACAGCAATATGAGCTGAAGGCTCTGTCTTCTCCGACGG	704	
QY	1136	AGGTAGCAAGCTGGGCCACTCGAACAGGACAGACAAGGGCCCTCGTGTGTCGCTCCCC	1195	
DB	705	AGGTAGCAAGCTGGGCCACTCGAACAGGACAGACAAGGGCCCTCGTGTGTCGCTCCCC	764	
QY	1196	CATCTCCACGGACGAGTGCAGCATCCAGGAGCTGGAAACAGAAAGCTGTGGAGAGGAGGG	1255	
DB	765	CATCTCCACGGACGAGTGCAGCATCCAGGAGCTGGAAACAGAAAGCTGTGGAGAGGAGGG	824	
QY	1256	CGCCCTCCAGAAAGTGCAGCGCAGCTTTGAGGAGAAAGAGCTTGCCTCCAGCTTGGCCTA	1315	
DB	825	CGCCCTCCAGAAAGTGCAGCGCAGCTTTGAGGAGAAAGAGCTTGCCTCCAGCTTGGCCTA	884	
QY	1316	CGAGGAGCGCCCGCGCTCGAGGACAGCTGGAGGGCCGAGGCCCAAGAGCGGCA	1375	
DB	885	CGAGGAGCGCCCGCGCTCGAGGACAGCTGGAGGGCCGAGGCCCAAGAGCGGCA	944	
QY	1376	CAAGCTCAAGCAGGCCCTCGCAGAAAGACCGACGCGCGCAGCTTCTGCACCTGCAAGT	1435	
DB	945	CAAGCTCAAGCAGGCCCTCGCAGAAAGACCGACGCGCGCAGCTTCTGCACCTGCAAGT	1004	
QY	1436	ACTGCAGCTTCAGCAGAGAAAGCGGACAGCTCCCGCAGAGACTCGAGAGCCTCATGAAGGA	1495	
DB	1005	ACTGCAGCTTCAGCAGAGAAAGCGGACAGCTCCCGCAGAGACTCGAGAGCCTCATGAAGGA	1064	
QY	1496	GCAGGACCTCTCGAGACCAAGCTCAGGTCCTTACGAGGGGAGAGACCAAGCTTCGCGCC	1555	
DB	1065	GCAGGACCTCTCGAGACCAAGCTCAGGTCCTTACGAGGGGAGAGACCAAGCTTCGCGCC	1124	
QY	1556	CGCGCTGGAGGAGACCCAGTGGGAGGTG	1583	

Db 1125 CGCGCTGGAGGAGACCCAGTGGGAGGTG 1152

RESULT 7

AAA64515

ID AAA64515 standard; cDNA; 1722 BP.

XX

AC AAA64515;

XX

DT 02-JAN-2001 (first entry)

XX DE Nucleotide sequence of truncated FEZ1 transcript G3612.

Human, FE21 gene; tumour suppressor gene, 8p22; cancer; tumour growth; tumour proliferation; tubulin; microtubule; protein ERI-gamma; tubulin polymerisation disorder; mitosis initiation; cell proliferation; cell growth; cell shape; cell rigidity; cell motility; DNA replication; tumorigenesis; tumour survival; metastasis; ss.

XX
OS
Homo sapiens.

[illegible]

Key	Location
FH	
Key	
Location	

1..1722

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:PT
/*tag= a

```

LET

XX

PN WO200050565-A2.

XX

PD 31-AUG-2000.

XX

PF 25-FEB-2000; 2000WO-

XX

PR 25-FEB-1999; 9905-0121537.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.

XX

PI	Croce CM, Ishii H;
XX	
XX	WPI; 2000-558396/51.
DR	P-PSDB; AAB08722.
DR	
XX	
PT	New polynucleotide homologous with a portion of one strand of the human
PT	PZ1 gene, useful for alleviating abnormal cell proliferation such as
PT	cancer -
XX	
XX	
PS	Disclosure: Fig 5H; 255pp; English.

The present sentence encodes a truncated human FEZ1 no-

the 3' flanking sequence encoded by the *FEZ1* gene. *FEZ1* is a tumour suppressor gene, located at chromosome location 8p22. Decreased or no expression of *FEZ1* is detected in a variety of cancer cells. Expression of *FEZ1* inhibits tumour growth and proliferation. *FEZ1* also interacts with tubulin, with microtubules, and with protein E1 γ . Post-translational phosphorylation and dephosphorylation modulates the effect of the *FEZ1* protein. Inhibitors of *FEZ1* gene expression are useful for inducing cells to proliferate. Compounds which modulate *FEZ1* association with tubulin are useful for alleviating tubulin hyper- or hypo- polymerisation disorders, such as those associated with aberrant initiation of mitosis, modulation of the initiation and rate of cell proliferation and cell growth, modulation of cell shape, cell rigidity, cell motility, rate and stage of cellular DNA replication, intracellular distribution of organelles, metastatic potential of cell and cellular transformation from a non-cancerous to cancerous phenotype. Compounds which modulate *FEZ1* binding and phosphorylation are also useful for alleviating a disorder, such as tumorigenesis, tumour survival, growth and metastasis.

QY 776 GGGTCCGAGAGGGTGCAGTGAGGCCACAGCCCTTCAAGCCTGTGTGTCACCGTCAAG 835
Db 345 GGGTCCGAGAGGGTGCAGTGAGGCCACAGCCCTTCAAGCCTGTGTGTCACCGTCAAG 404
QY 836 AGCCATCTGCACTCTCCCGGAGAGTGCAGCCAGCCAGTGCACCCGCTCCAGCA 895
Db 405 AGCCATCTGCACTCTCCCGGAGAGTGCAGCCAGCCAGTGCACCCGCTCCAGCA 464
QY 896 CAAGCCCAAGGAGCAGAGCTGAAGCCTGGCCTGTGTCTGGGGCGTGTGAGACTCCGG 955
Db 465 CAAGCCCAAGGAGCAGAGCTGAAGCCTGGCCTGTGTCTGGGGCGTGTGAGACTCCGG 524
QY 956 CCGGAATCTCATGTCCAGCCTGCCACACAGCAGCAGCAGCAGTACCAAGCTGGACCC 1015
Db 525 CCGGAATCTCATGTCCAGCCTGCCACACAGCAGCAGCAGTACCAAGCTGGACCC 584
QY 1016 GCTGGTACACCCGTGGGACCCACAGCCGTTTGGGGGCTCCGCCACATCACCAC 1075
Db 585 GCTGGTACACCCGTGGGACCCACAGCCGTTTGGGGGCTCCGCCACATCACCAC 644
QY 1076 GGGCATCTCTCCAGGACAGCAGCATGATGAGCTGAAGCTCTGTCTCTCCGACGG 1135
Db 645 GGGCATCTCTCCAGGACAGCAGCATGATGAGCTGAAGCTCTGTCTCTCCGACGG 704
QY 1136 AGGTAGCAAGCTGGGCCACTCGAACAAGGAGAGCAAGGGCCCTCGTGTGCTCCGC 1195
Db 705 AGGTAGCAAGCTGGGCCACTCGAACAAGGAGAGCAAGGGCCCTCGTGTGCTCCGC 764
QY 1196 CATCTCCAGCAGAGTGCAGCATCCAGGAGCTGGAAGAGTGTGGAGAGGAGGG 1255
Db 765 CATCTCCAGCAGAGTGCAGCATCCAGGAGCTGGAAGAGTGTGGAGAGGAGGG 824
QY 1256 CGCCCTCCAGAGCTGCAGCAGCTTTGAGGAGAGGAGCTTGCTCCAGCCTGGCCTA 1315
Db 825 CGCCCTCCAGAGCTGCAGCAGCTTTGAGGAGAGGAGCTTGCTCCAGCCTGGCCTA 884
QY 1316 CGAGAGCGGCGCGGCGCTCGAGGAGCAGCTGAGAGGCGCGGAGCCCAAGGCGGCA 1375
Db 885 CGAGAGCGGCGCGGCGCTCGAGGAGCAGCTGAGAGGCGCGGAGCCCAAGGCGGCA 944
QY 1376 CAAGTCCAGCAGGCTCGAGAGAGCAGCGCGGCGGAGCAGCTTGCACCTGCAGGT 1435
Db 945 CAAGTCCAGCAGGCTCGAGAGAGCAGCGCGGCGGAGCAGCTTGCACCTGCAGGT 1004
QY 1436 ACTGAGCTTCAGCAGGAGAGCGCAGCTCCGCGAGGAGCTCGAGAGCCTCATGAAGGA 1495
Db 1005 ACTGAGCTTCAGCAGGAGAGCGCAGCTCCGCGAGGAGCTCGAGAGCCTCATGAAGGA 1064
QY 1496 GCAGGACCTGTGGAGACCAAGCTCAGGTCTTACGAGGAGGAGAGCAGCTTCGGGCC 1555
Db 1065 GCAGGACCTGTGGAGACCAAGCTCAGGTCTTACGAGGAGGAGAGCAGCTTCGGGCC 1124
QY 1556 CGCGTGGAGAGACCCAGTGGAGGTG 1583
Db 1125 CGCGTGGAGAGACCCAGTGGAGGTG 1152

RESULT 8

AAA64509
ID AAA64509 standard; cDNA; 1791 BP.
XX
AC AAA64509;
XX
DT 02-JAN-2001 (first entry)
XX
DE cDNA sequence encoding a human FEZ1 polypeptide.
XX
KW Human; FEZ1 gene; tumour suppressor gene; 9p22; cancer; tumour growth;
KW tumour proliferation; tubulin; microtubule; protein EFL-gamma;
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT 1..1791
FT /*tag= a
FT /product= "FEZ1"
XX
PN WO2000050565-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000MO-US04950.
XX
PR 25-FEB-1999; 99US-0121537.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Ishii H;
XX
DR WPI; 2000-558396/51.
XX
DR P-PSDB; AAB08715.
XX
PT New polynucleotide homologous with a portion of one strand of the human
FEZ1 gene, useful for alleviating abnormal cell proliferation such as
cancer -
XX
PS Claim 7; Fig 5I; 255pp; English.
XX
CC The present sequence encodes a human FEZ1 polypeptide. FEZ1 is a
tumour suppressor gene, located at chromosome location 9p22. Decreased
or no expression of FEZ1 is detected in a variety of cancer cells.
CC Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
also interacts with tubulin, with microtubules, and with protein
EFL-gamma. Post-translational phosphorylation and dephosphorylation
modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
expression are useful for inducing cells to proliferate. Compounds
which modulate FEZ1 association with tubulin are useful for alleviating
CC tubulin hyper- or hypo- polymerisation disorders, such as those
associated with aberrant initiation of mitosis, modulation of the
initiation and rate of cell proliferation and cell growth, modulation of
cell shape, cell rigidity, cell motility, rate and stage of cellular
DNA replication, intracellular distribution of organelles, metastatic
potential of cell and cellular transformation from a non-cancerous to
cancerous phenotype. Compounds which modulate FEZ1 binding and
phosphorylation are also useful for alleviating a disorder, such as
tumorigenesis, tumour survival, growth and metastasis.
XX
SQ Sequence 1791 BP; 393 A; 561 C; 591 G; 246 T; 0 other;

Query Match 21.8%; Score 757; DB 21; Length 1791;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 776 GGGTCCGAGAGGGTGCAGTGAGGCCACAGCCCTTCAAGCCTGTGTGTCACCGTCAAG 835
Db 345 GGGTCCGAGAGGGTGCAGTGAGGCCACAGCCCTTCAAGCCTGTGTGTCACCGTCAAG 404
QY 836 AGCCATCTGCACTCTCCCGGAGAGTGCAGCCAGCCAGTGCACCCGCTCCAGCA 895
Db 405 AGCCATCTGCACTCTCCCGGAGAGTGCAGCCAGCCAGTGCACCCGCTCCAGCA 464
QY 896 CAAGCCCAAGGAGCAGAGCTGAAGCCTGGCCTGTGTCTGGGGCGTGTGAGACTCCGG 955
Db 465 CAAGCCCAAGGAGCAGAGCTGAAGCCTGGCCTGTGTCTGGGGCGTGTGAGACTCCGG 524
QY 956 CCGGAATCTCATGTCCAGCCTGCCACACAGCAGCAGCAGTACCAAGCTGGACCC 1015
Db 525 CCGGAATCTCATGTCCAGCCTGCCACACAGCAGCAGCAGTACCAAGCTGGACCC 584
QY 1016 GCTGGTACACCCGTGGGACCCACAGCCGTTTGGGGGCTCCGCCACATCACCAC 1075
Db 585 GCTGGTACACCCGTGGGACCCACAGCCGTTTGGGGGCTCCGCCACATCACCAC 644

Db 1116 ACTGCAGCTTCAGCAGGAGACCGCAGCTCGGCAGAGCTCGAGACCTCATGAAGGA 1175
QY 1496 GCAGGACCTGTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACCAAGCTTCGGGCC 1555
Db 1176 GCAGGACCTGTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACCAAGCTTCGGGCC 1235
QY 1556 CGCGCTGGAGAGACCCAGTGGAGGTG 1583
Db 1236 CGCGCTGGAGAGACCCAGTGGAGGTG 1263

RESULT 10

AAS30595
ID AAS30595 standard; cDNA; 560 BP.

XX AC AAS30595;

XX DT 21-NOV-2001 (first entry)

XX DE DNA encoding novel lung cancer antigen, Seq ID No 17.

XX KW Human; lung cancer; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nocotopic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; autoimmune disease; rheumatoid arthritis; neoplasm;
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; skin aging;
KW ocular disorder; wound healing; organ transplantation; ss.

XX OS Homo sapiens.

XX PN WO200155300-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01238.

XX PR 31-JAN-2000; 2000US-0179065.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Barash SC, Ruben SM;

XX DR WPI; 2001-465565/50.

XX PS P-PSDB; AAU18935.

PT Isolated nucleic acid molecule encoding a lung cancer antigen is used
in preventing, treating or ameliorating a medical condition -

XX Claim 1; SEQ ID No 17; 475pp; English.

XX CC The invention relates to novel isolated lung cancer antigen
CC polynucleotides (I) and polypeptides (II). (I) and (II) are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are
CC also used in diagnosing a pathological condition or susceptibility to a
CC pathological condition, in particular, lung cancer. The antibodies to
CC (II) can also be used in alleviating symptoms associated with the
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. AAS30580-AAS30685 represent novel human lung cancer antigen
CC coding sequences, PCR primers and related sequences of the invention.
CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 560 BP; 120 A; 196 C; 161 G; 83 T; 0 other;
Query Match 13.7%; Score 475; DB 22; Length 560;
Best Local Similarity 99.8%; Pred. No. 6.5e-210;
Matches 525; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 776 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCCTGTGTGTCACAGGTGAGG 835
Db 35 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCCTGTGTGTCACAGGTGAGG 94
QY 836 AGCCATCTGCACCTCTCTCCCGGAGAGTGCCAGCACCAGCTGCACCCGCCCTCCAGA 895
Db 95 AGCCATCTGCACCTCTCTCCCGGAGAGTGCCAGCACCAGCTGCACCCGCCCTCCAGA 154
QY 896 CAAGCCCAAGGAGGAGGAGCTGAAGCCTGGCCTGTGCTCGGGGGCTGTGAGACTCCGG 955
Db 155 CAAGCCCAAGGAGGAGGAGCTGAAGCCTGGCCTGTGCTCGGGGGCTGTGAGACTCCGG 214
QY 956 CCGGAATCTCCATGTCTCCAGCCTGCCACACACAGCACCAGCAGCAGCTACCACTGGACCC 1015
Db 215 CCGGAATCTCCATGTCTCCAGCCTGCCACACACAGCACCAGCAGCAGCTACCACTGGACCC 274
QY 1016 GCTGGTCCACACCCCGTGGGACCCCAAGCCGTTTTGGGGGGCTCCGCCCAACATCACCCA 1075
Db 275 GCTGGTCCACACCCCGTGGGACCCCAAGCCGTTTTGGGGGGCTCCGCCCAACATCACCCA 334
QY 1076 GGGCATCGTCTCCAGGACAGCAATGATGAGCCTGGAAGCCTGTGCTTCTTCGAGCG 1135
Db 335 GGGCATCGTCTCCAGGACAGCAATGATGAGCCTGGAAGCCTGTGCTTCTTCGAGCG 394
QY 1136 AGGTAGCAAGCTGGGGCCACTCGAACAGGAGCAAGGGCCCTCGTGTGTCCTCCCTCCC 1195
Db 395 AGGTAGCAAGCTGGGGCCACTCGAACAGGAGCAAGGGCCCTCGTGTGTCCTCCCTCCC 454
QY 1196 CATCTCCAGGACGAGTGCCAGCATCCAGGAGCTCGAACAGAGCTGTTGGAGAGGGAGGG 1255
Db 455 CATCTCCAGGACGAGTGCCAGCATCCAGGAGCTCGAACAGAGCTGTTGGAGAGGGAGGG 514
QY 1256 CGCCCTCCAGAGCTGCAGCGCAGCTTTGAGGAGAGAGGAGCTTCC 1301
Db 515 CGCCCTCCAGAGCTGCAGCGCAGCTTTGAGGAGAGAGGAGCTTCC 560

RESULT 11

AAS28127
ID AAS28127 standard; cDNA; 560 BP.

XX AC AAS28127;

XX DT 07-NOV-2001 (first entry)

XX DE Novel cDNA encoding for human respiratory antigen #259.

XX KW Human; respiratory antigen; respiratory disorder; throat disorder;
KW lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
KW anti allergic; anti aschmatic; anti inflammatory; oilyfactory;
KW respiratory active; ss.

XX OS Homo sapiens.

XX PN WO200155448-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01333.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217496.
 PR 11-JUL-2000; 2000US-0217497.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
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 PR 14-AUG-2000; 2000US-0225266.
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 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
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 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0232403.
 PR 14-SEP-2000; 2000US-0232404.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 25-SEP-2000; 2000US-0234999.
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 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
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 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
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 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
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 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246610.
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 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
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 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-476224/51.
 DR P-PSDB; AAU17943.
 XX
 PT Isolated polypeptide for treating, preventing and/ or prognosing
 PT disorders related to the respiratory system including respiratory
 PT cancers and also for testing and detection e.g. diagnosis -
 XX
 PS Claim 4; SED ID No 269; 546pp; English.
 XX

XX	Homo sapiens.
OS	
XX	
XX	
FH	Location/Qualifiers
FT	1..633
FT	CDS
FT	/*tag= a
FT	/product= "truncated FEZ1"
XX	
PN	WO200050565-A2.
XX	
XX	
PD	31-AUG-2000.
XX	
PF	25-FEB-2000; 2000WO-US04950.
XX	
PR	25-FEB-1999; 99US-0121537.
XX	

Croce CM, Ishii H;
 WPI: 2000-558396/51.
 P-PSDB; AAB08718.
 New polynucleotide homologous with a portion of one strand of the human
 FE21 gene, useful for alleviating abnormal cell proliferation such as
 cancer -
 Disclosure; Fig 5D; 255pp; English.
 The present sequence encodes a truncated human FE21 polypeptide. The
 encoding mRNA is transcribed by tumour cells. FE21 is a tumour
 suppressor gene, located at chromosome location 8p22. Decreased
 or no expression of FE21 is detected in a variety of cancer cells.
 Expression of FE21 inhibits tumour growth and proliferation. FE21
 also interacts with tubulin, with microtubules, and with protein
 ERI-gamma. Post-translational phosphorylation and dephosphorylation
 modulates the effect of the FE21 protein. Inhibitors of FE21 gene
 expression are useful for inducing cells to proliferate. Compounds
 which modulate FE21 association with tubulin are useful for alleviating
 tubulin hyper- or hypo- polymerisation disorders, such as those
 associated with aberrant initiation of mitosis, modulation of the
 initiation and rate of cell proliferation and cell growth, modulation of
 cell shape, cell rigidity, cell motility, rate and stage of cellular
 DNA replication, intracellular distribution of organelles, metastatic
 potential of cell and cellular transformation from a non-cancerous to
 cancerous phenotype. Compounds which modulate FE21 binding and
 phosphorylation are also useful for alleviating a disorder, such as
 tumorigenesis, tumour survival, growth and metastasis.
 Sequence 633 BP; 136 A; 217 C; 175 G; 105 T; 0 other;
 Query Match 6.2%; Score 214; DB 21; Length 633;
 Best Local Similarity 100.0%; Pred. No. 7.8e-89;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 776 GGCGTCCGAGAGGGGTGCACTGAGGCCACAGCTTCAAGCCGTGTGCTGCCAGGTCAGG 835

D0	345	GGGCTCCGAGAGGGGTGCAGGTGAGGCCCAAGCCCTTCAGAGCCTGTGCTGCCACGGTCAAG	404
Qy	836	AGCCATCTTGCACTCTCTCCCGAGAGTGCCAGCCACCAGCTGCACCCCGCCCTCCAGA	895
Db	405	AGCCATCTTGCACTCTCTCCCGAGAGTGCCAGCCACCAGCTGCACCCCGCCCTCCAGA	464
Qy	896	CAAGCCCAAGAGCAGGAGCTGAAGCCTGGCTGTGCTCTGGGGCGCTGTACAGACTCCG	955
Db	465	CAAGCCCAAGAGCAGGAGCTGAAGCCTGTGCTCTGGGGCGCTGTACAGACTCCG	524
Qy	956	CGGAACTCCATGTCCAGCCTGCCACACACAGC	989
Db	525	CGGAACTCCATGTCCAGCCTGCCACACACAGC	558

RESULT 13

XX New prostate-specific polypeptide for detecting, diagnosing,
PT monitoring, treating, staging and predicting cancers in humans having
PT cancer and non-cancerous prostate disease
XX
PS Claim 1; Page 213; 255pp; English.
XX
CC ABN89000 to ABN89111 represent human prostate specific nucleic acid
CC (PSNA) sequences which encode the human prostate specific proteins (PSP)
CC given in ABB81341 to ABB81439. PSNA and PSP sequences have cytostatic
CC activity, and can be used in gene therapy, antisense therapy and
CC vaccines. PSNA and PSP sequences can be used for diagnosing and
CC monitoring the presence and metastases of prostate cancer in a patient.
CC PSNA and PSP sequences are also useful: (i) for determining non-cancerous
CC prostate disease, by measuring their expression levels and/or structural
CC alterations; (ii) for determining that the sample that has prostate
CC tissue-like characteristics or is a prostate tissue; (iii) as elements
CC in an array or a multi-analyte test to recognise expression patterns
CC associated with prostate cancer and other prostate related disorders;
CC and (iv) as elements in a computer program for pattern recognition of
CC prostate disorders.
XX
SQ Sequence 881 BP; 353 A; 183 C; 217 G; 128 T; 0 other;

Query Match 0.9%; Score 32; DB 24; Length 881;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32	0.9	6769	1	US-08-480-784-20
C 2	32	0.9	6769	1	US-08-483-553-20
C 3	32	0.9	6769	1	US-08-487-002-20
C 4	32	0.9	6769	1	US-08-483-554B-20
C 5	32	0.9	6769	1	US-08-488-011B-20
C 6	32	0.9	6769	4	US-08-850-727-20
C 7	32	0.9	6769	5	PCT-US95-10202-20
C 8	32	0.9	6769	5	PCT-US95-10203-20
C 9	32	0.9	6769	5	PCT-US95-10220-20
C 10	28	0.8	19124	2	US-08-487-826B-13
C 11	26	0.7	1195	6	5240848-6
C 12	26	0.7	1618	1	US-08-236-918A-3
C 13	26	0.7	1618	4	US-09-150-864A-3
C 14	26	0.7	5526	3	US-08-751-359-21
C 15	26	0.7	5526	3	US-08-751-359-21
C 16	26	0.7	5526	4	US-08-907-146-21
C 17	26	0.7	5526	4	US-08-907-146-21
C 18	24	0.7	634	1	US-08-450-065-1
C 19	24	0.7	634	1	US-08-450-595-1
C 20	24	0.7	789	6	5219739-8
C 21	24	0.7	790	6	5194596-8
C 22	24	0.7	961	6	5194596-16
C 23	24	0.7	961	6	5219739-16
C 24	24	0.7	1543	6	532671-5
C 25	24	0.7	246240	2	US-08-724-394A-20
C 26	24	0.7	246240	2	US-08-724-394A-21
C 27	24	0.7	246240	2	US-08-724-394A-22
C 28	23	0.7	6124	4	US-09-313-300-6
C 29	23	0.7	8920	4	US-08-213-419B-3
C 30	23	0.7	8920	4	US-08-446-855A-1
C 31	23	0.7	8920	4	US-09-150-741-1
C 32	23	0.7	17949	4	US-09-087-465-3
C 33	22	0.6	750	1	US-08-224-195-1
C 34	22	0.6	780	1	US-08-224-195-2
C 35	22	0.6	937	4	US-08-927-219-48
C 36	22	0.6	1930	1	US-07-982-112-1
C 37	22	0.6	2634	3	US-08-949-386-26
C 38	22	0.6	2634	3	US-08-450-562-26
C 39	22	0.6	2634	4	US-08-984-709A-26
C 40	22	0.6	2634	4	US-08-450-272-26
C 41	22	0.6	2712	3	US-08-949-386-38
C 42	22	0.6	2712	3	US-08-450-562-38
C 43	22	0.6	2712	4	US-08-984-709A-38
C 44	22	0.6	2712	4	US-08-450-272-38
C 45	22	0.6	2970	3	US-08-949-386-37
C 46	22	0.6	2970	3	US-08-450-562-37
C 47	22	0.6	2970	4	US-08-984-709A-37
C 48	22	0.6	2970	4	US-08-450-272-37
C 49	22	0.6	2975	1	US-08-368-281-1
C 50	22	0.6	3059	4	US-09-484-970B-18
C 51	22	0.6	3240	1	US-08-368-281-3
C 52	22	0.6	3471	5	PCT-US93-00227-2
C 53	22	0.6	5923	4	US-09-064-922-3
C 54	22	0.6	10014	4	US-08-927-219-130
C 55	22	0.6	31571	1	US-08-323-443B-1
C 56	22	0.6	53526	3	US-08-658-136-2
C 57	22	0.6	53577	3	US-08-658-136-1
C 58	21	0.6	427	4	US-09-438-906-31
C 59	21	0.6	480	1	US-08-282-581-4
C 60	21	0.6	480	1	US-08-282-581-4
C 61	21	0.6	480	1	US-08-550-544-4
C 62	21	0.6	480	1	US-08-550-544-4
C 63	21	0.6	561	4	US-09-404-879A-50
C 64	21	0.6	625	4	US-09-328-111-593
C 65	21	0.6	949	4	US-09-247-155-148
C 66	21	0.6	1433	1	US-07-968-971A-11
C 67	21	0.6	1433	1	US-08-383-756-5
C 68	21	0.6	1433	1	US-08-424-406-2
C 69	21	0.6	1433	1	US-08-464-523B-8
C 70	21	0.6	1433	2	US-08-460-898-5
C 71	21	0.6	1524	4	US-09-056-105-2
C 72	21	0.6	1559	2	US-08-417-174-1
C 73	21	0.6	1559	2	US-08-231-565A-1
C 74	21	0.6	1559	2	US-09-007-961-1
C 75	21	0.6	1559	4	US-09-287-439-1
C 76	21	0.6	1600	2	US-08-487-113D-117
C 77	21	0.6	1600	2	US-08-720-420A-117
C 78	21	0.6	2340	3	US-08-742-877-3
C 79	21	0.6	2551	2	US-08-486-013-70
C 80	21	0.6	2551	2	US-08-482-279-70
C 81	21	0.6	2551	2	US-08-342-468-70
C 82	21	0.6	2551	3	US-09-015-968-70
C 83	21	0.6	2551	4	US-09-397-386-70
C 84	21	0.6	2775	4	US-09-053-871A-22
C 85	21	0.6	2781	3	US-08-749-522-4
C 86	21	0.6	2802	3	US-08-742-877-1
C 87	21	0.6	4673	1	US-07-638-431-1
C 88	21	0.6	4673	5	PCT-US92-00018-1
C 89	21	0.6	4880	4	US-09-402-929-5
C 90	21	0.6	4880	4	US-08-817-188-1
C 91	21	0.6	5238	3	US-09-080-855-1
C 92	21	0.6	5543	2	US-08-687-080-101
C 93	21	0.6	5560	3	US-08-817-188-5
C 94	21	0.6	5864	3	US-08-894-440-4
C 95	21	0.6	5864	4	US-09-458-093-4
C 96	21	0.6	6769	1	US-08-480-784-20
C 97	21	0.6	6769	1	US-08-483-553-20
C 98	21	0.6	6769	1	US-08-487-002-20
C 99	21	0.6	6769	1	US-08-483-554B-20
C 100	21	0.6	6769	1	US-08-488-011B-20

101	21	0.6	6769	4	US-08-850-727-20	Sequence 20, Appl	174	20	0.6	5319	2	US-08-861-464-7	Sequence 7, Appl
102	21	0.6	6769	5	PCT-US95-10202-20	Sequence 20, Appl	175	20	0.6	5319	2	US-08-396-001-7	Sequence 7, Appl
103	21	0.6	6769	5	PCT-US95-10203-20	Sequence 20, Appl	176	20	0.6	5319	2	US-09-323-433A-7	Sequence 7, Appl
104	21	0.6	6769	5	PCT-US95-10220-20	Sequence 20, Appl	177	20	0.6	6038	4	US-09-305-639-4	Sequence 4, Appl
105	21	0.6	12394	4	US-09-488-856A-10	Sequence 10, Appl	c 178	20	0.6	6124	4	US-08-213-419B-3	Sequence 3, Appl
106	21	0.6	16389	4	US-09-741-154-3	Sequence 3, Appl	179	20	0.6	6152	4	US-08-973-462-1	Sequence 1, Appl
107	21	0.6	21234	4	US-09-810-671-3	Sequence 3, Appl	180	20	0.6	6350	4	US-09-647-826-1	Sequence 1, Appl
108	21	0.6	32042	4	US-09-245-281-44	Sequence 44, Appl	c 181	20	0.6	6678	3	US-08-816-617A-1	Sequence 1, Appl
109	21	0.6	35060	3	US-08-814-095-7	Sequence 7, Appl	c 182	20	0.6	7622	4	US-09-305-639-1	Sequence 1, Appl
110	21	0.6	43950	4	US-09-735-934A-3	Sequence 3, Appl	183	20	0.6	9432	1	US-08-277-231A-1	Sequence 1, Appl
111	21	0.6	50000	4	US-09-146-053-4	Sequence 4, Appl	c 184	20	0.6	9432	2	US-08-277-231A-1	Sequence 1, Appl
112	21	0.6	59065	4	US-09-813-197-3	Sequence 3, Appl	c 185	20	0.6	9432	2	US-08-473-750-4	Sequence 4, Appl
113	21	0.6	59065	4	US-09-978-197-3	Sequence 3, Appl	c 186	20	0.6	9432	2	US-08-473-750-4	Sequence 4, Appl
114	21	0.6	80246	4	US-09-078-294-4	Sequence 4, Appl	187	20	0.6	9432	2	US-08-477-326-4	Sequence 4, Appl
115	21	0.6	80595	4	US-09-078-294-3	Sequence 3, Appl	c 188	20	0.6	9432	2	US-08-477-326-4	Sequence 4, Appl
116	21	0.6	111282	4	US-09-754-250-3	Sequence 3, Appl	189	20	0.6	10079	2	US-08-476-866-20	Sequence 20, Appl
117	21	0.6	112132	4	US-09-741-150-3	Sequence 3, Appl	190	20	0.6	11485	4	US-09-410-464-9	Sequence 9, Appl
118	21	0.6	162450	4	US-09-345-882-1	Sequence 1, Appl	191	20	0.6	11613	1	US-08-484-044-10	Sequence 10, Appl
119	21	0.6	168575	4	US-09-426-290-1	Sequence 1, Appl	192	20	0.6	12141	4	US-09-488-671-10	Sequence 10, Appl
120	21	0.6	246240	2	US-08-724-394A-20	Sequence 20, Appl	193	20	0.6	12793	4	US-09-004-838-124	Sequence 124, Appl
121	21	0.6	246240	2	US-08-724-394A-21	Sequence 21, Appl	c 194	20	0.6	15062	4	US-09-004-838-89	Sequence 89, Appl
122	21	0.6	246240	2	US-08-724-394A-22	Sequence 22, Appl	195	20	0.6	16063	4	US-09-801-052-3	Sequence 3, Appl
123	20	0.6	317	4	US-09-385-982-109	Sequence 109, App	c 196	20	0.6	17041	1	US-08-076-011-1	Sequence 1, Appl
124	20	0.6	341	4	US-09-404-879A-136	Sequence 136, App	197	20	0.6	17656	4	US-09-433-579-3	Sequence 3, Appl
125	20	0.6	461	4	US-09-404-879A-1	Sequence 1, Appl	198	20	0.6	19124	2	US-08-487-826B-13	Sequence 13, Appl
126	20	0.6	461	4	US-09-404-879A-3	Sequence 3, Appl	199	20	0.6	21234	4	US-09-810-671-3	Sequence 3, Appl
127	20	0.6	474	4	US-09-143-476-13	Sequence 13, Appl	200	20	0.6	29629	4	US-09-729-995-3	Sequence 3, Appl
128	20	0.6	602	1	US-08-764-100-8	Sequence 8, Appl	201	20	0.6	38682	4	US-08-943-731-2	Sequence 2, Appl
129	20	0.6	642	1	US-08-764-100-13	Sequence 13, Appl	202	20	0.6	38844	4	US-09-734-675-3	Sequence 3, Appl
130	20	0.6	643	1	US-08-764-100-7	Sequence 7, Appl	203	20	0.6	43676	3	US-09-356-952-12	Sequence 12, Appl
131	20	0.6	753	4	US-09-535-008-41	Sequence 41, Appl	c 204	20	0.6	50000	4	US-09-146-053-3	Sequence 3, Appl
132	20	0.6	790	6	5194596-8	Patent No. 5194596	205	20	0.6	51952	3	US-08-947-823-1	Sequence 1, Appl
133	20	0.6	935	2	US-08-892-770-1	Sequence 1, Appl	206	20	0.6	53526	3	US-08-658-136-2	Sequence 2, Appl
134	20	0.6	1001	4	US-09-641-638-259	Sequence 259, App	207	20	0.6	53577	3	US-08-658-136-2	Sequence 2, Appl
135	20	0.6	1095	4	US-09-276-531-55	Sequence 55, Appl	208	20	0.6	62804	4	US-09-800-960-3	Sequence 3, Appl
136	20	0.6	1106	3	US-08-755-587-18	Sequence 18, Appl	c 209	20	0.6	62804	4	US-09-800-960-3	Sequence 3, Appl
137	20	0.6	1181	2	US-08-632-598-2	Sequence 2, Appl	210	20	0.6	84495	4	US-09-797-906-3	Sequence 3, Appl
138	20	0.6	1181	4	US-09-231-240-2	Sequence 2, Appl	c 211	20	0.6	84495	4	US-09-797-906-3	Sequence 3, Appl
139	20	0.6	1278	4	US-08-943-731-63	Sequence 63, Appl	c 212	20	0.6	99500	4	US-09-798-096-10	Sequence 10, Appl
140	20	0.6	1368	3	US-08-874-563-5	Sequence 5, Appl	213	20	0.6	112132	4	US-09-741-150-3	Sequence 3, Appl
141	20	0.6	1442	2	US-08-577-483-14	Sequence 14, Appl	c 214	20	0.6	162450	4	US-09-345-882-1	Sequence 1, Appl
142	20	0.6	1442	2	US-08-454-557C-120	Sequence 120, App	c 215	19	0.5	258	1	US-07-711-615A-1	Sequence 1, Appl
143	20	0.6	1442	2	US-08-340-426D-120	Sequence 120, App	c 216	19	0.5	258	5	PCT-US92-04833-1	Sequence 1, Appl
144	20	0.6	1442	2	US-08-450-673C-120	Sequence 120, App	217	19	0.5	427	4	US-09-438-906-31	Sequence 31, Appl
145	20	0.6	1732	1	US-08-480-346-2	Sequence 2, Appl	c 218	19	0.5	602	1	US-08-764-100-8	Sequence 8, Appl
146	20	0.6	1732	2	US-08-243-541-2	Sequence 2, Appl	219	19	0.5	634	1	US-08-450-065-1	Sequence 1, Appl
147	20	0.6	1732	2	US-08-480-344-2	Sequence 2, Appl	220	19	0.5	634	1	US-08-450-065-1	Sequence 1, Appl
148	20	0.6	1854	3	US-09-486-581-1	Sequence 1, Appl	221	19	0.5	642	1	US-08-764-100-13	Sequence 13, Appl
149	20	0.6	1854	3	US-08-249-420-1	Sequence 3, Appl	c 222	19	0.5	643	1	US-08-764-100-7	Sequence 7, Appl
150	20	0.6	1854	2	US-08-737-663-1	Sequence 1, Appl	c 223	19	0.5	789	6	5219739-8	Patent No. 5219739
151	20	0.6	1939	6	5198542-3	Patent No. 5198542	c 224	19	0.5	935	2	US-08-892-770-1	Sequence 1, Appl
152	20	0.6	2099	4	US-08-938-669A-5	Sequence 5, Appl	225	19	0.5	961	6	5194596-16	Patent No. 5194596
153	20	0.6	2296	4	US-09-851-896-11	Sequence 11, Appl	226	19	0.5	961	6	5219739-16	Patent No. 5219739
154	20	0.6	2296	4	US-09-851-896-11	Sequence 11, Appl	227	19	0.5	1006	4	US-08-988-242-17	Sequence 17, Appl
155	20	0.6	2297	2	US-08-394-152A-48	Sequence 48, Appl	c 228	19	0.5	1006	4	US-08-988-242-17	Sequence 17, Appl
156	20	0.6	2993	1	US-08-764-100-2	Sequence 2, Appl	229	19	0.5	1095	4	US-09-276-531-55	Sequence 55, Appl
157	20	0.6	2993	1	US-08-764-100-10	Sequence 10, Appl	230	19	0.5	1172	4	US-08-969-046-5	Sequence 5, Appl
158	20	0.6	3000	1	US-08-764-100-9	Sequence 9, Appl	231	19	0.5	1181	2	US-08-632-598-2	Sequence 2, Appl
159	20	0.6	3001	1	US-08-764-100-1	Sequence 1, Appl	232	19	0.5	1181	4	US-09-231-240-2	Sequence 2, Appl
160	20	0.6	3017	2	US-08-394-152A-39	Sequence 39, Appl	233	19	0.5	1368	3	US-08-874-563-5	Sequence 5, Appl
161	20	0.6	3023	4	US-09-203-453-4	Sequence 4, Appl	234	19	0.5	1368	3	US-08-577-483-14	Sequence 14, Appl
162	20	0.6	3312	1	US-08-049-473-1	Sequence 1, Appl	c 235	19	0.5	1433	1	US-07-968-971A-11	Sequence 11, Appl
163	20	0.6	3312	1	US-08-312-648-1	Sequence 1, Appl	c 236	19	0.5	1433	1	US-08-383-756-5	Sequence 5, Appl
164	20	0.6	3312	5	PCT-US94-04190-1	Sequence 1, Appl	c 237	19	0.5	1433	1	US-08-424-406-2	Sequence 2, Appl
165	20	0.6	3319	1	US-08-006-676B-2	Sequence 2, Appl	c 238	19	0.5	1433	1	US-08-464-523B-8	Sequence 8, Appl
166	20	0.6	3319	1	US-08-282-845-1	Sequence 1, Appl	c 239	19	0.5	1433	1	US-08-460-898-5	Sequence 5, Appl
167	20	0.6	3319	5	US-08-428-414A-4	Sequence 4, Appl	240	19	0.5	1543	6	532671-5	Patent No. 532671
168	20	0.6	3319	5	PCT-US94-00324-2	Sequence 2, Appl	241	19	0.5	1732	2	US-08-480-346-2	Sequence 2, Appl
169	20	0.6	3536	3	US-09-418-640-3	Sequence 3, Appl	242	19	0.5	1732	2	US-08-243-541-2	Sequence 2, Appl
170	20	0.6	3550	4	US-09-398-395A-33	Sequence 33, Appl	243	19	0.5	1732	2	US-08-480-344-2	Sequence 2, Appl
171	20	0.6	4098	2	US-08-605-106-4	Sequence 4, Appl	244	19	0.5	1763	6	5198542-1	Patent No. 5198542
172	20	0.6	4253	3	US-08-577-483-7	Sequence 7, Appl	c 245	19	0.5	1763	6	5198542-1	Patent No. 5198542
173	20	0.6	4254	2	US-08-443-633-7	Sequence 7, Appl	c 246	19	0.5	1780	1	US-08-434-702-3	Sequence 3, Appl

C 247	19	0.5	1780	1	US-08-271-883-3	Sequence 3, Appl	C 320	19	0.5	51952	3	US-08-947-823-1	Sequence 1, Appl
C 248	19	0.5	1784	4	US-09-486-581-1	Sequence 1, Appl	C 321	19	0.5	56516	2	US-08-996-306-1	Sequence 1, Appl
C 249	19	0.5	1850	3	US-08-617-860B-32	Sequence 32, Appl	C 322	19	0.5	56516	4	US-09-338-907-1	Sequence 1, Appl
C 250	19	0.5	1856	1	US-08-464-523B-12	Sequence 12, Appl	C 323	19	0.5	56516	4	US-09-218-207-1	Sequence 1, Appl
C 251	19	0.5	1856	1	US-08-464-523B-12	Sequence 12, Appl	C 324	19	0.5	56520	4	US-09-338-907-179	Sequence 179, App
C 252	19	0.5	1939	6	5198542-3	Patent No. 5198542	C 325	19	0.5	56520	4	US-09-218-207-179	Sequence 7, Appl
C 253	19	0.5	1972	1	US-08-463-048-1	Sequence 1, Appl	C 326	19	0.5	72604	4	US-09-268-992-7	Sequence 7, Appl
C 254	19	0.5	1972	1	US-08-463-229-1	Sequence 1, Appl	C 327	19	0.5	72604	4	US-09-657-474-7	Sequence 7, Appl
C 255	19	0.5	2423	2	US-08-302-891-1	Sequence 1, Appl	C 328	19	0.5	99500	4	US-09-798-096-10	Sequence 10, Appl
C 256	19	0.5	2423	2	US-08-365-486A-25	Sequence 25, Appl	C 329	19	0.5	168575	4	US-09-426-230-1	Sequence 1, Appl
C 257	19	0.5	2423	1	US-08-880-342-25	Sequence 25, Appl	C 330	19	0.5	4403755	4	US-09-103-840A-2	Sequence 2, Appl
C 258	19	0.5	2551	1	US-08-486-013-70	Sequence 70, Appl	C 331	19	0.5	4411529	4	US-09-103-840A-1	Sequence 1, Appl
C 259	19	0.5	2551	2	US-08-482-279-70	Sequence 70, Appl	C 332	18	0.5	33	1	US-08-138-608-29	Sequence 29, Appl
C 260	19	0.5	2551	3	US-08-342-268-70	Sequence 70, Appl	C 333	18	0.5	36	2	US-08-669-721-5	Sequence 5, Appl
C 261	19	0.5	2551	3	US-09-015-968-70	Sequence 70, Appl	C 334	18	0.5	36	2	US-08-669-721-5	Sequence 5, Appl
C 262	19	0.5	2551	4	US-09-397-386-70	Sequence 70, Appl	C 335	18	0.5	36	4	US-09-189-344-5	Sequence 5, Appl
C 263	19	0.5	2610	1	US-08-374-834-17	Sequence 17, Appl	C 336	18	0.5	36	4	US-09-189-344-5	Sequence 5, Appl
C 264	19	0.5	2610	1	US-08-644-271-28	Sequence 28, Appl	C 337	18	0.5	40	2	US-08-849-021-1	Sequence 1, Appl
C 265	19	0.5	2610	4	US-09-077-955-32	Sequence 32, Appl	C 338	18	0.5	40	2	US-08-849-021-1	Sequence 1, Appl
C 266	19	0.5	2975	1	US-08-368-281-1	Sequence 1, Appl	C 339	18	0.5	40	2	US-08-849-021-2	Sequence 2, Appl
C 267	19	0.5	2993	1	US-08-764-100-2	Sequence 2, Appl	C 340	18	0.5	40	2	US-08-849-021-2	Sequence 2, Appl
C 268	19	0.5	2993	1	US-08-764-100-10	Sequence 10, Appl	C 341	18	0.5	43	2	US-08-849-021-85	Sequence 85, Appl
C 269	19	0.5	3000	1	US-08-764-100-9	Sequence 9, Appl	C 342	18	0.5	43	2	US-08-849-021-85	Sequence 85, Appl
C 270	19	0.5	3001	1	US-08-764-100-1	Sequence 1, Appl	C 343	18	0.5	43	2	US-08-849-021-86	Sequence 86, Appl
C 271	19	0.5	3023	4	US-09-203-453-4	Sequence 4, Appl	C 344	18	0.5	43	2	US-08-849-021-86	Sequence 86, Appl
C 272	19	0.5	3240	1	US-08-368-281-3	Sequence 3, Appl	C 345	18	0.5	57	1	US-08-222-177A-163	Sequence 163, App
C 273	19	0.5	3300	3	US-08-913-842-4	Sequence 4, Appl	C 346	18	0.5	57	1	US-08-222-177A-163	Sequence 163, App
C 274	19	0.5	3312	1	US-08-049-473-1	Sequence 1, Appl	C 347	18	0.5	66	1	US-08-222-177A-301	Sequence 301, App
C 275	19	0.5	3312	1	US-08-312-648-1	Sequence 1, Appl	C 348	18	0.5	67	3	US-09-050-559C-36	Sequence 36, Appl
C 276	19	0.5	3312	5	PCT-US94-04190-1	Sequence 1, Appl	C 349	18	0.5	87	3	US-09-050-559C-36	Sequence 36, Appl
C 277	19	0.5	3319	1	US-08-006-676B-2	Sequence 2, Appl	C 350	18	0.5	128	1	US-07-922-723A-8	Sequence 8, Appl
C 278	19	0.5	3319	1	US-08-282-845-1	Sequence 1, Appl	C 351	18	0.5	128	1	US-07-922-723A-8	Sequence 8, Appl
C 279	19	0.5	3319	2	US-08-428-414A-4	Sequence 4, Appl	C 352	18	0.5	128	1	US-07-922-723A-8	Sequence 8, Appl
C 280	19	0.5	3319	5	PCT-US94-00324-2	Sequence 2, Appl	C 353	18	0.5	128	1	US-07-922-723A-8	Sequence 8, Appl
C 281	19	0.5	3387	5	US-08-261-822A-5	Sequence 5, Appl	C 354	18	0.5	128	1	US-07-922-723A-8	Sequence 8, Appl
C 282	19	0.5	3387	5	PCT-US95-07744A-5	Sequence 5, Appl	C 355	18	0.5	128	1	US-08-074-275-8	Sequence 8, Appl
C 283	19	0.5	3950	4	US-09-398-395A-33	Sequence 33, Appl	C 356	18	0.5	128	1	US-08-074-275-8	Sequence 8, Appl
C 284	19	0.5	4098	2	US-08-605-106-4	Sequence 4, Appl	C 357	18	0.5	128	1	US-08-480-366-8	Sequence 8, Appl
C 285	19	0.5	4253	3	US-08-577-483-7	Sequence 7, Appl	C 358	18	0.5	128	1	US-08-480-366-8	Sequence 8, Appl
C 286	19	0.5	4254	2	US-08-443-639-7	Sequence 7, Appl	C 359	18	0.5	128	2	US-07-952-277A-8	Sequence 8, Appl
C 287	19	0.5	4853	4	US-08-881-450A-22	Sequence 22, Appl	C 360	18	0.5	129	1	US-08-616-368A-26	Sequence 26, Appl
C 288	19	0.5	5238	3	US-09-080-855-1	Sequence 1, Appl	C 361	18	0.5	129	1	US-08-616-368A-26	Sequence 26, Appl
C 289	19	0.5	5319	2	US-08-861-464-7	Sequence 7, Appl	C 362	18	0.5	129	3	US-09-054-298-26	Sequence 26, Appl
C 290	19	0.5	5319	2	US-08-396-001-7	Sequence 7, Appl	C 363	18	0.5	129	3	US-09-054-298-26	Sequence 26, Appl
C 291	19	0.5	5319	4	US-09-323-433A-7	Sequence 7, Appl	C 364	18	0.5	129	4	US-08-818-655-26	Sequence 26, Appl
C 292	19	0.5	5852	1	US-07-867-106-2	Sequence 2, Appl	C 365	18	0.5	129	4	US-08-818-655-26	Sequence 26, Appl
C 293	19	0.5	5923	4	US-09-064-922-3	Sequence 3, Appl	C 366	18	0.5	210	2	US-08-875-972-18	Sequence 18, Appl
C 294	19	0.5	6038	4	US-08-305-639-4	Sequence 4, Appl	C 367	18	0.5	258	1	US-07-711-615A-1	Sequence 1, Appl
C 295	19	0.5	6138	4	US-09-067-800-4	Sequence 4, Appl	C 368	18	0.5	258	5	PCT-US92-04833-1	Sequence 1, Appl
C 296	19	0.5	6138	4	US-09-067-800-4	Sequence 4, Appl	C 369	18	0.5	297	1	US-08-616-368A-17	Sequence 17, Appl
C 297	19	0.5	6138	4	US-09-349-677-4	Sequence 4, Appl	C 370	18	0.5	297	1	US-08-616-368A-17	Sequence 17, Appl
C 298	19	0.5	6138	4	US-09-647-826-1	Sequence 1, Appl	C 371	18	0.5	297	3	US-09-054-298-17	Sequence 17, Appl
C 299	19	0.5	6350	4	US-08-305-639-1	Sequence 1, Appl	C 372	18	0.5	297	3	US-09-054-298-17	Sequence 17, Appl
C 300	19	0.5	7622	4	US-08-545-860D-63	Sequence 63, Appl	C 373	18	0.5	297	4	US-08-818-655-17	Sequence 17, Appl
C 301	19	0.5	8342	3	PCT-US94-04496-63	Sequence 63, Appl	C 374	18	0.5	297	4	US-08-818-655-17	Sequence 17, Appl
C 302	19	0.5	8392	1	US-08-080-255-6	Sequence 6, Appl	C 375	18	0.5	353	4	US-09-366-887A-21	Sequence 21, Appl
C 303	19	0.5	8392	1	US-08-465-713-6	Sequence 6, Appl	C 376	18	0.5	406	4	US-08-868-452-35	Sequence 35, Appl
C 304	19	0.5	8392	5	PCT-US93-05857-6	Sequence 6, Appl	C 377	18	0.5	406	4	US-08-868-452-35	Sequence 35, Appl
C 305	19	0.5	8453	4	US-08-167-681-45	Sequence 45, Appl	C 378	18	0.5	473	1	US-08-764-100-16	Sequence 16, Appl
C 306	19	0.5	8920	2	US-08-446-855A-1	Sequence 1, Appl	C 379	18	0.5	587	4	US-09-123-912-102	Sequence 102, App
C 307	19	0.5	8920	4	US-09-150-741-1	Sequence 1, Appl	C 380	18	0.5	587	4	US-09-643-597-102	Sequence 102, App
C 308	19	0.5	10007	4	US-09-410-464-13	Sequence 13, Appl	C 381	18	0.5	587	4	US-09-643-597-102	Sequence 102, App
C 309	19	0.5	10007	4	US-09-410-464-13	Sequence 13, Appl	C 382	18	0.5	587	4	US-09-643-597-102	Sequence 102, App
C 310	19	0.5	11485	4	US-09-410-464-9	Sequence 9, Appl	C 383	18	0.5	605	4	US-09-366-887A-26	Sequence 26, Appl
C 311	19	0.5	12793	4	US-08-004-838-124	Sequence 124, App	C 384	18	0.5	615	4	US-09-385-982-240	Sequence 240, App
C 312	19	0.5	15062	4	US-09-004-838-89	Sequence 89, Appl	C 385	18	0.5	615	4	US-09-385-982-240	Sequence 240, App
C 313	19	0.5	17041	1	US-08-076-011-1	Sequence 1, Appl	C 386	18	0.5	618	4	US-08-961-810-17	Sequence 17, Appl
C 314	19	0.5	17656	4	US-09-433-579-3	Sequence 3, Appl	C 387	18	0.5	618	4	US-08-961-810-17	Sequence 17, Appl
C 315	19	0.5	17949	4	US-09-087-465-3	Sequence 3, Appl	C 388	18	0.5	618	4	US-08-352-902D-17	Sequence 17, Appl
C 316	19	0.5	38564	4	US-09-734-673-3	Sequence 3, Appl	C 389	18	0.5	684	1	US-08-352-902D-17	Sequence 17, Appl
C 317	19	0.5	38844	4	US-09-734-675-3	Sequence 3, Appl	C 390	18	0.5	684	1	US-08-577-463A-1	Sequence 1, Appl
C 318	19	0.5	43676	3	US-09-356-952-12	Sequence 12, Appl	C 391	18	0.5	684	1	US-08-577-463A-1	Sequence 1, Appl
C 319	19	0.5	43676	3	US-09-356-952-12	Sequence 12, Appl	C 392	18	0.5	713	4	US-09-149-476-72	Sequence 72, Appl

C 393	18	0.5	713	4	US-09-149-476-72	Sequence 72, Appl	466	18	0.5	1453	6	5194600-1	Patent No. 5194600
C 394	18	0.5	804	1	US-08-126-593A-3	Sequence 3, Appl	467	18	0.5	1468	6	5187075-4	Patent No. 5187075
C 395	18	0.5	804	1	US-08-126-593A-3	Sequence 3, Appl	C 468	18	0.5	1468	6	5187075-4	Patent No. 5187075
C 396	18	0.5	804	1	US-08-454-039A-3	Sequence 3, Appl	C 469	18	0.5	1499	4	US-09-484-970B-157	Sequence 157, App
C 397	18	0.5	804	1	US-08-454-039A-3	Sequence 3, Appl	C 470	18	0.5	1529	6	US-08-448-110-1	Sequence 1, Appl
C 398	18	0.5	828	4	US-08-998-416-360	Sequence 360, App	C 471	18	0.5	1529	6	5436393-2	Patent No. 5436393
C 399	18	0.5	828	4	US-08-998-416-360	Sequence 360, App	C 472	18	0.5	1570	3	US-08-617-860B-20	Sequence 20, Appl
C 400	18	0.5	830	4	US-09-149-476-236	Sequence 236, App	C 473	18	0.5	1570	3	US-08-617-860B-20	Sequence 20, Appl
C 401	18	0.5	830	4	US-09-149-476-236	Sequence 236, App	C 474	18	0.5	1601	3	US-08-817-188-3	Sequence 3, Appl
C 402	18	0.5	831	4	US-09-118-554-66	Sequence 66, Appl	C 475	18	0.5	1601	3	US-08-817-188-3	Sequence 3, Appl
C 403	18	0.5	831	4	US-09-118-554-66	Sequence 66, Appl	C 476	18	0.5	1607	1	US-07-679-451-1	Sequence 1, Appl
C 404	18	0.5	831	4	US-09-118-627-66	Sequence 66, Appl	C 477	18	0.5	1607	1	US-07-679-451-1	Sequence 1, Appl
C 405	18	0.5	831	4	US-09-118-627-66	Sequence 66, Appl	C 478	18	0.5	1607	2	US-07-989-847-1	Sequence 1, Appl
C 406	18	0.5	831	4	US-09-602-877A-66	Sequence 66, Appl	C 479	18	0.5	1607	2	US-07-989-847-1	Sequence 1, Appl
C 407	18	0.5	831	4	US-09-602-877A-66	Sequence 66, Appl	C 480	18	0.5	1607	3	US-07-721-847A-3	Sequence 3, Appl
C 408	18	0.5	883	4	US-09-171-209-25	Sequence 25, Appl	C 481	18	0.5	1607	3	US-07-721-847A-3	Sequence 3, Appl
C 409	18	0.5	883	4	US-09-171-209-25	Sequence 25, Appl	C 482	18	0.5	1607	4	US-08-469-411-1	Sequence 1, Appl
C 410	18	0.5	888	4	US-09-171-209-20	Sequence 20, Appl	C 483	18	0.5	1607	4	US-08-469-411-1	Sequence 1, Appl
C 411	18	0.5	888	4	US-09-171-209-20	Sequence 20, Appl	C 484	18	0.5	1607	4	US-08-925-779-3	Sequence 3, Appl
C 412	18	0.5	972	3	US-09-286-690-1	Sequence 1, Appl	C 485	18	0.5	1607	4	US-08-925-779-3	Sequence 3, Appl
C 413	18	0.5	1001	4	US-09-641-638-387	Sequence 387, App	C 486	18	0.5	1607	6	516058-3	Patent No. 516058
C 414	18	0.5	1001	4	US-09-641-638-387	Sequence 387, App	C 487	18	0.5	1607	6	516058-3	Patent No. 516058
C 415	18	0.5	1001	4	US-09-641-638-388	Sequence 388, App	C 488	18	0.5	1618	1	US-08-236-918A-3	Sequence 3, Appl
C 416	18	0.5	1001	4	US-09-641-638-388	Sequence 388, App	C 489	18	0.5	1618	4	US-09-150-864A-3	Sequence 3, Appl
C 417	18	0.5	1020	2	US-07-757-606B-3	Sequence 3, Appl	C 490	18	0.5	1646	1	US-07-995-950-2	Sequence 2, Appl
C 418	18	0.5	1020	2	US-07-757-606B-3	Sequence 3, Appl	C 491	18	0.5	1646	1	US-07-995-950-2	Sequence 2, Appl
C 419	18	0.5	1140	4	US-08-893-654B-3	Sequence 3, Appl	C 492	18	0.5	1646	1	US-08-300-582-2	Sequence 2, Appl
C 420	18	0.5	1140	4	US-08-893-654B-3	Sequence 3, Appl	C 493	18	0.5	1646	1	US-08-300-582-2	Sequence 2, Appl
C 421	18	0.5	1142	1	US-08-006-082A-5	Sequence 5, Appl	C 494	18	0.5	1690	4	US-08-943-731-166	Sequence 166, App
C 422	18	0.5	1142	1	US-08-006-082A-5	Sequence 5, Appl	C 495	18	0.5	1744	4	US-09-380-262B-3	Sequence 3, Appl
C 423	18	0.5	1160	1	US-08-006-082A-4	Sequence 4, Appl	C 496	18	0.5	1890	6	5312912-3	Patent No. 5312912
C 424	18	0.5	1160	1	US-08-006-082A-4	Sequence 4, Appl	C 497	18	0.5	1890	6	5312912-3	Patent No. 5312912
C 425	18	0.5	1172	4	US-08-969-046-5	Sequence 5, Appl	C 498	18	0.5	1906	1	US-08-207-904-18	Sequence 18, Appl
C 426	18	0.5	1260	1	US-07-841-646-4	Sequence 4, Appl	C 499	18	0.5	1906	1	US-08-207-904-18	Sequence 18, Appl
C 427	18	0.5	1260	1	US-07-841-646-4	Sequence 4, Appl	C 500	18	0.5	1934	1	US-07-941-651-1	Sequence 1, Appl
C 428	18	0.5	1260	1	US-07-901-703-14	Sequence 14, Appl	C 501	18	0.5	1934	1	US-07-941-651-1	Sequence 1, Appl
C 429	18	0.5	1260	1	US-07-901-703-14	Sequence 14, Appl	C 502	18	0.5	1934	1	US-08-279-996-1	Sequence 1, Appl
C 430	18	0.5	1260	1	US-08-147-023-4	Sequence 4, Appl	C 503	18	0.5	1934	1	US-08-279-996-1	Sequence 1, Appl
C 431	18	0.5	1260	1	US-08-147-023-4	Sequence 4, Appl	C 504	18	0.5	1975	6	5436393-1	Patent No. 5436393
C 432	18	0.5	1260	1	US-08-447-570-4	Sequence 4, Appl	C 505	18	0.5	1983	1	US-08-383-756-3	Sequence 3, Appl
C 433	18	0.5	1260	1	US-08-447-570-4	Sequence 4, Appl	C 506	18	0.5	1983	1	US-08-383-756-3	Sequence 3, Appl
C 434	18	0.5	1260	1	US-08-449-700-4	Sequence 4, Appl	C 507	18	0.5	1983	2	US-08-460-898-3	Sequence 3, Appl
C 435	18	0.5	1260	2	US-08-449-700-4	Sequence 4, Appl	C 508	18	0.5	1983	2	US-08-460-898-3	Sequence 3, Appl
C 436	18	0.5	1260	2	US-08-449-700-4	Sequence 4, Appl	C 509	18	0.5	2000	4	US-09-338-907-180	Sequence 180, App
C 437	18	0.5	1260	2	US-08-449-699A-4	Sequence 4, Appl	C 510	18	0.5	2000	4	US-09-338-907-180	Sequence 180, App
C 438	18	0.5	1260	5	PCT-US93-05446-14	Sequence 14, Appl	C 511	18	0.5	2000	4	US-09-218-207-180	Sequence 180, App
C 439	18	0.5	1260	5	PCT-US93-05446-14	Sequence 14, Appl	C 512	18	0.5	2073	4	US-09-134-001C-1731	Sequence 1731, Ap
C 440	18	0.5	1264	1	US-08-006-082A-1	Sequence 1, Appl	C 513	18	0.5	2076	2	US-08-617-101-1	Sequence 1, Appl
C 441	18	0.5	1264	1	US-08-006-082A-1	Sequence 1, Appl	C 514	18	0.5	2076	2	US-08-617-101-1	Sequence 1, Appl
C 442	18	0.5	1265	1	US-08-182-060A-5	Sequence 5, Appl	C 515	18	0.5	2251	4	US-08-991-677-11	Sequence 11, Appl
C 443	18	0.5	1265	1	US-08-182-060A-5	Sequence 5, Appl	C 516	18	0.5	2251	4	US-08-991-677-11	Sequence 11, Appl
C 444	18	0.5	1265	1	US-08-712-702A-5	Sequence 5, Appl	C 517	18	0.5	2267	4	US-09-142-569-5	Sequence 5, Appl
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C 447	18	0.5	1360	1	US-08-383-756-2	Sequence 2, Appl	C 520	18	0.5	2310	1	US-08-461-690B-1	Sequence 1, Appl
C 448	18	0.5	1360	2	US-08-460-898-2	Sequence 2, Appl	C 521	18	0.5	2311	1	US-08-103-445-1	Sequence 1, Appl
C 449	18	0.5	1360	2	US-08-460-898-2	Sequence 2, Appl	C 522	18	0.5	2311	1	US-08-103-445-1	Sequence 1, Appl
C 450	18	0.5	1380	1	US-08-599-252-82	Sequence 82, Appl	C 523	18	0.5	2340	3	US-08-742-877-3	Sequence 3, Appl
C 451	18	0.5	1380	1	US-08-599-252-82	Sequence 82, Appl	C 524	18	0.5	2401	1	US-08-480-346-1	Sequence 1, Appl
C 452	18	0.5	1380	1	US-08-436-074-55	Sequence 55, Appl	C 525	18	0.5	2401	1	US-08-480-346-1	Sequence 1, Appl
C 453	18	0.5	1380	1	US-08-436-074-55	Sequence 55, Appl	C 526	18	0.5	2401	1	US-08-480-346-1	Sequence 1, Appl
C 454	18	0.5	1380	5	PCT-US96-06352-82	Sequence 82, Appl	C 527	18	0.5	2401	2	US-08-243-541-1	Sequence 1, Appl
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C 456	18	0.5	1380	5	PCT-US96-06583-82	Sequence 82, Appl	C 529	18	0.5	2401	2	US-08-480-344-1	Sequence 1, Appl
C 457	18	0.5	1429	5	PCT-US96-06583-82	Sequence 82, Appl	C 530	18	0.5	2403	1	US-08-480-344-1	Sequence 1, Appl
C 458	18	0.5	1429	2	US-08-244-205-6	Sequence 6, Appl	C 531	18	0.5	2403	1	US-08-441-139-17	Sequence 17, Appl
C 459	18	0.5	1429	2	US-08-244-205-6	Sequence 6, Appl	C 532	18	0.5	2403	1	US-08-441-139-17	Sequence 17, Appl
C 460	18	0.5	1429	2	US-08-244-205-8	Sequence 8, Appl	C 533	18	0.5	2437	1	US-07-795-859B-5	Sequence 5, Appl
C 461	18	0.5	1429	2	US-08-244-205-8	Sequence 8, Appl	C 534	18	0.5	2437	1	US-07-795-859B-5	Sequence 5, Appl
C 462	18	0.5	1429	5	PCT-US92-10284-6	Sequence 6, Appl	C 535	18	0.5	2437	1	US-08-457-616-5	Sequence 5, Appl
C 463	18	0.5	1429	5	PCT-US92-10284-6	Sequence 6, Appl	C 536	18	0.5	2437	1	US-08-457-616-5	Sequence 5, Appl
C 464	18	0.5	1429	5	PCT-US92-10284-8	Sequence 8, Appl	C 537	18	0.5	2437	4	US-09-235-538-1	Sequence 1, Appl
C 465	18	0.5	1429	5	PCT-US92-10284-8	Sequence 8, Appl	C 538	18	0.5	2437	4	US-09-235-538-1	Sequence 1, Appl

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c 540	18	0.5	2473	2	US-08-540-804-3	Sequence 3, Appli	Sequence 3, Appli
541	18	0.5	2473	2	US-08-218-265-3	Sequence 3, Appli	Sequence 3, Appli
c 542	18	0.5	2473	2	US-08-218-265-3	Sequence 3, Appli	Sequence 3, Appli
543	18	0.5	2473	3	US-08-521-872-3	Sequence 3, Appli	Sequence 3, Appli
c 544	18	0.5	2473	3	US-08-521-872-3	Sequence 3, Appli	Sequence 3, Appli
545	18	0.5	2473	4	US-08-590-399-3	Sequence 3, Appli	Sequence 1, Appli
c 546	18	0.5	2473	4	US-08-590-399-3	Sequence 3, Appli	Sequence 22, Appli
547	18	0.5	2612	4	US-09-105-390-7	Sequence 7, Appli	Sequence 1, Appli
c 548	18	0.5	2612	4	US-09-105-390-7	Sequence 7, Appli	Sequence 14, Appli
549	18	0.5	2663	1	US-08-136-743B-3	Sequence 3, Appli	Sequence 14, Appli
c 550	18	0.5	2663	1	US-08-136-743B-3	Sequence 3, Appli	Sequence 20, Appli
551	18	0.5	2747	2	US-08-874-347-1	Sequence 1, Appli	Sequence 20, Appli
c 552	18	0.5	2747	3	US-09-093-522-1	Sequence 1, Appli	Sequence 1, Appli
553	18	0.5	2775	4	US-09-053-871A-22	Sequence 22, Appli	Sequence 28, Appli
c 554	18	0.5	2781	3	US-08-749-522-4	Sequence 4, Appli	Sequence 28, Appli
555	18	0.5	2802	3	US-08-742-877-1	Sequence 1, Appli	Sequence 28, Appli
c 556	18	0.5	3072	4	US-08-522-217-55	Sequence 55, Appli	Sequence 28, Appli
557	18	0.5	3072	4	US-08-522-217-55	Sequence 55, Appli	Sequence 5, Appli
c 558	18	0.5	3183	2	US-08-939-218A-1	Sequence 1, Appli	Sequence 1, Appli
559	18	0.5	3183	2	US-08-939-218A-1	Sequence 1, Appli	Sequence 1, Appli
c 560	18	0.5	3187	5	PCT-US95-06815-1	Sequence 1, Appli	Sequence 4, Appli
561	18	0.5	3187	5	PCT-US95-06815-1	Sequence 1, Appli	Sequence 4, Appli
c 562	18	0.5	3192	1	US-08-706-037-26	Sequence 26, Appli	Sequence 1, Appli
563	18	0.5	3192	1	US-08-706-037-26	Sequence 26, Appli	Sequence 1, Appli
c 564	18	0.5	3192	1	US-08-940-661A-1	Sequence 1, Appli	Sequence 1, Appli
565	18	0.5	3192	1	US-08-940-661A-1	Sequence 1, Appli	Sequence 1, Appli
c 566	18	0.5	3192	2	US-09-083-485-1	Sequence 1, Appli	Sequence 5, Appli
567	18	0.5	3192	2	US-09-083-485-1	Sequence 1, Appli	Sequence 5, Appli
c 568	18	0.5	3192	2	US-09-083-485-1	Sequence 1, Appli	Sequence 5, Appli
569	18	0.5	3192	2	US-09-005-397-26	Sequence 26, Appli	Sequence 1, Appli
c 570	18	0.5	3387	5	PCT-US95-07744A-5	Sequence 5, Appli	Sequence 1, Appli
571	18	0.5	3387	5	PCT-US95-07744A-5	Sequence 5, Appli	Sequence 1, Appli
c 572	18	0.5	3395	4	US-09-103-478-3	Sequence 3, Appli	Sequence 2, Appli
573	18	0.5	3395	4	US-09-103-478-3	Sequence 3, Appli	Sequence 2, Appli
c 574	18	0.5	3395	4	US-09-193-931C-3	Sequence 3, Appli	Sequence 4, Appli
575	18	0.5	3395	4	US-09-193-931C-3	Sequence 3, Appli	Sequence 4, Appli
c 576	18	0.5	3511	4	US-09-380-262B-5	Sequence 5, Appli	Sequence 4, Appli
577	18	0.5	3528	4	US-08-984-320-2	Sequence 2, Appli	Sequence 10, Appli
c 578	18	0.5	3528	4	US-08-984-320-2	Sequence 2, Appli	Sequence 11, Appli
579	18	0.5	3528	4	US-08-487-087A-2	Sequence 2, Appli	Sequence 11, Appli
c 580	18	0.5	3528	4	US-08-487-087A-2	Sequence 2, Appli	Sequence 11, Appli
581	18	0.5	3623	2	US-07-989-847-13	Sequence 13, Appli	Sequence 11, Appli
c 582	18	0.5	3623	2	US-07-989-847-13	Sequence 13, Appli	Sequence 11, Appli
583	18	0.5	3623	4	US-08-469-411-13	Sequence 13, Appli	Sequence 11, Appli
c 584	18	0.5	3623	4	US-08-469-411-13	Sequence 13, Appli	Sequence 11, Appli
585	18	0.5	3627	1	US-08-104-072B-6	Sequence 6, Appli	Sequence 1, Appli
c 586	18	0.5	3627	1	US-08-104-072B-6	Sequence 6, Appli	Sequence 1, Appli
587	18	0.5	3627	1	US-08-351-413-7	Sequence 7, Appli	Sequence 1, Appli
c 588	18	0.5	3627	1	US-08-351-413-7	Sequence 7, Appli	Sequence 1, Appli
589	18	0.5	3627	2	US-09-025-583-7	Sequence 7, Appli	Sequence 2, Appli
c 590	18	0.5	3627	2	US-09-025-583-7	Sequence 7, Appli	Sequence 2, Appli
591	18	0.5	3697	1	US-08-571-758-1	Sequence 1, Appli	Sequence 5, Appli
c 592	18	0.5	3697	1	US-08-571-758-1	Sequence 1, Appli	Sequence 5, Appli
593	18	0.5	3697	1	US-08-909-984A-1	Sequence 1, Appli	Sequence 15, Appli
c 594	18	0.5	3697	1	US-08-909-984A-1	Sequence 1, Appli	Sequence 15, Appli
595	18	0.5	3697	1	US-08-909-983-1	Sequence 1, Appli	Sequence 16, Appli
c 596	18	0.5	3697	1	US-08-909-983-1	Sequence 1, Appli	Sequence 16, Appli
597	18	0.5	3744	4	US-08-961-527-263	Sequence 263, App	Sequence 1, Appli
c 598	18	0.5	3744	4	US-08-961-527-263	Sequence 263, App	Sequence 1, Appli
599	18	0.5	4084	3	US-08-866-340-1	Sequence 1, Appli	Sequence 3, Appli
c 600	18	0.5	4084	3	US-08-866-340-1	Sequence 1, Appli	Sequence 3, Appli
601	18	0.5	4383	4	US-08-397-653B-2	Sequence 2, Appli	Sequence 31, Appli
c 602	18	0.5	4383	4	US-08-397-653B-2	Sequence 2, Appli	Sequence 31, Appli
603	18	0.5	4383	6	5175095-4	Patent No. 5175095	Sequence 31, Appli
c 604	18	0.5	4383	6	5175095-4	Patent No. 5175095	Sequence 36, Appli
605	18	0.5	4383	6	5177307-1	Patent No. 5177307	Sequence 36, Appli
c 606	18	0.5	4383	6	5177307-1	Patent No. 5177307	Sequence 36, Appli
607	18	0.5	4456	3	US-08-321-686B-1	Sequence 1, Appli	Sequence 36, Appli
c 608	18	0.5	4456	3	US-08-321-686B-1	Sequence 1, Appli	Sequence 36, Appli
609	18	0.5	4460	4	US-09-103-875-4	Sequence 4, Appli	Sequence 36, Appli
c 610	18	0.5	4460	4	US-09-103-875-4	Sequence 4, Appli	Sequence 36, Appli
611	18	0.5	4507	2	US-08-568-459A-3	Sequence 3, Appli	Sequence 36, Appli

c 685	18	0.5	12124	1	US-08-456-265A-36	Sequence 36, Appl	c 758	17	0.5	24	2	US-08-849-021-70	Sequence 70, Appl
c 686	18	0.5	12124	1	US-08-455-416-36	Sequence 36, Appl	759	17	0.5	56	4	US-09-636-735A-4	Sequence 4, Appl
c 687	18	0.5	12124	1	US-08-455-416-36	Sequence 36, Appl	c 760	17	0.5	56	4	US-09-636-735A-4	Sequence 4, Appl
c 688	18	0.5	12124	1	US-08-455-244-36	Sequence 36, Appl	761	17	0.5	148	4	US-08-991-789A-229	Sequence 229, App
c 689	18	0.5	12124	1	US-08-455-244-36	Sequence 36, Appl	762	17	0.5	148	4	US-09-062-451-229	Sequence 229, App
c 690	18	0.5	12124	1	US-08-454-876-36	Sequence 36, Appl	763	17	0.5	148	4	US-09-598-326-229	Sequence 229, App
c 691	18	0.5	12124	1	US-08-454-876-36	Sequence 36, Appl	c 764	17	0.5	165	1	US-08-209-747-9	Sequence 9, Appl
c 692	18	0.5	12124	2	US-08-457-364-36	Sequence 36, Appl	c 765	17	0.5	165	1	US-08-458-298-9	Sequence 9, Appl
c 693	18	0.5	12124	2	US-08-457-364-36	Sequence 36, Appl	766	17	0.5	182	4	US-09-712-016-53	Sequence 53, Appl
c 694	18	0.5	12124	2	US-08-456-262-36	Sequence 36, Appl	c 767	17	0.5	231	4	US-08-943-731-12	Sequence 12, Appl
c 695	18	0.5	12124	2	US-08-456-262-36	Sequence 36, Appl	c 768	17	0.5	231	4	US-09-328-111-287	Sequence 287, App
c 696	18	0.5	12124	2	US-08-456-240-36	Sequence 36, Appl	769	17	0.5	232	4	US-08-971-188-7	Sequence 7, Appl
c 697	18	0.5	12124	2	US-08-456-240-36	Sequence 36, Appl	770	17	0.5	250	4	US-08-971-188-6	Sequence 6, Appl
c 698	18	0.5	12124	2	US-08-455-736-36	Sequence 36, Appl	771	17	0.5	306	4	US-09-605-785-650	Sequence 650, App
c 699	18	0.5	12124	2	US-08-455-736-36	Sequence 36, Appl	772	17	0.5	349	4	US-09-484-970B-108	Sequence 108, App
c 700	18	0.5	12124	2	US-08-971-217-36	Sequence 36, Appl	c 773	17	0.5	425	2	US-08-967-101-102	Sequence 102, App
c 701	18	0.5	12124	2	US-08-971-217-36	Sequence 36, Appl	c 774	17	0.5	425	2	US-08-952-541-102	Sequence 102, App
c 702	18	0.5	12124	4	US-09-350-600-36	Sequence 36, Appl	c 775	17	0.5	425	3	US-09-124-698-102	Sequence 102, App
c 703	18	0.5	12124	4	US-09-350-600-36	Sequence 36, Appl	c 776	17	0.5	425	4	US-09-127-480-102	Sequence 102, App
c 704	18	0.5	12730	4	US-09-004-838-91	Sequence 91, Appl	c 777	17	0.5	425	4	US-08-496-841C-102	Sequence 102, App
c 705	18	0.5	12730	4	US-09-004-838-91	Sequence 91, Appl	c 778	17	0.5	435	4	US-09-124-523-102	Sequence 102, App
c 706	18	0.5	13158	2	US-08-687-080-105	Sequence 105, App	779	17	0.5	484	6	5496550-5	Patent No. 5496550
c 707	18	0.5	15144	3	US-08-458-434A-6	Sequence 6, Appl	780	17	0.5	500	4	US-09-328-111-343	Sequence 343, App
c 708	18	0.5	15144	3	US-08-458-434A-6	Sequence 6, Appl	c 781	17	0.5	570	4	US-09-385-982-417	Sequence 417, App
c 709	18	0.5	17341	4	US-09-415-946-1	Sequence 1, Appl	782	17	0.5	575	3	US-08-726-807B-6	Sequence 6, Appl
c 710	18	0.5	17341	4	US-09-415-946-1	Sequence 1, Appl	c 783	17	0.5	575	3	US-08-726-807B-6	Sequence 6, Appl
c 711	18	0.5	17606	4	US-08-943-731-4	Sequence 4, Appl	784	17	0.5	575	3	US-09-258-367-6	Sequence 6, Appl
c 712	18	0.5	22846	2	US-08-469-461-3	Sequence 3, Appl	c 785	17	0.5	575	3	US-09-258-367-6	Sequence 6, Appl
c 713	18	0.5	22846	2	US-08-469-461-3	Sequence 3, Appl	786	17	0.5	575	4	US-09-546-550-6	Sequence 6, Appl
c 714	18	0.5	22846	3	US-07-890-609-3	Sequence 3, Appl	c 787	17	0.5	575	4	US-09-546-550-6	Sequence 6, Appl
c 715	18	0.5	22846	3	US-07-890-609-3	Sequence 3, Appl	788	17	0.5	575	4	US-09-431-414-6	Sequence 6, Appl
c 716	18	0.5	29604	3	US-08-781-891-207	Sequence 207, App	c 789	17	0.5	575	4	US-09-431-414-6	Sequence 6, Appl
c 717	18	0.5	29604	3	US-08-781-891-207	Sequence 207, App	790	17	0.5	575	4	US-09-225-670-6	Sequence 6, Appl
c 718	18	0.5	32207	2	US-08-770-379-20	Sequence 20, Appl	c 791	17	0.5	575	4	US-09-225-670-6	Sequence 6, Appl
c 719	18	0.5	32207	4	US-08-757-669A-20	Sequence 20, Appl	792	17	0.5	575	4	US-09-431-349C-6	Sequence 6, Appl
c 720	18	0.5	32207	4	US-09-230-371A-20	Sequence 20, Appl	c 793	17	0.5	575	4	US-09-431-349C-6	Sequence 6, Appl
c 721	18	0.5	35100	2	US-08-770-379-17	Sequence 17, Appl	794	17	0.5	592	3	US-07-721-847A-1	Sequence 1, Appl
c 722	18	0.5	35100	4	US-08-757-669A-17	Sequence 17, Appl	c 795	17	0.5	592	3	US-07-721-847A-1	Sequence 1, Appl
c 723	18	0.5	35100	4	US-09-230-371A-17	Sequence 3, Appl	796	17	0.5	592	4	US-08-925-779-1	Sequence 1, Appl
c 724	18	0.5	36651	4	US-09-738-894A-3	Sequence 3, Appl	c 797	17	0.5	592	4	US-08-925-779-1	Sequence 1, Appl
c 725	18	0.5	43795	3	US-08-742-185-101	Sequence 101, App	798	17	0.5	592	6	5166058-1	Patent No. 5166058
c 726	18	0.5	43795	3	US-08-742-185-101	Sequence 101, App	c 799	17	0.5	592	6	5166058-1	Patent No. 5166058
c 727	18	0.5	43950	4	US-09-146-053-5	Sequence 5, Appl	800	17	0.5	631	4	US-08-991-789A-34	Sequence 34, Appl
c 728	18	0.5	44543	4	US-09-146-053-5	Sequence 5, Appl	c 801	17	0.5	631	4	US-08-991-789A-34	Sequence 34, Appl
c 729	18	0.5	45546	4	US-09-146-053-6	Sequence 6, Appl	802	17	0.5	631	4	US-09-062-451-34	Sequence 34, Appl
c 730	18	0.5	45546	4	US-09-146-053-6	Sequence 6, Appl	c 803	17	0.5	631	4	US-09-062-451-34	Sequence 34, Appl
c 731	18	0.5	45716	4	US-08-965-048-5	Sequence 5, Appl	804	17	0.5	631	4	US-09-598-326-34	Sequence 34, Appl
c 732	18	0.5	45716	4	US-08-965-048-5	Sequence 5, Appl	c 805	17	0.5	636	4	US-09-598-326-34	Sequence 34, Appl
c 733	18	0.5	45989	4	US-08-965-048-6	Sequence 6, Appl	c 806	17	0.5	636	4	US-09-221-017B-1004	Sequence 1004, Ap
c 734	18	0.5	45989	4	US-08-965-048-6	Sequence 6, Appl	c 807	17	0.5	645	4	US-09-328-111-106	Sequence 106, App
c 735	18	0.5	55516	2	US-08-996-306-1	Sequence 1, Appl	c 808	17	0.5	645	4	US-09-288-143-22	Sequence 22, Appl
c 736	18	0.5	55516	4	US-09-338-907-1	Sequence 1, Appl	c 809	17	0.5	646	4	US-09-288-143-22	Sequence 22, Appl
c 737	18	0.5	56516	4	US-09-218-207-1	Sequence 1, Appl	c 810	17	0.5	671	4	US-09-643-597-131	Sequence 131, App
c 738	18	0.5	56520	4	US-09-338-907-179	Sequence 179, App	c 811	17	0.5	676	4	US-09-490-818-1	Sequence 1, Appl
c 739	18	0.5	56520	4	US-09-218-207-179	Sequence 179, App	812	17	0.5	705	4	US-09-328-111-674	Sequence 674, App
c 740	18	0.5	65042	4	US-09-784-316-3	Sequence 3, Appl	c 813	17	0.5	705	4	US-09-328-111-674	Sequence 674, App
c 741	18	0.5	65042	4	US-09-784-316-3	Sequence 3, Appl	c 814	17	0.5	740	4	US-08-998-416-771	Sequence 771, App
c 742	18	0.5	72604	4	US-09-268-992-7	Sequence 7, Appl	c 815	17	0.5	741	4	US-09-149-476-202	Sequence 202, App
c 743	18	0.5	72604	4	US-09-657-474-7	Sequence 7, Appl	816	17	0.5	750	1	US-08-224-195-1	Sequence 1, Appl
c 744	18	0.5	87350	3	US-08-781-891-79	Sequence 79, Appl	c 817	17	0.5	773	4	US-09-149-476-20	Sequence 20, Appl
c 745	18	0.5	87350	3	US-08-781-891-79	Sequence 79, Appl	818	17	0.5	780	1	US-08-224-195-2	Sequence 2, Appl
c 746	18	0.5	87543	4	US-09-791-211-3	Sequence 3, Appl	819	17	0.5	842	2	US-08-820-170A-3	Sequence 3, Appl
c 747	18	0.5	87543	4	US-09-791-211-3	Sequence 3, Appl	820	17	0.5	842	3	US-09-055-699-3	Sequence 3, Appl
c 748	18	0.5	98844	4	US-09-791-211-10	Sequence 10, Appl	821	17	0.5	842	4	US-09-273-565-3	Sequence 3, Appl
c 749	18	0.5	98844	4	US-09-791-211-10	Sequence 10, Appl	822	17	0.5	842	4	US-09-565-538-3	Sequence 3, Appl
c 750	18	0.5	152331	3	US-09-128-155-16	Sequence 16, Appl	823	17	0.5	842	4	US-09-661-468-3	Sequence 3, Appl
c 751	18	0.5	152331	3	US-09-128-155-16	Sequence 16, Appl	824	17	0.5	852	2	US-09-069-330-1	Sequence 1, Appl
c 752	18	0.5	169998	4	US-09-676-610B-24	Sequence 24, Appl	c 825	17	0.5	860	2	US-08-310-416A-19	Sequence 19, Appl
c 753	18	0.5	169998	4	US-09-676-610B-24	Sequence 24, Appl	826	17	0.5	860	2	US-08-888-171-19	Sequence 19, Appl
c 754	18	0.5	176373	3	US-09-128-155-17	Sequence 17, Appl	c 827	17	0.5	901	4	US-09-475-316A-12	Sequence 12, Appl
c 755	17	0.5	22	2	US-08-849-021-84	Sequence 84, Appl	c 828	17	0.5	901	4	US-09-475-316A-12	Sequence 12, Appl
c 756	17	0.5	22	2	US-08-849-021-84	Sequence 84, Appl	829	17	0.5	917	2	US-08-924-759-17	Sequence 17, Appl
c 757	17	0.5	24	2	US-08-849-021-70	Sequence 70, Appl	c 830	17	0.5	917	2	US-08-924-759-17	Sequence 17, Appl

C 831	17	0.5	917	3	US-09-248-335-17	Sequence 17, Appl	904	17	0.5	1972	1	US-08-463-048-1	Sequence 1, Appl
C 832	17	0.5	917	3	US-09-248-335-17	Sequence 17, Appl	905	17	0.5	1972	1	US-08-463-229-1	Sequence 1, Appl
C 833	17	0.5	939	4	US-09-079-029-7	Sequence 7, Appl	906	17	0.5	1972	2	US-08-302-891-1	Sequence 1, Appl
C 834	17	0.5	1006	4	US-09-058-368-4	Sequence 4, Appl	C 907	17	0.5	1997	4	US-09-269-731-3	Sequence 3, Appl
C 835	17	0.5	1048	2	US-08-897-340-3	Sequence 3, Appl	C 908	17	0.5	2019	4	US-09-160-494-3	Sequence 3, Appl
C 836	17	0.5	1048	3	US-09-252-329-3	Sequence 3, Appl	C 909	17	0.5	2030	2	US-08-923-536A-1	Sequence 1, Appl
C 837	17	0.5	1068	4	US-09-235-103-3	Sequence 3, Appl	C 910	17	0.5	2030	2	US-08-923-536A-1	Sequence 1, Appl
C 838	17	0.5	1146	2	US-08-504-265B-74	Sequence 74, Appl	C 911	17	0.5	2065	2	US-08-968-751-1	Sequence 1, Appl
C 839	17	0.5	1195	6	5240848-6	Patent No. 5240848	C 912	17	0.5	2071	1	US-07-923-724-1	Sequence 1, Appl
C 840	17	0.5	1279	4	US-09-277-716-31	Sequence 31, Appl	C 913	17	0.5	2071	2	US-08-609-426A-1	Sequence 1, Appl
C 841	17	0.5	1279	4	US-09-277-716-31	Sequence 31, Appl	C 914	17	0.5	2071	2	US-08-374-652C-3	Sequence 3, Appl
C 842	17	0.5	1279	4	US-09-609-161B-31	Sequence 31, Appl	C 915	17	0.5	2075	1	US-08-167-628-1	Sequence 1, Appl
C 843	17	0.5	1279	4	US-09-609-161B-31	Sequence 31, Appl	C 916	17	0.5	2075	1	US-08-167-628-1	Sequence 1, Appl
C 844	17	0.5	1280	4	US-09-096-776B-4	Sequence 4, Appl	C 917	17	0.5	2075	1	US-08-386-680-1	Sequence 1, Appl
C 845	17	0.5	1320	4	US-09-370-838-22	Sequence 22, Appl	C 918	17	0.5	2075	1	US-08-386-680-1	Sequence 1, Appl
C 846	17	0.5	1328	4	US-09-370-838-24	Sequence 24, Appl	C 919	17	0.5	2075	1	US-08-459-717-1	Sequence 1, Appl
C 847	17	0.5	1330	2	US-09-036-582-33	Sequence 33, Appl	C 920	17	0.5	2075	1	US-08-459-717-1	Sequence 1, Appl
C 848	17	0.5	1330	2	US-09-036-582-33	Sequence 33, Appl	C 921	17	0.5	2075	1	US-08-712-302-1	Sequence 1, Appl
C 849	17	0.5	1331	4	US-09-370-838-27	Sequence 27, Appl	C 922	17	0.5	2075	1	US-08-712-302-1	Sequence 1, Appl
C 850	17	0.5	1333	4	US-09-370-838-28	Sequence 28, Appl	C 923	17	0.5	2075	2	US-08-880-031-1	Sequence 1, Appl
C 851	17	0.5	1347	4	US-09-286-529-18	Sequence 18, Appl	C 924	17	0.5	2075	2	US-08-880-031-1	Sequence 1, Appl
C 852	17	0.5	1355	4	US-09-370-838-31	Sequence 31, Appl	C 925	17	0.5	2075	3	US-09-097-179-1	Sequence 1, Appl
C 853	17	0.5	1356	1	US-08-592-936B-22	Sequence 22, Appl	C 926	17	0.5	2075	3	US-09-097-179-1	Sequence 1, Appl
C 854	17	0.5	1356	1	US-08-788-928A-2	Sequence 2, Appl	C 927	17	0.5	2075	4	US-09-080-715-1	Sequence 1, Appl
C 855	17	0.5	1356	2	US-09-111-573-22	Sequence 22, Appl	C 928	17	0.5	2075	4	US-09-080-715-1	Sequence 1, Appl
C 856	17	0.5	1362	4	US-08-979-608A-12	Sequence 12, Appl	C 929	17	0.5	2075	4	US-09-142-569-7	Sequence 7, Appl
C 857	17	0.5	1362	4	US-08-979-608A-12	Sequence 12, Appl	C 930	17	0.5	2075	4	US-09-142-569-7	Sequence 7, Appl
C 858	17	0.5	1407	4	US-09-134-001C-1162	Sequence 1162, Ap	C 931	17	0.5	2075	5	PCT-US96-08140-1	Sequence 1, Appl
C 859	17	0.5	1422	4	US-08-979-608A-13	Sequence 13, Appl	C 932	17	0.5	2075	5	PCT-US96-08140-1	Sequence 1, Appl
C 860	17	0.5	1422	4	US-08-979-608A-13	Sequence 13, Appl	C 933	17	0.5	2096	1	US-08-458-084-1	Sequence 1, Appl
C 861	17	0.5	1450	3	US-08-617-860B-22	Sequence 22, Appl	C 934	17	0.5	2096	1	US-08-205-508-1	Sequence 1, Appl
C 862	17	0.5	1450	3	US-08-617-860B-22	Sequence 22, Appl	C 935	17	0.5	2096	1	US-08-278-630A-10	Sequence 10, Appl
C 863	17	0.5	1494	4	US-09-255-502-1	Sequence 1, Appl	C 936	17	0.5	2096	5	PCT-US95-02945-1	Sequence 1, Appl
C 864	17	0.5	1496	6	RE34606-1	Patent No. RE34606	C 937	17	0.5	2099	4	US-09-643-597-158	Sequence 158, App
C 865	17	0.5	1497	1	US-08-322-677A-6	Sequence 6, Appl	C 938	17	0.5	2101	2	US-08-860-150-1	Sequence 1, Appl
C 866	17	0.5	1497	1	US-08-322-677A-6	Sequence 6, Appl	C 939	17	0.5	2101	3	US-09-338-132-1	Sequence 1, Appl
C 867	17	0.5	1497	3	US-08-898-218-6	Sequence 6, Appl	C 940	17	0.5	2116	1	US-07-811-048-9	Sequence 9, Appl
C 868	17	0.5	1497	3	US-08-848-793-6	Sequence 6, Appl	C 941	17	0.5	2145	2	US-08-592-936B-16	Sequence 16, Appl
C 869	17	0.5	1497	4	US-09-445-270-1	Sequence 1, Appl	C 942	17	0.5	2145	2	US-09-111-573-16	Sequence 16, Appl
C 870	17	0.5	1497	6	5472855-1	Patent No. 5472855	C 943	17	0.5	2160	4	US-09-382-256-15	Sequence 15, Appl
C 871	17	0.5	1499	4	US-09-484-970B-157	Sequence 157, App	C 944	17	0.5	2160	4	US-09-395-115-15	Sequence 15, Appl
C 872	17	0.5	1513	4	US-09-178-155-1	Sequence 1, Appl	C 945	17	0.5	2160	4	US-08-436-265-15	Sequence 15, Appl
C 873	17	0.5	1519	1	US-07-971-759-19	Sequence 19, Appl	C 946	17	0.5	2160	4	US-09-679-187-15	Sequence 15, Appl
C 874	17	0.5	1519	1	US-07-971-759-19	Sequence 19, Appl	C 947	17	0.5	2190	4	US-09-625-188-19	Sequence 19, Appl
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C 877	17	0.5	1556	1	US-08-457-135-3	Sequence 3, Appl	C 950	17	0.5	2213	1	US-08-788-928A-1	Sequence 1, Appl
C 878	17	0.5	1573	1	US-08-597-545-4	Sequence 4, Appl	C 951	17	0.5	2213	2	US-09-111-573-12	Sequence 12, Appl
C 879	17	0.5	1573	1	US-08-457-135-4	Sequence 4, Appl	C 952	17	0.5	2218	2	US-08-421-044-1	Sequence 1, Appl
C 880	17	0.5	1608	2	PCT-US94-02891-68	Sequence 1, Appl	C 953	17	0.5	2234	1	US-07-811-048-10	Sequence 10, Appl
C 881	17	0.5	1608	5	PCT-US94-02891-68	Sequence 68, Appl	C 954	17	0.5	2236	3	US-08-829-525-23	Sequence 23, Appl
C 882	17	0.5	1617	4	US-08-979-608A-11	Sequence 11, Appl	C 955	17	0.5	2236	4	US-08-609-583A-23	Sequence 23, Appl
C 883	17	0.5	1617	4	US-08-979-608A-11	Sequence 11, Appl	C 956	17	0.5	2236	4	US-08-937-389-23	Sequence 23, Appl
C 884	17	0.5	1627	4	US-09-484-970B-19	Sequence 19, Appl	C 957	17	0.5	2236	4	US-09-310-367-23	Sequence 23, Appl
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C 886	17	0.5	1670	3	US-08-709-838-1	Sequence 1, Appl	C 959	17	0.5	2238	3	US-08-617-860B-28	Sequence 28, Appl
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C 894	17	0.5	1756	2	US-08-879-260-3	Sequence 3, Appl	C 967	17	0.5	2847	3	US-08-483-433-2	Sequence 2, Appl
C 895	17	0.5	1758	4	US-09-370-838-25	Sequence 25, Appl	C 968	17	0.5	2847	4	US-09-484-970B-22	Sequence 22, Appl
C 896	17	0.5	1811	3	US-09-231-529-5	Sequence 5, Appl	C 969	17	0.5	2847	5	PCT-US92-05920-2	Sequence 2, Appl
C 897	17	0.5	1811	4	US-08-577-816-5	Sequence 5, Appl	C 970	17	0.5	2877	4	US-09-235-103-1	Sequence 1, Appl
C 898	17	0.5	1868	1	US-08-069-863-1	Sequence 1, Appl	C 971	17	0.5	2917	1	US-08-592-936B-20	Sequence 20, Appl
C 899	17	0.5	1868	1	US-08-309-069-1	Sequence 1, Appl	C 972	17	0.5	2917	2	US-09-111-573-20	Sequence 20, Appl
C 900	17	0.5	1868	1	US-08-562-833-1	Sequence 1, Appl	C 973	17	0.5	2998	3	US-09-054-368-1	Sequence 1, Appl
C 901	17	0.5	1868	5	PCT-US95-05520-1	Sequence 1, Appl	C 974	17	0.5	2998	3	US-09-054-368-1	Sequence 1, Appl
C 902	17	0.5	1910	4	US-09-071-709-8	Sequence 8, Appl	C 975	17	0.5	2998	3	US-09-054-274-1	Sequence 1, Appl
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1  RESULT 3
2  US-08-487-002-20/c
3  ; Sequence 20, Application US/08487002
4  ; Patent No. 5710001
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Shattuck-Eidens, Donna M.
7  ; APPLICANT: Simard, Jacques
8  ; APPLICANT: Emi, Mitsuru
9  ; APPLICANT: Nakamura, Yusuke
10 ; APPLICANT: Durocher, Francine
11 ; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
12 ; TITLE OF INVENTION: Susceptibility Gene
13 ; NUMBER OF SEQUENCES: 85
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
16 ; STREET: 1201 New York Avenue, N.W., Suite 1000
17 ; CITY: Washington
18 ; STATE: DC
19 ; COUNTRY: USA
20 ; ZIP: 20005
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Floppy disk
23 ; COMPUTER: IBM PC compatible
24 ; OPERATING SYSTEM: PC-DOS/MS-DOS
25 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08/487,002
28 ; FILING DATE:
29 ; CLASSIFICATION: 424
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER: US 08/409,305
32 ; FILING DATE: 24-MAR-1995
33 ; PRIOR APPLICATION DATA:
34 ; APPLICATION NUMBER: US 08/348,824

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 APPLICATION NUMBER: PCT/US95/10202
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/409,305
 FILING DATE: 24-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,824
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08-308,104
 FILING DATE: 16-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/300,266
 FILING DATE: 02-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,221
 FILING DATE: 12-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109347
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6769 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 PCT-US95-10202-20

Query Match 0.9%; Score 32; DB 5; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 32: Conservative 0; Mismatches 0 Indels

[illegible]

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Sequence 20. Application PC/TUS9510203
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast
; TITLE OF INVENTION: Susceptibility G

Query Match 0.7%; Score 26; DB 6; Length 1195;

RESULT 13
US-09-150-864A-3/c
; Sequence 3, Application US/09150864A

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Patent No. 6355779
GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
TITLE OF INVENTION: That Binds Thereto
FILE REFERENCE: 2801-B
CURRENT APPLICATION NUMBER: US/09/150,864A
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 08/060,843
PRIOR FILING DATE: 1993-05-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1618
TYPE: DNA
ORGANISM: Homo sapiens(clone: human4-1BB-L(7A))
FEATURE:
NAME/KEY: CDS
LOCATION: (4)..(765)
US-09-150-864A-3

Query Match      0.7%; Score 26; DB 4; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3216 ATATATATATATATATATATATATATA 3241
Db 1005 ATATATATATATATATATATATATA 980

RESULT 14
US-08-751-359-21
Sequence 21, Application US/08751359
Patent No. 6143559
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: Concurrently Herewith
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: Concurrently Herewith
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 5526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-751-359-21
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Query Match      0.7%; Score 26; DB 3; Length 5526;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3395 TATATTTTATATATATATATAA 3420

RESULT 15
US-08-751-359-21/c
Sequence 21, Application US/08751359
Patent No. 6143559
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: Concurrently Herewith
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 5526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-751-359-21

Query Match      0.7%; Score 26; DB 3; Length 5526;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3208 TATATTTTATATATATATATAA 3233
Db 3426 TATATTTTATATATATATAA 3401

Search completed: June 17, 2003, 06:27:32
Job time : 165.951 secs
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 367.156 Seconds
(without alignments)

13697.491 Million cell updates/sec

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1677	48.3	2411	9	US-10-091-548-89
3	1677	48.3	2411	9	US-10-074-095-1133
4	1677	48.3	2411	10	US-09-764-860-1133
5	475	13.7	560	9	US-09-764-904-17
6	475	13.7	560	9	US-10-091-548-17
7	475	13.7	560	9	US-10-074-095-269
8	475	13.7	560	10	US-09-764-860-269
9	32	0.9	64	9	US-10-057-940-2
10	32	0.9	881	9	US-10-001-876-93
11	32	0.9	5908	9	US-10-239-676-93
12	32	0.9	32203	9	US-10-091-504-1849
13	32	0.9	32203	10	US-09-764-869-1849
14	32	0.9	1691139	9	US-10-067-514-1
15	29	0.8	148	10	US-09-969-373-172
16	29	0.8	158	9	US-09-754-853A-247
17	29	0.8	549	9	US-09-991-936-1786
18	29	0.8	2000	9	US-09-938-842A-5364
19	29	0.8	4096	9	US-10-037-598-27

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Sequence 13, Appl
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94	23	0.7	1966	10	US-09-925-301-58	Sequence 58, Appl	167	22	0.6	23544	9	US-09-764-891-8517	Sequence 8517, Ap
95	23	0.7	2000	9	US-09-938-842A-3679	Sequence 3679, Ap	168	22	0.6	30781	9	US-10-092-308-37	Sequence 37, Appl
96	23	0.7	2000	9	US-09-938-842A-4634	Sequence 4634, Ap	169	22	0.6	32193	9	US-09-764-868-1508	Sequence 1508, Ap
97	23	0.7	5498	9	US-10-198-846-12674	Sequence 12674, A	170	22	0.6	32248	10	US-09-764-864-1769	Sequence 1769, Ap
98	23	0.7	5908	9	US-10-233-676-93	Sequence 93, Appl	171	22	0.6	32248	10	US-09-764-877-3487	Sequence 3487, Ap
99	23	0.7	6025	9	US-10-233-676-43	Sequence 43, Appl	172	22	0.6	38186	9	US-09-373-658-38	Sequence 38, Appl
100	23	0.7	7404	9	US-10-198-846-10404	Sequence 10404, A	173	22	0.6	53522	9	US-09-904-968A-1	Sequence 1, Appli
101	23	0.7	8588	9	US-10-233-676-177	Sequence 177, App	174	22	0.6	66804	10	US-09-740-041-3	Sequence 3, Appli
102	23	0.7	9566	10	US-09-764-864-1768	Sequence 1768, Ap	175	22	0.6	84539	10	US-09-962-436-36	Sequence 36, Appl
103	23	0.7	9566	10	US-09-764-877-3486	Sequence 3486, Ap	176	22	0.6	98865	10	US-09-770-689A-3	Sequence 3, Appli
104	23	0.7	11221	10	US-09-778-963A-3	Sequence 3, Appli	177	22	0.6	106344	10	US-09-910-185-10	Sequence 10, Appl
105	23	0.7	18648	10	US-09-954-456-11150	Sequence 1150, Ap	178	22	0.6	126112	10	US-09-804-474A-3	Sequence 3, Appli
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107	23	0.7	31718	9	US-09-764-872-813	Sequence 813, App	180	22	0.6	132893	9	US-10-161-510-1	Sequence 1, Appli
108	23	0.7	31718	9	US-09-764-891-9103	Sequence 9103, Ap	181	22	0.6	175561	9	US-10-017-721-3	Sequence 3, Appli
109	23	0.7	31718	9	US-09-764-891-9104	Sequence 9104, Ap	182	22	0.6	203654	10	US-09-820-905-3	Sequence 3, Appli
110	23	0.7	39776	9	US-10-160-293-3	Sequence 3, Appli	183	22	0.6	326014	10	US-09-731-231A-3	Sequence 3, Appli
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112	23	0.7	335913	9	US-09-754-853A-2	Sequence 2, Appli	185	22	0.6	1503841	9	US-09-946-807-1	Sequence 1, Appli
113	23	0.7	335913	9	US-09-754-853A-3	Sequence 3, Appli	186	22	0.6	1503841	10	US-09-795-668-1	Sequence 1, Appli
114	23	0.7	513509	9	US-09-754-853A-4	Sequence 4, Appli	187	22	0.6	1691139	10	US-09-795-668-1	Sequence 1, Appli
115	22	0.6	159	10	US-09-969-373-1250	Sequence 1250, Ap	188	22	0.6	1067	10	US-10-067-514-1	Sequence 1, Appli
116	22	0.6	161	10	US-09-969-373-1319	Sequence 1319, Ap	189	21	0.6	70	10	US-09-969-373-1343	Sequence 1343, Ap
117	22	0.6	200	10	US-09-867-701-9056	Sequence 9056, Ap	190	21	0.6	98	10	US-09-969-373-448	Sequence 448, App
118	22	0.6	200	10	US-09-969-373-1045	Sequence 1045, Ap	191	21	0.6	106	10	US-09-867-701-4719	Sequence 4719, Ap
119	22	0.6	202	10	US-09-969-373-5	Sequence 5, Appli	192	21	0.6	110	10	US-09-969-373-714	Sequence 714, App
120	22	0.6	205	10	US-09-969-373-690	Sequence 690, App	193	21	0.6	150	10	US-09-969-373-94	Sequence 94, Appl
121	22	0.6	217	10	US-09-969-373-685	Sequence 685, App	194	21	0.6	160	9	US-09-754-853A-104	Sequence 104, App
122	22	0.6	271	10	US-09-969-373-317	Sequence 317, App	195	21	0.6	162	10	US-09-969-373-930	Sequence 930, App
123	22	0.6	284	10	US-09-969-373-2	Sequence 2, Appli	196	21	0.6	167	10	US-09-969-373-1331	Sequence 1331, Ap
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129	22	0.6	419	10	US-09-867-701-10237	Sequence 10237, A	202	21	0.6	188	9	US-09-754-853A-298	Sequence 298, Appl
130	22	0.6	426	10	US-09-960-352-13080	Sequence 13080, A	203	21	0.6	196	10	US-09-969-373-850	Sequence 850, App
131	22	0.6	431	10	US-09-969-373-739	Sequence 739, App	204	21	0.6	202	10	US-09-969-373-380	Sequence 380, App
132	22	0.6	496	10	US-09-867-701-9793	Sequence 9793, Ap	205	21	0.6	206	10	US-09-969-373-1214	Sequence 1214, Ap
133	22	0.6	538	9	US-09-918-995-23771	Sequence 23771, A	206	21	0.6	220	10	US-09-969-373-794	Sequence 794, App
134	22	0.6	549	9	US-09-991-936-1711	Sequence 1711, Ap	207	21	0.6	223	10	US-09-969-373-1183	Sequence 1183, Ap
135	22	0.6	549	9	US-09-991-936-1801	Sequence 1801, Ap	208	21	0.6	227	9	US-09-754-853A-152	Sequence 152, App
136	22	0.6	748	10	US-09-910-943-370	Sequence 370, App	209	21	0.6	232	10	US-09-969-373-863	Sequence 863, App
137	22	0.6	819	9	US-09-822-846-232	Sequence 232, App	210	21	0.6	237	10	US-09-969-373-800	Sequence 800, App
138	22	0.6	1167	9	US-09-804-409A-18	Sequence 18, Appl	211	21	0.6	239	9	US-09-784-891-7091	Sequence 7091, Ap
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163	22	0.6	11836	9	US-10-239-676-102	Sequence 102, App	236	21	0.6	466	9	US-10-198-846-12101	Sequence 12101, A
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272	21	0.6	800	9	US-10-198-846-3900	Sequence 3900, Ap	c 345	21	0.6	7260	10	US-09-919-497-24	Sequence 24, Appli
273	21	0.6	832	9	US-09-974-879-37	Sequence 37, Appli	c 346	21	0.6	7260	10	US-09-880-107-3739	Sequence 3739, Ap
274	21	0.6	832	9	US-09-305-736-37	Sequence 37, Appli	c 347	21	0.6	7448	9	US-10-270-333-82	Sequence 82, Appli
c 275	21	0.6	839	8	US-08-927-939-51	Sequence 51, Appli	c 348	21	0.6	7606	9	US-10-074-095-800	Sequence 800, App
276	21	0.6	879	10	US-09-764-853-13	Sequence 13, Appli	c 349	21	0.6	7606	10	US-09-764-860-800	Sequence 801, App
c 277	21	0.6	925	9	US-10-198-846-4101	Sequence 4101, Ap	c 350	21	0.6	7608	9	US-10-074-095-801	Sequence 801, App
c 278	21	0.6	950	9	US-10-198-846-7276	Sequence 7276, Ap	c 351	21	0.6	7608	10	US-09-764-860-801	Sequence 801, App
c 279	21	0.6	955	9	US-10-037-270-228	Sequence 228, App	c 352	21	0.6	7739	10	US-09-764-877-3189	Sequence 3189, Ap
c 280	21	0.6	955	9	US-09-938-842A-3324	Sequence 3324, Ap	c 353	21	0.6	8205	9	US-09-860-670-276	Sequence 276, App
c 281	21	0.6	1232	9	US-10-198-846-7269	Sequence 7269, Ap	c 354	21	0.6	8701	9	US-10-052-154-1976	Sequence 1976, Ap
282	21	0.6	1261	9	US-10-198-846-10840	Sequence 10840, A	c 355	21	0.6	8701	10	US-09-764-847-1976	Sequence 1976, Ap
283	21	0.6	1453	10	US-09-764-877-2774	Sequence 2774, Ap	c 356	21	0.6	8794	9	US-09-764-891-8933	Sequence 8933, Ap
c 284	21	0.6	1503	9	US-10-198-846-14076	Sequence 14076, A	c 357	21	0.6	9496	9	US-09-764-891-5542	Sequence 5542, Ap
c 285	21	0.6	1524	9	US-09-922-405B-1	Sequence 1, Appli	c 358	21	0.6	9821	9	US-09-764-891-5933	Sequence 5933, Ap
c 286	21	0.6	1524	9	US-10-066-474-1	Sequence 1, Appli	c 359	21	0.6	9824	9	US-09-764-891-5934	Sequence 5934, Ap
287	21	0.6	1550	10	US-09-764-877-2178	Sequence 2178, Ap	c 360	21	0.6	9887	9	US-10-000-639-7	Sequence 7, Appli
288	21	0.6	1600	10	US-09-753-436-117	Sequence 117, App	c 361	21	0.6	10619	9	US-10-239-676-1	Sequence 1, Appli
289	21	0.6	1707	10	US-09-884-901-7	Sequence 7, Appli	c 362	21	0.6	10758	9	US-10-091-504-1647	Sequence 1647, Ap
c 290	21	0.6	1837	9	US-09-823-846-502	Sequence 502, App	c 363	21	0.6	10758	9	US-10-091-504-1650	Sequence 1650, Ap
c 291	21	0.6	1971	10	US-09-864-761-13921	Sequence 13921, A	c 364	21	0.6	10758	10	US-09-764-869-1647	Sequence 1647, Ap
292	21	0.6	1991	10	US-09-848-852A-4	Sequence 4, Appli	c 365	21	0.6	10758	10	US-09-764-869-1650	Sequence 1650, Ap
c 293	21	0.6	2000	9	US-09-938-842A-2717	Sequence 2717, Ap	c 366	21	0.6	10759	10	US-09-764-869-1649	Sequence 1649, Ap
c 294	21	0.6	2000	9	US-09-938-842A-3293	Sequence 3293, Ap	c 367	21	0.6	10759	10	US-09-764-869-1649	Sequence 1649, Ap
c 295	21	0.6	2000	9	US-09-938-842A-3384	Sequence 3384, Ap	c 368	21	0.6	11036	9	US-10-239-676-117	Sequence 117, App
296	21	0.6	2000	9	US-09-938-842A-3641	Sequence 3641, Ap	c 369	21	0.6	11036	9	US-10-239-676-118	Sequence 118, App
c 297	21	0.6	2000	9	US-09-938-842A-4474	Sequence 4474, Ap	c 370	21	0.6	11036	9	US-10-239-676-118	Sequence 118, App
c 298	21	0.6	2000	9	US-09-938-842A-4951	Sequence 4951, Ap	c 371	21	0.6	11809	9	US-09-764-891-10172	Sequence 10172, A
c 299	21	0.6	2000	9	US-09-938-842A-4998	Sequence 4998, Ap	c 372	21	0.6	11821	10	US-09-764-877-2857	Sequence 2857, Ap
300	21	0.6	2004	9	US-09-938-842A-5078	Sequence 5078, Ap	c 373	21	0.6	11870	9	US-09-764-891-10016	Sequence 10016, A
301	21	0.6	2004	10	US-09-887-576-159	Sequence 159, App	c 374	21	0.6	11870	9	US-09-764-891-10017	Sequence 10017, A
c 302	21	0.6	2012	10	US-09-887-576-242	Sequence 242, App	c 375	21	0.6	12192	9	US-10-074-095-629	Sequence 629, App
303	21	0.6	2027	9	US-10-132-652-1	Sequence 1, Appli	c 376	21	0.6	12192	10	US-09-764-860-629	Sequence 629, App
304	21	0.6	2029	9	US-10-037-270-306	Sequence 306, App	c 377	21	0.6	13606	9	US-10-239-676-166	Sequence 166, App
c 305	21	0.6	2029	9	US-10-037-270-306	Sequence 306, App	c 378	21	0.6	13743	9	US-09-764-872-615	Sequence 615, App
306	21	0.6	2080	9	US-10-037-270-305	Sequence 305, App	c 379	21	0.6	13996	9	US-10-125-540-602	Sequence 602, App
c 307	21	0.6	2080	9	US-10-037-270-305	Sequence 305, App	c 380	21	0.6	13996	9	US-10-125-540-602	Sequence 602, App
308	21	0.6	2297	9	US-09-764-891-8760	Sequence 8760, Ap	c 381	21	0.6	13996	10	US-09-764-870-602	Sequence 602, App
309	21	0.6	2297	9	US-09-764-891-8763	Sequence 8763, Ap	c 382	21	0.6	13996	10	US-09-764-870-602	Sequence 602, App
310	21	0.6	2563	9	US-09-764-891-8395	Sequence 8395, App	c 383	21	0.6	14001	9	US-10-125-540-601	Sequence 601, App
311	21	0.6	2613	10	US-09-822-830A-518	Sequence 518, App	c 384	21	0.6	14001	9	US-10-125-540-601	Sequence 601, App

385	21	0.6	14001	10	US-09-764-870-601	Sequence 601, App	c 458	21	0.6	80595	9	US-09-728-552-3	Sequence 3, Appli
386	21	0.6	14001	10	US-09-764-870-601	Sequence 601, App	c 459	21	0.6	81826	9	US-10-175-523-197	Sequence 197, App
387	21	0.6	14040	9	US-09-764-891-5478	Sequence 5478, App	c 460	21	0.6	82938	9	US-09-818-657-3	Sequence 3, Appli
388	21	0.6	14040	9	US-09-764-891-5478	Sequence 5478, App	c 461	21	0.6	84539	9	US-09-962-436-36	Sequence 36, Appli
389	21	0.6	14093	10	US-10-092-154-1744	Sequence 1744, App	c 462	21	0.6	99014	10	US-09-880-107-3428	Sequence 3428, Ap
390	21	0.6	14093	10	US-09-764-847-1744	Sequence 1744, App	c 463	21	0.6	108359	9	US-10-191-807-3	Sequence 3, Appli
391	21	0.6	15362	10	US-09-764-877-2856	Sequence 2856, App	c 464	21	0.6	110079	9	US-10-175-523-96	Sequence 96, Appli
392	21	0.6	15335	10	US-09-764-877-2856	Sequence 2856, App	c 465	21	0.6	111282	12	US-10-094-989-3	Sequence 3, Appli
393	21	0.6	15732	9	US-10-239-676-96	Sequence 96, Appli	c 466	21	0.6	116592	10	US-09-818-512-3	Sequence 3, Appli
394	21	0.6	17142	9	US-10-239-676-99	Sequence 99, Appli	c 467	21	0.6	116840	9	US-10-020-141-3	Sequence 3, Appli
395	21	0.6	17419	9	US-10-239-676-100	Sequence 100, App	c 468	21	0.6	118951	9	US-10-161-572-11	Sequence 11, Appli
396	21	0.6	17419	9	US-10-239-676-100	Sequence 100, App	c 469	21	0.6	126512	10	US-09-804-474A-3	Sequence 3, Appli
397	21	0.6	17450	9	US-09-764-891-8641	Sequence 8641, App	c 470	21	0.6	127197	9	US-09-754-853A-1	Sequence 3, Appli
398	21	0.6	17498	9	US-10-074-095-798	Sequence 798, App	c 471	21	0.6	148567	9	US-10-254-869-3	Sequence 3, Appli
399	21	0.6	17498	10	US-09-764-860-798	Sequence 798, App	c 472	21	0.6	148567	10	US-09-801-876B-3	Sequence 3, Appli
400	21	0.6	18408	9	US-09-764-891-7441	Sequence 7441, App	c 473	21	0.6	172637	10	US-09-805-458A-3	Sequence 3, Appli
401	21	0.6	18408	9	US-09-764-891-7441	Sequence 7441, App	c 474	21	0.6	174424	10	US-09-967-768A-314	Sequence 314, App
402	21	0.6	18409	9	US-09-764-868-1457	Sequence 1457, App	c 475	21	0.6	183337	9	US-10-020-141-5	Sequence 5, Appli
403	21	0.6	20268	9	US-10-072-349-173	Sequence 173, App	c 476	21	0.6	185695	9	US-10-020-141-11	Sequence 11, Appli
404	21	0.6	20268	10	US-09-764-855-173	Sequence 173, App	c 477	21	0.6	185695	9	US-10-017-721-1	Sequence 1, Appli
405	21	0.6	21234	12	US-10-109-854-3	Sequence 3, Appli	c 478	21	0.6	203654	10	US-09-820-905-3	Sequence 3, Appli
406	21	0.6	21936	9	US-09-764-891-8807	Sequence 8807, App	c 479	21	0.6	225883	9	US-10-175-523-57	Sequence 57, Appli
407	21	0.6	21936	9	US-09-764-891-8446	Sequence 8446, App	c 480	21	0.6	235033	9	US-10-301-844-1	Sequence 1, Appli
408	21	0.6	23603	9	US-09-860-670-264	Sequence 264, App	c 481	21	0.6	237326	9	US-10-301-844-2	Sequence 2, Appli
409	21	0.6	23613	9	US-09-860-670-258	Sequence 258, App	c 482	21	0.6	335913	9	US-09-754-853A-2	Sequence 2, Appli
410	21	0.6	24023	9	US-10-094-679-1	Sequence 1, Appli	c 483	21	0.6	335913	9	US-09-754-853A-3	Sequence 3, Appli
411	21	0.6	24218	9	US-09-860-670-263	Sequence 263, App	c 484	21	0.6	659158	9	US-09-771-208-20	Sequence 20, Appli
412	21	0.6	25423	9	US-10-072-349-193	Sequence 193, App	c 485	21	0.6	684973	10	US-09-263-959-1	Sequence 1, Appli
413	21	0.6	25423	10	US-09-764-855-193	Sequence 193, App	c 486	21	0.6	89	10	US-09-969-373-1247	Sequence 1247, App
414	21	0.6	25424	9	US-10-072-349-194	Sequence 194, App	c 487	20	0.6	94	10	US-09-969-373-1228	Sequence 1228, Ap
415	21	0.6	25424	10	US-09-764-855-194	Sequence 194, App	c 488	20	0.6	108	10	US-09-969-373-1338	Sequence 1338, Ap
416	21	0.6	25701	9	US-09-764-891-9766	Sequence 9766, App	c 489	20	0.6	111	10	US-09-969-373-1205	Sequence 1205, Ap
417	21	0.6	25758	9	US-09-764-891-9765	Sequence 9765, App	c 490	20	0.6	111	10	US-09-969-373-1205	Sequence 1205, Ap
418	21	0.6	26320	9	US-10-166-221-3	Sequence 3, Appli	c 491	20	0.6	123	10	US-09-969-373-539	Sequence 539, App
419	21	0.6	27118	9	US-09-764-891-10230	Sequence 10230, A	c 492	20	0.6	123	10	US-09-969-373-235	Sequence 235, App
420	21	0.6	31154	9	US-09-764-891-8396	Sequence 8396, App	c 493	20	0.6	129	10	US-09-969-373-747	Sequence 747, App
421	21	0.6	31168	9	US-09-764-868-1464	Sequence 1464, App	c 494	20	0.6	131	10	US-09-969-373-809	Sequence 809, App
422	21	0.6	31314	10	US-09-764-877-3875	Sequence 3875, App	c 495	20	0.6	132	10	US-09-969-373-868	Sequence 868, App
423	21	0.6	31474	9	US-09-764-891-8149	Sequence 8149, App	c 496	20	0.6	135	10	US-09-969-373-767	Sequence 767, App
424	21	0.6	31994	9	US-09-764-904-71	Sequence 71, Appli	c 497	20	0.6	135	10	US-09-969-373-1018	Sequence 1018, Ap
425	21	0.6	31994	9	US-10-091-548-71	Sequence 71, Appli	c 498	20	0.6	137	10	US-09-969-373-1223	Sequence 1223, Ap
426	21	0.6	31994	9	US-10-074-095-599	Sequence 599, App	c 499	20	0.6	137	10	US-09-969-373-1223	Sequence 1223, Ap
427	21	0.6	31994	10	US-09-764-860-599	Sequence 599, App	c 500	20	0.6	138	10	US-09-864-864-101	Sequence 101, App
428	21	0.6	32042	9	US-10-118-984-44	Sequence 44, Appli	c 501	20	0.6	142	10	US-09-969-373-177	Sequence 177, App
429	21	0.6	32042	10	US-09-728-721-63	Sequence 63, Appli	c 502	20	0.6	142	10	US-09-969-373-210	Sequence 210, App
430	21	0.6	32082	9	US-09-764-891-9679	Sequence 9679, App	c 503	20	0.6	143	10	US-09-969-373-829	Sequence 829, App
431	21	0.6	32146	9	US-10-074-095-797	Sequence 797, App	c 504	20	0.6	143	10	US-09-969-373-1272	Sequence 1272, Ap
432	21	0.6	32169	10	US-09-764-860-797	Sequence 797, App	c 505	20	0.6	144	10	US-09-969-373-698	Sequence 698, App
433	21	0.6	32169	9	US-09-764-891-8605	Sequence 8605, App	c 506	20	0.6	147	9	US-09-754-853A-354	Sequence 354, App
434	21	0.6	32185	10	US-09-764-877-3171	Sequence 3171, App	c 507	20	0.6	148	10	US-09-969-373-429	Sequence 429, Appli
435	21	0.6	32189	9	US-09-764-891-8604	Sequence 8604, App	c 508	20	0.6	149	10	US-09-969-373-429	Sequence 429, Appli
436	21	0.6	32190	9	US-09-860-670-255	Sequence 255, App	c 509	20	0.6	150	10	US-09-969-373-94	Sequence 94, Appli
437	21	0.6	32195	9	US-10-102-627-92	Sequence 92, Appli	c 510	20	0.6	152	9	US-09-754-853A-227	Sequence 227, App
438	21	0.6	32220	10	US-09-764-877-3933	Sequence 3933, App	c 511	20	0.6	152	9	US-09-969-373-833	Sequence 833, App
439	21	0.6	32248	9	US-10-074-095-802	Sequence 802, App	c 512	20	0.6	153	9	US-09-969-373-1380	Sequence 1380, Ap
440	21	0.6	32248	10	US-09-764-860-802	Sequence 802, App	c 513	20	0.6	153	10	US-09-754-853A-363	Sequence 363, App
441	21	0.6	32249	9	US-09-860-670-260	Sequence 260, App	c 514	20	0.6	153	10	US-09-864-761-26437	Sequence 26437, A
442	21	0.6	32249	9	US-09-860-670-260	Sequence 260, App	c 515	20	0.6	153	10	US-09-969-373-173	Sequence 173, App
443	21	0.6	32429	10	US-09-764-891-7364	Sequence 7364, App	c 516	20	0.6	153	10	US-09-969-373-1194	Sequence 1194, App
444	21	0.6	32429	10	US-09-880-107-2125	Sequence 2125, App	c 517	20	0.6	158	10	US-09-969-373-533	Sequence 533, App
445	21	0.6	38186	9	US-09-373-658-38	Sequence 38, Appli	c 518	20	0.6	168	10	US-09-969-373-203	Sequence 203, App
446	21	0.6	40090	10	US-09-820-004-3	Sequence 3, Appli	c 519	20	0.6	170	10	US-09-969-373-82	Sequence 82, Appli
447	21	0.6	43950	12	US-10-060-332-3	Sequence 3, Appli	c 520	20	0.6	173	10	US-09-969-373-1083	Sequence 1083, Ap
448	21	0.6	46050	10	US-09-820-003A-3	Sequence 3, Appli	c 521	20	0.6	174	9	US-09-754-853A-276	Sequence 276, App
449	21	0.6	48436	10	US-09-927-602-38	Sequence 38, Appli	c 522	20	0.6	178	10	US-09-969-373-972	Sequence 972, App
450	21	0.6	49984	10	US-09-739-457-5	Sequence 5, Appli	c 523	20	0.6	180	10	US-09-969-373-1248	Sequence 1248, Ap
451	21	0.6	50000	9	US-10-060-763-4	Sequence 4, Appli	c 524	20	0.6	184	9	US-09-754-853A-292	Sequence 292, App
452	21	0.6	50354	10	US-09-742-311-3	Sequence 3, Appli	c 525	20	0.6	186	10	US-09-969-373-1464	Sequence 1464, Ap
453	21	0.6	53542	10	US-09-801-574-61	Sequence 61, Appli	c 526	20	0.6	190	9	US-09-796-692-4244	Sequence 4244, Ap
454	21	0.6	57130	10	US-09-835-081-3	Sequence 1, Appli	c 527	20	0.6	190	9	US-10-040-862-4244	Sequence 4244, Ap
455	21	0.6	64779	9	US-10-041-856-1	Sequence 1, Appli	c 528	20	0.6	193	10	US-09-969-373-253	Sequence 253, App
456	21	0.6	66686	10	US-09-736-960-86	Sequence 86, Appli	c 529	20	0.6	194	10	US-09-969-373-1113	Sequence 1113, Ap
457	21	0.6	80246	9	US-09-728-552-4	Sequence 4, Appli	c 530	20	0.6	194	10	US-09-969-373-1217	Sequence 1217, Ap

531	20	0.6	197	10	US-09-369-373-1022	Sequence 1022, Ap	604	20	0.6	403	10	US-09-878-574-3960	Sequence 3960, Ap
532	20	0.6	199	10	US-09-369-373-931	Sequence 931, App	c 605	20	0.6	407	10	US-09-864-761-3134	Sequence 3134, Ap
533	20	0.6	199	10	US-09-369-373-1193	Sequence 1193, Ap	c 606	20	0.6	407	10	US-09-969-373-1315	Sequence 1315, Ap
c 534	20	0.6	203	10	US-09-369-373-961	Sequence 961, App	c 607	20	0.6	408	9	US-09-946-807-1477	Sequence 1477, Ap
535	20	0.6	205	9	US-09-754-853A-310	Sequence 310, App	c 608	20	0.6	408	9	US-09-918-995-5372	Sequence 5372, Ap
c 536	20	0.6	209	10	US-09-369-373-1107	Sequence 1107, Ap	c 609	20	0.6	408	10	US-09-795-668-1477	Sequence 1477, Ap
c 537	20	0.6	212	10	US-09-369-373-1097	Sequence 1097, Ap	c 610	20	0.6	408	10	US-09-969-373-236	Sequence 236, App
538	20	0.6	217	9	US-10-060-036-2965	Sequence 2965, Ap	c 611	20	0.6	411	10	US-09-918-995-33135	Sequence 33135, A
c 539	20	0.6	219	10	US-09-369-373-246	Sequence 246, App	c 612	20	0.6	416	9	US-09-803-719-1868	Sequence 1868, Ap
540	20	0.6	230	10	US-09-369-373-110	Sequence 110, App	c 613	20	0.6	417	9	US-09-969-373-237	Sequence 237, App
541	20	0.6	230	10	US-09-369-373-111	Sequence 111, App	c 614	20	0.6	419	10	US-09-918-995-3758	Sequence 3758, Ap
542	20	0.6	234	10	US-09-369-373-1527	Sequence 1527, Ap	c 615	20	0.6	420	10	US-09-925-297-370	Sequence 10528, A
c 543	20	0.6	238	9	US-09-754-853A-155	Sequence 155, App	c 616	20	0.6	421	10	US-09-867-701-10528	Sequence 10528, A
544	20	0.6	241	9	US-10-091-504-188	Sequence 188, App	c 617	20	0.6	430	9	US-09-918-995-34767	Sequence 34767, A
c 545	20	0.6	241	10	US-09-764-869-188	Sequence 188, App	c 618	20	0.6	431	9	US-09-918-995-17488	Sequence 17488, A
c 546	20	0.6	241	10	US-09-369-373-396	Sequence 396, App	c 619	20	0.6	431	9	US-09-918-995-16881	Sequence 16881, A
c 547	20	0.6	243	10	US-09-369-373-874	Sequence 874, App	c 620	20	0.6	436	10	US-09-867-701-7782	Sequence 7782, Ap
c 548	20	0.6	243	10	US-09-369-373-874	Sequence 874, App	c 621	20	0.6	437	9	US-09-918-995-17116	Sequence 17116, A
c 549	20	0.6	252	10	US-09-369-373-1061	Sequence 1061, Ap	c 622	20	0.6	443	9	US-09-969-708-377	Sequence 27709, A
c 550	20	0.6	256	10	US-09-369-373-1312	Sequence 1312, Ap	c 623	20	0.6	448	10	US-09-918-995-2177	Sequence 2177, Ap
551	20	0.6	262	10	US-09-954-456-1999	Sequence 1999, Ap	c 624	20	0.6	453	9	US-09-867-701-9387	Sequence 9387, Ap
552	20	0.6	262	10	US-09-880-107-827	Sequence 827, App	c 625	20	0.6	454	10	US-09-864-761-14466	Sequence 14466, A
553	20	0.6	263	10	US-09-867-701-9223	Sequence 9223, Ap	c 626	20	0.6	458	10	US-09-907-969-3	Sequence 1, Appli
554	20	0.6	265	10	US-09-369-373-1074	Sequence 1074, Ap	c 627	20	0.6	461	9	US-09-884-441-1	Sequence 1, Appli
555	20	0.6	266	9	US-09-754-853A-161	Sequence 161, App	c 628	20	0.6	461	10	US-09-867-701-10022	Sequence 10022, A
c 556	20	0.6	266	9	US-09-754-853A-161	Sequence 161, App	c 629	20	0.6	461	9	US-09-918-995-34582	Sequence 34582, Ap
c 557	20	0.6	275	10	US-09-867-701-8770	Sequence 8770, Ap	c 630	20	0.6	461	9	US-09-918-995-24980	Sequence 24980, A
c 558	20	0.6	275	10	US-09-867-701-8897	Sequence 8897, Ap	c 631	20	0.6	470	9	US-09-918-995-26052	Sequence 26052, A
c 559	20	0.6	276	10	US-09-369-373-630	Sequence 630, App	c 632	20	0.6	473	9	US-09-918-995-34501	Sequence 34501, A
c 560	20	0.6	276	10	US-09-369-373-1465	Sequence 1465, Ap	c 633	20	0.6	474	9	US-09-918-995-21585	Sequence 21585, A
c 561	20	0.6	280	9	US-10-037-598-21	Sequence 21, Appl	c 634	20	0.6	480	9	US-09-918-995-19161	Sequence 19161, A
c 562	20	0.6	291	9	US-09-803-719-1252	Sequence 1252, Ap	c 635	20	0.6	481	9	US-09-918-995-25363	Sequence 25363, A
563	20	0.6	291	9	US-09-803-719-1453	Sequence 1453, Ap	c 636	20	0.6	484	9	US-09-918-995-4434	Sequence 4434, Ap
564	20	0.6	293	10	US-09-764-877-2750	Sequence 2750, Ap	c 637	20	0.6	485	10	US-09-864-761-10125	Sequence 10125, A
565	20	0.6	294	10	US-09-867-701-9509	Sequence 9509, Ap	c 638	20	0.6	489	9	US-09-918-995-30715	Sequence 30715, A
c 566	20	0.6	296	10	US-09-369-373-974	Sequence 974, App	c 639	20	0.6	489	9	US-09-918-995-26874	Sequence 26874, A
c 567	20	0.6	297	9	US-10-091-504-2400	Sequence 2400, Ap	c 640	20	0.6	489	9	US-09-918-995-17588	Sequence 17588, A
c 568	20	0.6	297	9	US-09-918-995-1002	Sequence 1002, Ap	c 641	20	0.6	490	9	US-09-918-995-28954	Sequence 28954, A
c 569	20	0.6	297	9	US-09-918-995-1002	Sequence 1002, Ap	c 642	20	0.6	492	9	US-10-198-846-1525	Sequence 1525, Ap
c 570	20	0.6	297	10	US-09-764-869-2400	Sequence 2400, Ap	c 643	20	0.6	501	9	US-09-918-995-14033	Sequence 14033, A
c 571	20	0.6	300	9	US-10-033-329-3	Sequence 3, Appli	c 644	20	0.6	509	10	US-10-091-504-2116	Sequence 2116, Ap
c 572	20	0.6	304	9	US-10-091-504-2406	Sequence 2406, Ap	c 645	20	0.6	509	10	US-09-764-869-2115	Sequence 2115, Ap
c 573	20	0.6	304	10	US-09-764-869-2406	Sequence 2406, Ap	c 646	20	0.6	509	10	US-09-764-869-2116	Sequence 2116, Ap
c 574	20	0.6	313	10	US-09-369-373-1463	Sequence 1463, Ap	c 647	20	0.6	509	10	US-09-764-877-3964	Sequence 3964, Ap
c 575	20	0.6	317	10	US-09-871-161-109	Sequence 109, App	c 648	20	0.6	509	10	US-09-764-877-3965	Sequence 3965, Ap
c 576	20	0.6	317	10	US-09-960-352-1366	Sequence 356, Ap	c 649	20	0.6	512	10	US-09-783-590-2879	Sequence 2879, Ap
c 577	20	0.6	318	9	US-09-764-891-7651	Sequence 7651, Ap	c 650	20	0.6	521	9	US-09-918-995-25752	Sequence 25752, A
c 578	20	0.6	322	10	US-09-369-373-1065	Sequence 1065, Ap	c 651	20	0.6	524	9	US-09-764-891-7075	Sequence 7075, Ap
c 579	20	0.6	325	10	US-09-369-373-1339	Sequence 1339, Ap	c 652	20	0.6	531	9	US-09-764-891-7076	Sequence 7076, Ap
580	20	0.6	332	9	US-09-803-719-1292	Sequence 1292, Ap	c 653	20	0.6	532	9	US-09-918-995-3769	Sequence 3769, Ap
581	20	0.6	334	10	US-09-867-701-9936	Sequence 9936, Ap	c 654	20	0.6	532	9	US-09-991-936-1786	Sequence 1786, Ap
582	20	0.6	337	10	US-09-764-877-3785	Sequence 3785, Ap	c 655	20	0.6	532	9	US-09-918-995-29443	Sequence 29443, A
c 583	20	0.6	341	9	US-09-907-969-136	Sequence 136, App	c 656	20	0.6	533	10	US-09-864-761-9392	Sequence 9392, Ap
c 584	20	0.6	341	10	US-09-884-441-136	Sequence 136, App	c 657	20	0.6	533	10	US-09-864-761-9392	Sequence 9392, Ap
c 585	20	0.6	356	10	US-09-369-373-825	Sequence 825, App	c 658	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 586	20	0.6	356	10	US-09-369-373-825	Sequence 825, App	c 659	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 587	20	0.6	356	10	US-09-369-373-827	Sequence 827, App	c 660	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 588	20	0.6	359	10	US-09-369-373-1006	Sequence 1006, App	c 661	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 589	20	0.6	373	10	US-09-962-436-492	Sequence 492, App	c 662	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 590	20	0.6	375	10	US-09-369-373-1369	Sequence 1369, Ap	c 663	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 591	20	0.6	377	9	US-09-918-995-29856	Sequence 29856, A	c 664	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
592	20	0.6	388	9	US-09-918-995-27277	Sequence 27277, A	c 665	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
593	20	0.6	399	9	US-09-918-995-16899	Sequence 16899, A	c 666	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
594	20	0.6	400	9	US-09-918-995-33367	Sequence 33367, A	c 667	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
595	20	0.6	401	9	US-09-946-807-275	Sequence 275, App	c 668	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 596	20	0.6	401	9	US-09-946-807-275	Sequence 275, App	c 669	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 597	20	0.6	401	9	US-09-946-807-1090	Sequence 1090, Ap	c 670	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
598	20	0.6	401	10	US-09-795-668-274	Sequence 274, App	c 671	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
599	20	0.6	401	10	US-09-795-668-275	Sequence 275, App	c 672	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 600	20	0.6	401	10	US-09-795-668-1090	Sequence 1090, Ap	c 673	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 601	20	0.6	401	10	US-09-795-668-274	Sequence 274, App	c 674	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 602	20	0.6	401	10	US-09-795-668-275	Sequence 275, App	c 675	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A
c 603	20	0.6	401	10	US-09-795-668-1090	Sequence 1090, Ap	c 676	20	0.6	533	10	US-09-918-995-29443	Sequence 29443, A

677	20	0.6	650	10	US-09-263-959-385	Sequence 385, Appl	c	750	20	0.6	2000	9	US-09-938-842A-4888	Sequence 4888, Ap
678	20	0.6	656	9	US-09-986-480-84	Sequence 84, Appl		751	20	0.6	2000	9	US-09-938-842A-4951	Sequence 4951, Ap
679	20	0.6	658	9	US-09-893-191A-143	Sequence 143, Appl		752	20	0.6	2000	9	US-09-938-842A-4963	Sequence 4963, Ap
680	20	0.6	659	10	US-09-764-877-2785	Sequence 2785, Ap		753	20	0.6	2000	9	US-09-938-842A-4994	Sequence 4994, Ap
681	20	0.6	679	9	US-10-073-961-633	Sequence 633, Appl	c	754	20	0.6	2000	9	US-09-938-842A-5087	Sequence 5087, Ap
682	20	0.6	679	10	US-09-764-887-633	Sequence 633, Appl	c	755	20	0.6	2000	9	US-09-938-842A-5099	Sequence 5099, Ap
683	20	0.6	683	10	US-09-764-877-2393	Sequence 2393, Ap	c	756	20	0.6	2000	9	US-09-938-842A-5122	Sequence 5122, Ap
684	20	0.6	696	10	US-09-910-943-288	Sequence 288, Appl	c	757	20	0.6	2000	9	US-09-938-842A-5287	Sequence 5287, Ap
685	20	0.6	714	9	US-10-198-846-6487	Sequence 6487, Ap	c	758	20	0.6	2002	10	US-09-887-576-324	Sequence 324, Appl
686	20	0.6	725	9	US-10-202-193-295	Sequence 295, Appl	c	759	20	0.6	2003	10	US-09-887-576-15	Sequence 15, Appl
687	20	0.6	736	9	US-10-202-193-294	Sequence 294, Appl	c	760	20	0.6	2018	9	US-10-091-504-1568	Sequence 1568, Ap
688	20	0.6	736	10	US-09-772-134B-53	Sequence 53, Appl	c	761	20	0.6	2018	10	US-09-764-869-1568	Sequence 1568, Ap
689	20	0.6	803	10	US-10-091-504-2437	Sequence 2437, Ap	c	762	20	0.6	2009	9	US-10-244-633-5	Sequence 5, Appl
690	20	0.6	803	10	US-09-764-869-2437	Sequence 2437, Ap	c	763	20	0.6	2119	9	US-10-091-504-2439	Sequence 2439, Ap
691	20	0.6	867	9	US-09-764-891-8794	Sequence 8794, Ap	c	764	20	0.6	2119	10	US-09-764-869-2439	Sequence 2439, Ap
692	20	0.6	875	9	US-10-198-846-3516	Sequence 3516, Ap	c	765	20	0.6	2142	9	US-10-091-504-2440	Sequence 2440, Ap
693	20	0.6	884	9	US-10-198-846-3350	Sequence 3350, Ap	c	766	20	0.6	2142	10	US-09-764-869-2440	Sequence 2440, Ap
694	20	0.6	921	9	US-10-198-846-7263	Sequence 7263, Ap	c	767	20	0.6	2172	9	US-09-966-880A-15	Sequence 15, Appl
695	20	0.6	942	9	US-09-764-891-9845	Sequence 9845, Ap	c	768	20	0.6	2241	10	US-09-822-849A-230	Sequence 230, Appl
696	20	0.6	988	9	US-10-195-781A-1	Sequence 1, Appl	c	769	20	0.6	2390	9	US-09-374-046A-91	Sequence 91, Appl
697	20	0.6	997	10	US-09-764-877-2210	Sequence 2210, Ap	c	770	20	0.6	2410	10	US-09-771-161A-66	Sequence 66, Appl
698	20	0.6	1005	9	US-10-079-854-102	Sequence 102, Appl	c	771	20	0.6	2437	9	US-09-764-904-102	Sequence 102, Appl
699	20	0.6	1005	9	US-10-074-095-301	Sequence 301, Appl	c	772	20	0.6	2437	9	US-10-091-548-102	Sequence 102, Appl
700	20	0.6	1005	10	US-09-764-878-102	Sequence 102, Appl	c	773	20	0.6	2437	9	US-10-074-095-1157	Sequence 1157, Ap
701	20	0.6	1005	10	US-09-764-860-301	Sequence 301, Appl	c	774	20	0.6	2437	10	US-09-764-860-1157	Sequence 1157, Ap
702	20	0.6	1060	10	US-09-764-877-2730	Sequence 2730, Appl	c	775	20	0.6	2460	9	US-10-198-846-11526	Sequence 11526, A
703	20	0.6	1086	10	US-09-529-063-6	Sequence 6, Appl	c	776	20	0.6	2547	10	US-09-764-877-2582	Sequence 2582, Ap
704	20	0.6	1149	9	US-10-198-846-4399	Sequence 4399, Ap	c	777	20	0.6	2550	10	US-09-764-864-318	Sequence 318, Appl
705	20	0.6	1151	9	US-09-974-879-105	Sequence 105, Appl	c	778	20	0.6	2567	9	US-09-510-332-146	Sequence 146, App
706	20	0.6	1151	9	US-09-305-736-105	Sequence 105, Appl	c	779	20	0.6	2600	9	US-10-073-961-526	Sequence 526, App
707	20	0.6	1360	9	US-10-198-846-12833	Sequence 12833, A	c	780	20	0.6	2600	10	US-09-764-887-526	Sequence 526, App
708	20	0.6	1382	9	US-10-092-154-1253	Sequence 1253, Ap	c	781	20	0.6	2750	9	US-09-822-846-63	Sequence 63, Appl
709	20	0.6	1382	10	US-09-764-847-1253	Sequence 1253, Ap	c	782	20	0.6	2769	9	US-10-119-926-105	Sequence 105, Appl
710	20	0.6	1442	9	US-10-146-130-1	Sequence 1, Appl	c	783	20	0.6	2818	9	US-09-966-880A-7	Sequence 7, Appl
711	20	0.6	1442	9	US-09-964-667-1	Sequence 1, Appl	c	784	20	0.6	2831	9	US-09-764-891-6097	Sequence 6097, Ap
712	20	0.6	1442	9	US-09-872-968-1	Sequence 1, Appl	c	785	20	0.6	2998	9	US-10-195-781A-3	Sequence 3, Appl
713	20	0.6	1442	9	US-10-092-934-1	Sequence 1, Appl	c	786	20	0.6	3023	9	US-10-066-443-4	Sequence 4, Appl
714	20	0.6	1442	9	US-10-153-334-53	Sequence 53, Appl	c	787	20	0.6	3023	10	US-10-256-889-4	Sequence 4, Appl
715	20	0.6	1442	9	US-10-198-069-48	Sequence 48, Appl	c	788	20	0.6	3023	10	US-09-900-236-4	Sequence 4, Appl
716	20	0.6	1442	10	US-09-964-666-1	Sequence 1, Appl	c	789	20	0.6	3190	9	US-10-153-668-165	Sequence 165, App
717	20	0.6	1442	10	US-09-964-412-1	Sequence 1, Appl	c	790	20	0.6	3381	9	US-09-764-891-5397	Sequence 5397, Ap
718	20	0.6	1491	9	US-09-938-842A-4918	Sequence 4918, Appl	c	791	20	0.6	3425	10	US-09-764-877-3888	Sequence 3888, Ap
719	20	0.6	1506	10	US-09-815-242-7845	Sequence 7845, Ap	c	792	20	0.6	3536	10	US-09-880-107-3271	Sequence 3271, Ap
720	20	0.6	1544	10	US-09-880-107-2122	Sequence 2122, Ap	c	793	20	0.6	3631	10	US-09-764-864-738	Sequence 738, App
721	20	0.6	1547	9	US-10-073-961-525	Sequence 525, Appl	c	794	20	0.6	3813	10	US-09-764-877-3325	Sequence 3325, Ap
722	20	0.6	1547	10	US-09-764-887-525	Sequence 525, Appl	c	795	20	0.6	3830	9	US-10-037-598-26	Sequence 26, Appl
723	20	0.6	1625	9	US-10-198-846-13305	Sequence 13305, A	c	796	20	0.6	3950	9	US-09-900-797-33	Sequence 33, Appl
724	20	0.6	1635	9	US-10-092-154-1075	Sequence 1075, Ap	c	797	20	0.6	3950	10	US-09-887-586A-33	Sequence 33, Appl
725	20	0.6	1635	10	US-09-764-847-1075	Sequence 1075, Ap	c	798	20	0.6	3950	10	US-09-903-012-33	Sequence 33, Appl
726	20	0.6	1681	9	US-09-986-480-40	Sequence 40, Appl	c	799	20	0.6	3971	9	US-09-764-891-5821	Sequence 5821, Ap
727	20	0.6	1704	9	US-10-198-846-10761	Sequence 10761, A	c	800	20	0.6	4071	9	US-10-091-504-2040	Sequence 2040, Ap
728	20	0.6	1764	10	US-09-947-027-3	Sequence 3, Appl	c	801	20	0.6	4071	10	US-09-764-869-2040	Sequence 2040, Ap
729	20	0.6	1764	12	US-10-091-009-3	Sequence 3, Appl	c	802	20	0.6	4394	10	US-09-764-877-2127	Sequence 2127, Ap
730	20	0.6	1803	10	US-09-887-576-268	Sequence 268, Appl	c	803	20	0.6	4400	10	US-09-764-877-2128	Sequence 2128, Ap
731	20	0.6	1823	9	US-09-938-842A-4744	Sequence 4744, Ap	c	804	20	0.6	4535	9	US-10-175-523-24	Sequence 24, Appl
732	20	0.6	1881	9	US-09-938-842A-3346	Sequence 3346, Ap	c	805	20	0.6	4589	9	US-09-764-891-8845	Sequence 8845, Ap
733	20	0.6	1897	10	US-09-799-777-85	Sequence 85, Appl	c	806	20	0.6	4590	9	US-09-764-891-8846	Sequence 8846, Ap
734	20	0.6	1956	10	US-09-828-830A-190	Sequence 190, Appl	c	807	20	0.6	4606	12	US-10-044-090-773	Sequence 773, Appl
735	20	0.6	1991	10	US-09-848-852A-4	Sequence 4, Appl	c	808	20	0.6	4824	9	US-10-171-581-82	Sequence 82, Appl
736	20	0.6	2000	9	US-09-938-842A-2717	Sequence 2717, Ap	c	809	20	0.6	4824	10	US-09-960-253-160	Sequence 160, Appl
737	20	0.6	2000	9	US-09-938-842A-2789	Sequence 2789, Ap	c	810	20	0.6	5150	9	US-09-764-904-94	Sequence 94, Appl
738	20	0.6	2000	9	US-09-938-842A-3254	Sequence 3254, Ap	c	811	20	0.6	5150	9	US-10-091-548-94	Sequence 94, Appl
739	20	0.6	2000	9	US-09-938-842A-3285	Sequence 3285, Ap	c	812	20	0.6	5150	9	US-10-074-095-1138	Sequence 1138, Ap
740	20	0.6	2000	9	US-09-938-842A-3330	Sequence 3330, Ap	c	813	20	0.6	5150	10	US-09-764-860-1138	Sequence 1138, Ap
741	20	0.6	2000	9	US-09-938-842A-3987	Sequence 3987, Ap	c	814	20	0.6	5159	10	US-09-764-877-3707	Sequence 3707, Ap
742	20	0.6	2000	9	US-09-938-842A-4246	Sequence 4246, Ap	c	815	20	0.6	5209	9	US-09-822-846-64	Sequence 64, Appl
743	20	0.6	2000	9	US-09-938-842A-4315	Sequence 4315, Ap	c	816	20	0.6	5242	9	US-09-764-891-8877	Sequence 8877, Ap
744	20	0.6	2000	9	US-09-938-842A-4413	Sequence 4413, Ap	c	817	20	0.6	5319	10	US-09-826-752-7	Sequence 7, Appl
745	20	0.6	2000	9	US-09-938-842A-4650	Sequence 4650, Ap	c	818	20	0.6	5345	9	US-09-764-868-1356	Sequence 1356, Ap
746	20	0.6	2000	9	US-09-938-842A-4679	Sequence 4679, Ap	c	819	20	0.6	5345	9	US-10-092-154-1729	Sequence 1729, Ap
747	20	0.6	2000	9	US-09-938-842A-4748	Sequence 4748, Ap	c	820	20	0.6	5345	10	US-09-764-847-1729	Sequence 1729, Ap
748	20	0.6	2000	9	US-09-938-842A-4854	Sequence 4854, Ap	c	821	20	0.6	5359	9	US-10-197-666A-139	Sequence 139, App
749	20	0.6	2000	9	US-09-938-842A-4871	Sequence 4871, Ap	c	822	20	0.6	5530	9	US-09-764-904-112	Sequence 112, App

823	20	0.6	5530	9	US-10-091-548-112	Sequence 112, App	c 896	20	0.6	10198	9	US-09-764-891-8744	Sequence 8744, Ap
824	20	0.6	5530	9	US-10-074-095-1167	Sequence 1167, Ap	897	20	0.6	10445	9	US-09-764-891-6380	Sequence 6380, Ap
825	20	0.6	5530	10	US-09-764-860-1167	Sequence 1167, Ap	898	20	0.6	10855	9	US-09-764-891-7965	Sequence 7965, Ap
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c 999 20 0.6 24218 9 US-09-860-670-263 Sequence 263, App
c1000 20 0.6 24533 9 US-09-764-868-1349 Sequence 1349, Ap

ALIGNMENTS

RESULT 1
US-09-764-904-89
; Sequence 89, Application US/09764904
; Patent No. US20020173454A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122
; CURRENT APPLICATION NUMBER: US/09/764,904
; CURRENT FILING DATE: 2001-01-17
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; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-904-89
Query Match 48.3%; Score 1677; DB 9; Length 2411;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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; PRIOR APPLICATION NUMBER: 60/237,037
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; PRIOR APPLICATION NUMBER: 60/237,040
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; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
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; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match 48.3%; Score 1677; DB 9; Length 2411;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGCTGCGCCTGGGGGCATCTTTGAATACAGGCTGGAGTTTGTGCATCCATTTACCAGAGA 60
Db 531 AGCTGCGCCTGGGGGCATCTTTGAATACAGGCTGGAGTTTGTGCATCCATTTACCAGAGA 590
Qy 61 CTAGGGCAAGAGGGCCCGGCACTGAGAAATCCAGCCCTCACACAGCTCAAGCCCTCG 120
Db 591 TTAGGGCAAGAGGGCCCGGCACTGAGAAATCCAGCCCTCACACAGCTCAAGCCCTCG 650
Qy 121 TGGTCCACAGTGGGACACTGAAATCAATTTTCTATTGAGTCTCTGCCCCCTTGCCCT 180
Db 651 TGGTCCACAGTGGGACACTGAAATCAATTTTCTATTGAGTCTCTGCCCCCTTGCCCT 710
Qy 181 GGGGAAATGAATCCCGGCTTTGATTTTACTAGGAAAGAGCCCTTATGTTTGCATAGAGC 240
Db 711 GGGGAAATGAATCCCGGCTTTGATTTTACTAGGAAAGAGCCCTTATGTTTGCATAGAGC 770
Qy 241 ATTCAGCTTTTCAAAATTAAGGGCTTGTAACTGTGAAGCACTCTACAGGAAAAATTAC 300
Db 771 ATTCAGCTTTTCAAAATTAAGGGCTTGTAACTGTGAAGCACTCTACAGGAAAAATTAC 830
Qy 301 AGTTTAAAAAGGATCGTGAATTTGGAGTGAGCTCCCAACCCCTGTAAAGGAGCCAGTC 360
Db 831 AGTTTAAAAAGGATCGTGAATTTGGAGTGAGCTCCCAACCCCTGTAAAGGAGCCAGTC 890
Qy 361 CGTGTCTTGTCTCCAGGCTTTAATGGAAGAGGCACTGATGCCCTAACTTGGCCCAACAGGAGTGGACCTAA 420
Db 891 CGTGTCTTGTCTCCAGGCTTTAATGGAAGAGGCACTGATGCCCTAACTTGGCCCAACAGGAGTGGACCTAA 950
Qy 421 AGAGGACAGCAAGCTCGGCCAGCCTGATGCCCTAACTTGGCCCAACAGGAGCTTAGAG 480
Db 951 AGAGGACAGCAAGCTCGGCCAGCCTGATGCCCTAACTTGGCCCAACAGGAGCTTAGAG 1010
Qy 481 CAGGAGCTCAAGATGGTATTATACCTCGGGAGGCTGGGGCAAGCTGGTGCAGGTT 540
Db 1011 CAGGAGCTCAAGATGGTATTATACCTCGGGAGGCTGGGGCAAGCTGGTGCAGGTT 1070

QY 541 GCTATTTTCATAGAACAAAGTCGCCAATTTAGGGTTTTTCCCTCCTAAGAGAT 600
Db 1071 GCTATTTTCATAGAACAAAGTCGCCAATTTAGGGTTTTTCCCTCCTAAGAGAT 1130
QY 601 GACATTCAGCTGCTTCAAAGCAACAGGCAAGGTCTGCTGAGACAATTGACCAAGAGGGGT 660
Db 1131 GACATTCAGCTGCTTCAAAGCAACAGGCAAGGTCTGCTGAGACAATTGACCAAGAGGGGT 1190
QY 661 GCTGCTGCTGCTCAGAGAGCCAGACTGCTCAAGGTTCGCGACGCGTCTGGGAGGGA 720
Db 1191 GCTGCTGCTGCTCAGAGAGCCAGACTGCTCAAGGTTCGCGACGCGTCTGGGAGGGA 1250
QY 721 GGGTCAATGCGCGCGAGGGAGGATGATGATCAAGGTTCGCGACGCGTCTGGGAGGGA 780
Db 1251 GGGTCAATGCGCGCGAGGGAGGATGATGATCAAGGTTCGCGACGCGTCTGGGAGGGA 1310
QY 781 CCGAGAAGGGTGCAGTGAGGGCCACAGACTTCAAGCTTGTGTCGACGCTCAGGAGCCA 840
Db 1311 CCGAGAAGGGTGCAGTGAGGGCCACAGACTTCAAGCTTGTGTCGACGCTCAGGAGCCA 1370
QY 841 TCCTGCACTCTCCCGGAGAGTGCCAGCCACAGCTGCACCCGCGCTCCAGACAGC 900
Db 1371 TCCTGCACTCTCCCGGAGAGTGCCAGCCACAGCTGCACCCGCGCTCCAGACAGC 1430
QY 901 CCAAGGACGAGCTGAAGCTGCGCTGTGCTCTGGGGCGCTGTCAGACTCCGCGCGGA 960
Db 1431 CCAAGGACGAGCTGAAGCTGCGCTGTGCTCTGGGGCGCTGTCAGACTCCGCGCGGA 1490
QY 961 ACTCATCTCAGCGCTGCCACACACAGCAGCAGCAGCTACAGCTGACCGCTGG 1020
Db 1491 ACTCATCTCAGCGCTGCCACACACAGCAGCAGCAGCTACAGCTGACCGCTGG 1550
QY 1021 TCACACCGTGGGACCCACAGCGCTTTGGGGGCTCGGCCACAAATCATCCAGGGCA 1080
Db 1551 TCACACCGTGGGACCCACAGCGCTTTGGGGGCTCGGCCACAAATCATCCAGGGCA 1610
QY 1081 TCGTCTCCAGGACAGCACATGATGAGCTGAGGCTCTGCTTCTCCGACGAGGTA 1140
Db 1611 TCGTCTCCAGGACAGCACATGATGAGCTGAGGCTCTGCTTCTCCGACGAGGTA 1670
QY 1141 GCAAGCTGGGCACTCGAACAGGAGCAGAACAGGCGCTCTGCTGTCGCTCCCGCATCT 1200
Db 1671 GCAAGCTGGGCACTCGAACAGGAGCAGAACAGGCGCTCTGCTGTCGCTCCCGCATCT 1730
QY 1201 CCACGAGAGTGAGCTCAGAGCTCAGAGCTGGAACAGAGCTGTTGAGAGGAGGCGGCC 1260
Db 1731 CCACGAGAGTGAGCTCAGAGCTCAGAGCTGGAACAGAGCTGTTGAGAGGAGGCGGCC 1790
QY 1261 TCCAGAAGCTGAGCGAGCTTTGAGGAGAGGAGCTTGCCTTCCAGCTGCGCTACGAGG 1320
Db 1791 TCCAGAAGCTGAGCGAGCTTTGAGGAGAGGAGCTTGCCTTCCAGCTGCGCTACGAGG 1850
QY 1321 AGCGGCGCGGCTGCGAGGAGCAGCTGAGGCGCGGAGCCTCAAGAGCGGCAACAGC 1380
Db 1851 AGCGGCGCGGCTGCGAGGAGCAGCTGAGGCGCGGAGCCTCAAGAGCGGCAACAGC 1910
QY 1381 TCAAGCAGGCTCGCAGAGAGCAGCGGCGGAGAGCTCTGACCTGAGGAGTACTGC 1440
Db 1911 TCAAGCAGGCTCGCAGAGAGCAGCGGCGGAGAGCTCTGACCTGAGGAGTACTGC 1970
QY 1441 AGCTTTCAGCAGGAGAGCGGAGCTCCGCGAGGAGCTCGAGAGCTCATGAGGAGCAGG 1500
Db 1971 AGCTTTCAGCAGGAGAGCGGAGCTCCGCGAGGAGCTCGAGAGCTCATGAGGAGCAGG 2030
QY 1501 ACCTCTGAGACCAAGCTCAGTCTTCTACGAGAGGAGAGCAGCTTCGCGCGCGCGC 1560
Db 2031 ACCTCTGAGACCAAGCTCAGTCTTCTACGAGAGGAGAGCAGCTTCGCGCGCGCGC 2090
QY 1561 TGGAGGAGCCAGTGGGAGGTGAGGCCACACAGGCTCATGGGTTTGGTGGTTCAGCGG 1620
Db 2091 TGGAGGAGCCAGTGGGAGGTGAGGCCACACAGGCTCATGGGTTTGGTGGTTCAGCGG 2150
QY 1621 TTTGGGCGCAGTACCCCTCTCTCTTCTGCTGCTGCGCAATAGCGTGCAGAACACAGACCG 1680

Db 2151 TTTGGGCGCAGTACCCCTCTCTCTTCTGCTGCGGCAATAGCTGCAACACAGACCG 2210
QY 1681 CGCAGGCAAGCGGGCTTAATGCTGCTTATACCCAAAGAGGGGCTCCCTGCAAC 1740
Db 2211 CGCAGGCAAGCGGGCTTAATGCTGCTTATACCCAAAGAGGGGCTCCCTGCAAC 2270
QY 1741 CATGTTGGGGATGCACTTACATCTGAGCTTCTCTGCTCCACCATCACCTCATGGC 1800
Db 2271 CATGTTGGGGATGCACTTACATCTGAGCTTCTCTGCTCCACCATCACCTCATGGC 2330
QY 1801 TCCTAGATTTTCAAGTTCCTCAAGTGAGCATTAAATCATGAAGCGGAGCAGATGACCA 1860
Db 2331 TCCTAGATTTTCAAGTTCCTCAAGTGAGCATTAAATCATGAAGCGGAGCAGATGACCA 2390
QY 1861 AGCCCAAGCAGGCTGTGGC 1881
Db 2391 AGCCCAAGCAGGCTGTGGC 2411

RESULT 4
US-09-764-860-1133
; Sequence 1133, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1133
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1133

Query Match 48.3%; Score 1677; DB 10; Length 2411;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCTGCGCGCTGGGGCATCTTGAATACAGGCTGGAGTTTGTCTCATCTTACCAGAGA 60
Db 531 AGCTGCGCGCTGGGGCATCTTGAATACAGGCTGGAGTTTGTCTCATCTTACCAGAGA 590
QY 61 CTAGGGCAAGAGGAGGCGCCAGGCACTGAGAAATCCAGGCCCTCACACAGCTCAAGCCCTCG 120
Db 591 TTAGGGCAAGAGGAGGCGCCAGGCACTGAGAAATCCAGGCCCTCACACAGCTCAAGCCCTCG 650
QY 121 TCGCTCCACAGAGTGGACACTGAAATCAATTTTCTATTGAGTCTCTGCGCCCTTGCCCT 180
Db 651 TCGCTCCACAGAGTGGACACTGAAATCAATTTTCTATTGAGTCTCTGCGCCCTTGCCCT 710
QY 181 GGGGAATGATCCCGGCTTTGATTTACTAGGAAGAGCTCTTATGTTGTCATAGAGC 240
Db 711 GGGGAATGATCCCGGCTTTGATTTACTAGGAAGAGCTCTTATGTTGTCATAGAGC 770
QY 241 ATTCAAGCTTTTCAAAATTAAGGGCTTGTAAATCTGTGAAGCACTCTACAGGAGAAATTTAC 300
Db 771 ATTCAAGCTTTTCAAAATTAAGGGCTTGTAAATCTGTGAAGCACTCTACAGGAGAAATTTAC 830
QY 301 AGTTTTAAAGAGATCGTATTTGGAGTGAGCTTCCACCTCTGAAGGAGGCGAGTC 360
Db 831 AGTTTTAAAGAGATCGTATTTGGAGTGAGCTTCCACCTCTGAAGGAGGCGAGTC 890
QY 361 CGTCTCTGCTCAGGCTTAATGGAAGAGCAGTGAACAGAGAGAGGAGTGCACCTAA 420
Db 891 CGTCTCTGCTCAGGCTTAATGGAAGAGCAGTGAACAGAGAGAGGAGTGCACCTAA 950
QY 421 AGAGGAGCAGCAAGCTCGGCGAGCTGATGCTTAACTTGTCCCAACAGAGACTAGAG 480

Qy	1561	TGAGGAGACCCAGTGGGAGGTGAGGCCACACAGGGCTCATGGTTGGGTGGTTCAGCGG	1620
Db	2091	TGGAGGAGACCCAGTGGGAGGTGAGGCCACACAGGGCTCATGGTTGGGTGGTTCAGCGG	2150
Qy	1621	TTTGGGCCAGTACCCCCCTCTCTTCTGTGTGTGGCCAAATAGCGTGCAAAACACAGACCG	1680
Db	2151	TTTGGGCCAGTACCCCCCTCTCTTCTGTGTGTGGCCAAATAGCGTGCAAAACACAGACCG	2210
Qy	1681	CGCAGGCAAGCGGGGCTTAATGCTGCTTTATCACCACCAAGAGGGGCTCCCTGCACAC	1740
Db	2211	CGCAGGCAAGCGGGGCTTAATGCTGCTTTATCACCACCAAGAGGGGCTCCCTGCACAC	2270
Qy	1741	CATGTTGGGGATCGACTTACATCTGAGCTTCCTCTGTCCCCACCATCACCTCATGGC	1800
Db	2271	CATGTTGGGGATCGACTTACATCTGAGCTTCCTCTGTCCCCACCATCACCTCATGGC	2330
Qy	1801	TCCTAGATTTTCAGTTTCCCAAGTGAGCCATTAAATCATGAAGCGGAGCCAGATGACCA	1860
Db	2331	TCCTAGATTTTCAGTTTCCCAAGTGAGCCATTAAATCATGAAGCGGAGCCAGATGACCA	2390
Qy	1861	AGGCCACGAGGCTGTGGGC	1881
Db	2391	AGGCCACGAGGCTGTGGGC	2411

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RESULT 5
US-09-764-904-17
; Sequence 17, Application US/09764904
; Patent No. US20020173454A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122
; CURRENT APPLICATION NUMBER: US/09/764,904
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patent In Ver. 2.0

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Query Match 13.7%; Score 475; DB 9; Length 560;
Best Local Similarity 99.8%; Pred. No. 1.7e-240;

Qy	776	GGGTC	CGAGAA	GGGTG	CACTG	AGGCC	CCACAG	CCCTT	CAAGC	CTGTG	TGTC	CCACGGT	CAGG	8335
Db	35	GGGTC	CGAGAA	GGGTG	CACTG	AGGCC	CCACAG	CCCTT	CAAGC	CTGTG	TGTC	CCACGGT	CAGG	94
Qy	836	AGCCAT	CCTGCA	CTCTC	CCGAGAG	TGCCAG	CACAGCT	GCACCC	CGCCCT	CCAGA				895
Db	95	AGCCAT	CCTGCA	CTCTC	CCGAGAG	TGCCAG	CACAGCT	GCACCC	CGCCCT	CCAGA				154
Qy	896	CAAGCC	CAAGAG	CAGAG	CTGAAG	CGTGC	CTGTG	CTGGG	CGCTG	TCAGAC	TC	CCGG		955
Db	155	CAAGCC	CAAGAG	CAGAG	CTGAAG	CGTGC	CTGTG	CTGGG	CGCTG	TCAGAC	TC	CCGG		214
Qy	956	CCGGAA	CTCCAT	GTCCAG	CCCTG	CCCA	CACACAG	CACAG	CAGAG	CTAC	CAGCTG	GACCC		1015
Db	215	CCGGAA	CTCCAT	GTCCAG	CCCTG	CCCA	CACACAG	CACAG	CAGAG	CTAC	CAGCTG	GACCC		274
Qy	1016	GCTGGT	CACACC	GTGGAG	CCCA	CAAG	CCCGTTTT	TGGGG	GTCCG	CCCA	CAACAT	CA	CCCA	1075
Db	275	GCTGGT	CACACC	GTGGAG	CCCA	CAAG	CCCGTTTT	TGGGG	GTCCG	CCCA	CAACAT	CA	CCCA	334
Qy	1076	GGGCAT	CGTCC	TCCAG	GACAG	CAACAT	GATG	AGCTG	GAAG	GGCTG	CTG	CTT	TCCG	ACGG 1135
Db	335	GGGCAT	CGTCC	TCCAG	GACAG	CAACAT	GATG	AGCTG	GAAG	GGCTG	CTG	CTT	TCCG	ACGG 394

QY 1136 AGGTAGCAAGCTGGCCACTCGAACACAGGACAGACAGGGCCCTCGTGTGCTCCCTCCC 1195
Db 395 AGGTAGCAAGCTGGCCACTCGAACACAGGACAGACAGGGCCCTCGTGTGCTCCCTCCC 454
QY 1196 CATCTCCACGACGAGTGCAGCATCCAGAGCTGGAAACAGAGCTGTTGGAGAGGAGGG 1255
Db 455 CATCTCCACGACGAGTGCAGCATCCAGAGCTGGAGCAGAGCTGTTGGAGAGGAGGG 514
QY 1256 CGCCTCCAGAGCTGCAGCGCAGCTTTGAGAGAGAGGAGTTGCC 1301
Db 515 CGCCTCCAGAGCTGCAGCGCAGCTTTGAGAGAGAGGAGTTGCC 560

RESULT 6

US-10-091-548-17
; Sequence 17, Application US/10091548
; Publication No. US20030049703A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122CI
; CURRENT APPLICATION NUMBER: US/10/091,548
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 137
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-548-17

Query Match 13.7%; Score 475; DB 9; Length 560;
Best Local Similarity 99.8%; Pred. No. 1.7e-240;
Matches 525; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 776 GGGCTCCAGAGGGTGCAGTGAGGCCACACAGCTTCAAGCTGTGCTGCCACGGTCAGG 835
Db 35 GGGCTCCAGAGGGTGCAGTGAGGCCACACAGCTTCAAGCTGTGCTGCCACGGTCAGG 94
QY 836 AGCCATCTGCACCTCTCTCCCGGAGGTGCCAGCCACAGCTGCACCCCGCCCTCCAGA 895
Db 95 AGCCATCTGCACCTCTCTCCCGGAGGTGCCAGCCACAGCTGCACCCCGCCCTCCAGA 154
QY 896 CAAGCCCAAGAGCAGAGCTGAAGCTTGGCTGTGGGGGGCTGTGAGACTCCGG 955
Db 155 CAAGCCCAAGAGCAGAGCTGAAGCTTGGCTGTGGGGGGCTGTGAGACTCCGG 214
QY 956 CCGGAATCTCATGTCTCAGCTGCCACACACAGCAGCAGCAGCTACAGCTGGACCC 1015
Db 215 CCGGAATCTCATGTCTCAGCTGCCACACACAGCAGCAGCAGCTACAGCTGGACCC 274
QY 1016 GCTGTGTACACCCGCTGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACATCACCCA 1075
Db 275 GCTGTGTACACCCGCTGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACATCACCCA 334
QY 1076 GGGCATCTGCTCCAGGACAGCAACATGATGAGCTGAAGCTGTCTCTCTCCGAGCG 1135
Db 335 GGGCATCTGCTCTCCAGGACAGCAACATGATGAGCTGAAGCTGTCTCTCTCCGAGCG 394
QY 1136 AGGTAGCAAGCTGGCCACTCGAACACAGGACAGACAGGGCCCTCGTGTGCTCCCTCCC 1195
Db 395 AGGTAGCAAGCTGGCCACTCGAACACAGGACAGACAGGGCCCTCGTGTGCTCCCTCCC 454
QY 1196 CATCTCCACGACGAGTGCAGCATCCAGAGCTGGAAACAGAGCTGTTGGAGAGGAGGG 1255
Db 455 CATCTCCACGACGAGTGCAGCATCCAGAGCTGGAGCAGAGCTGTTGGAGAGGAGGG 514
QY 1256 CGCCTCCAGAGCTGCAGCGCAGCTTTGAGAGAGAGGAGTTGCC 1301
Db 515 CGCCTCCAGAGCTGCAGCGCAGCTTTGAGAGAGAGGAGTTGCC 560

RESULT 7

US-10-074-095-269
; Sequence 269, Application US/10074095
; Publication No. US2003007704A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C1
; CURRENT APPLICATION NUMBER: US/10/074,095
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
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; PRIOR FILING DATE: 2000-07-26
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; PRIOR FILING DATE: 2000-07-11
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; PRIOR APPLICATION NUMBER: 60/226,868
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; PRIOR APPLICATION NUMBER: 60/216,647
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; PRIOR APPLICATION NUMBER: 60/230,438
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; PRIOR APPLICATION NUMBER: 60/215,135
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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match 13.7%; Score 475; DB 9; Length 560;

Best Local Similarity 99.8%; Pred No. 1.7e-240;

Matches 525; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 172, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A

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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 3946.59 Seconds
(without alignments)
14252.028 Million cell updates/sec

Title: US-09-513-888C-1_COPY_871_4343

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	381	11.0	668	12 BF058214	BF058214 7k28d05.x
C 4	333	9.6	547	12 BF590813	BF590813 7h42e07.x
C 5	287	8.3	531	10 BE276168	BE276168 601144424
C 6	283	8.1	743	10 BE410921	BE410921 601303579

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BE384131	601272956	673	4.8	165	C 8
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AA644373	af64c10.s	153	3.5	122	C 10
AW028197	wv84a01.x	397	2.0	168	C 11
BF725320	bxi4e11.y	714	1.1	37	C 12
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AV663618	AV663618	596	1.0	35	C 14
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BQ739770	PfESToab4	34	1.0	34	C 16
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BF505681	BB170032B	717	1.0	34	C 18
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BM259700	CH230-113	491	1.0	33	C 21
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AU086887	AU086887	500	1.0	33	C 23
AU088222	AU088222	500	1.0	33	C 24
AU088256	AU088256	501	1.0	33	C 25
BI814790	PfESToaa0	523	1.0	33	C 26
BM273468	PfESToaa5	94	1.0	32	C 27
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AL779579	AL779579	227	0.9	32	C 29
BM274140	PfESToaa6	262	0.9	32	C 30
BH043946	RPCI-24-2	264	0.9	32	C 31
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AA287156	zs58a01.r	356	0.9	32	C 40
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AZ284683	RPCI-23-1	437	0.9	32	C 47
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AQ984657	RPCI-23-3	474	0.9	32	C 53
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AU087803	AU087803	500	0.9	32	C 57
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AQ838282	HS_5175.B	518	0.9	32	C 62
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AZ063844	RPCI-23-4	533	0.9	32	C 64
AZ262620	RPCI-23-1	533	0.9	32	C 65
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374	28	0.8	812	17	BH178455	C 447	27	0.8	516	12	BM160403	BF33007.1
375	28	0.8	812	17	CNS07KRM	C 448	27	0.8	518	14	BQ603144	MI-P-NA-a
376	28	0.8	815	17	BH352602	C 449	27	0.8	524	13	BI289404	UI-R-DK0
377	28	0.8	835	17	AZ695866	C 450	27	0.8	525	17	BH121510	RPCI-24-3
378	28	0.8	1299	13	BM334791	C 451	27	0.8	527	17	AQ100252	HS 3179.8
379	28	0.8	1652	13	BM395003	C 452	27	0.8	528	17	AQ800724	HS 5315.B
380	27	0.8	200	14	BQ596826	C 453	27	0.8	528	17	BH310462	CH230-193
381	27	0.8	207	17	AQ539388	C 454	27	0.8	530	17	AZ886419	RPCI-23-1
382	27	0.8	236	14	N98064	C 455	27	0.8	533	17	AQ591933	HS 5414.A
383	27	0.8	266	14	N98016	C 456	27	0.8	536	17	AQ211941	HS 3241.B
384	27	0.8	266	17	AZ583402	C 457	27	0.8	537	17	BH323914	CH230-104
385	27	0.8	273	13	BM268056	C 458	27	0.8	541	13	BM273797	PFEStoaas
386	27	0.8	274	13	BM274634	C 459	27	0.8	545	13	BI506833	BI170028B
387	27	0.8	280	9	AU087647	C 460	27	0.8	546	10	AW638015	b165b11.w
388	27	0.8	281	14	BQ596510	C 461	27	0.8	550	13	AW531801	BI160014B
389	27	0.8	286	9	AU087673	C 462	27	0.8	552	17	AQ538004	RPCI-11-3
390	27	0.8	314	14	N97597	C 463	27	0.8	553	13	BI670695	PFEStoaas
391	27	0.8	318	13	BI517121	C 464	27	0.8	554	9	AU149369	AU149369
392	27	0.8	320	17	AZ928031	C 465	27	0.8	554	13	BM274761	BM274761
393	27	0.8	321	13	BQ54962	C 466	27	0.8	561	17	BH078344	BM274761
394	27	0.8	328	17	AQ017800	C 467	27	0.8	563	13	BI670535	PFEStoaas
395	27	0.8	342	10	AV691884	C 468	27	0.8	563	13	BM275212	PFEStoaas
396	27	0.8	343	9	AU086817	C 469	27	0.8	563	17	AQ561057	HS 5342.B
397	27	0.8	347	17	AZ389560	C 470	27	0.8	565	17	AQ79015	CIT-HSP-2
398	27	0.8	348	17	CNS045F8	C 471	27	0.8	572	17	BH313000	CH230-12D
399	27	0.8	354	17	AQ246404	C 472	27	0.8	573	13	BM275162	PFEStoaas
400	27	0.8	361	9	AI133217	C 473	27	0.8	583	17	AQ774291	HS 3086.A
401	27	0.8	366	14	BQ452441	C 474	27	0.8	588	9	AL632384	AL632384
402	27	0.8	376	13	BI184954	C 475	27	0.8	592	17	CNS0207F	Tetraodon
403	27	0.8	377	13	BM273826	C 476	27	0.8	602	13	BI516270	BI160021B
404	27	0.8	381	13	BM273527	C 477	27	0.8	608	13	BM161711	EST564234
405	27	0.8	390	9	AU086299	C 478	27	0.8	615	9	AL712274	DKSP6860
406	27	0.8	396	17	BH358845	C 479	27	0.8	615	12	BE806160	ss54hl0.1.y
407	27	0.8	403	14	N97876	C 480	27	0.8	617	17	AZ095099	RPCI-23-1
408	27	0.8	416	17	AZ928053	C 481	27	0.8	623	17	BH363698	CH230-60A
409	27	0.8	420	12	BF770455	C 482	27	0.8	627	10	AW222691	EST299502
410	27	0.8	421	9	AU087621	C 483	27	0.8	631	13	BM276345	PFEStoaas
411	27	0.8	423	13	BI936135	C 484	27	0.8	642	13	BM267903	MEST373-G
412	27	0.8	424	14	BQ633388	C 485	27	0.8	649	14	BM922058	RPCI-23-1
413	27	0.8	426	9	AU087549	C 486	27	0.8	652	9	AU134513	AU134513
414	27	0.8	427	17	AQ022939	C 487	27	0.8	653	17	AA550371	1517m3.gm
415	27	0.8	427	17	AQ051379	C 488	27	0.8	656	12	BF296492	037PBG11
416	27	0.8	450	13	BM275482	C 489	27	0.8	664	17	AZ316496	BM0334J08
417	27	0.8	450	17	AZ193756	C 490	27	0.8	681	17	BH207155	Sn1-51M13
418	27	0.8	453	9	AU087959	C 491	27	0.8	704	17	AZ230276	RPCI-23-6
419	27	0.8	456	13	BI814644	C 492	27	0.8	713	17	AZ660488	AW6538A08
420	27	0.8	460	17	AQ530955	C 493	27	0.8	716	17	AQ574273	nmxb0083P
421	27	0.8	469	13	BI815280	C 494	27	0.8	717	13	BQ405445	BQ405445
422	27	0.8	469	17	AQ816884	C 495	27	0.8	719	13	BI938844	dj33e05.x
423	27	0.8	473	13	BM274148	C 496	27	0.8	725	17	AZ561119	RPCI-23-2
424	27	0.8	475	17	AZ262310	C 497	27	0.8	729	17	AZ660406	AW6538A06
425	27	0.8	489	17	AZ060178	C 498	27	0.8	737	17	CNS04MGM	AL297401
426	27	0.8	491	13	BM274073	C 499	27	0.8	741	13	BM028532	IPskn0078
427	27	0.8	498	10	AW232842	C 500	27	0.8	748	14	BQ103768	ESTBB1700
428	27	0.8	500	9	AU086152	C 501	27	0.8	753	17	BH314212	CH230-63A
429	27	0.8	500	9	AU086589	C 502	27	0.8	767	17	BH599469	CH230-63A
430	27	0.8	500	9	AU086643	C 503	27	0.8	803	10	AV700369	AV700369
431	27	0.8	500	9	AU087045	C 504	27	0.8	830	17	BH445595	RPCI-24-2
432	27	0.8	500	9	AU087082	C 505	27	0.8	845	17	BH491488	BOGJY56TR
433	27	0.8	500	9	AU087328	C 506	27	0.8	848	17	CNS03N06	Tetraodon
434	27	0.8	500	9	AU087403	C 507	27	0.8	853	17	AQ750271	HS 5576.A
435	27	0.8	500	9	AU087483	C 508	27	0.8	869	12	BG657230	602660466
436	27	0.8	500	9	AU087584	C 509	27	0.8	911	17	CNS07375	clone BA0
437	27	0.8	500	9	AU087888	C 510	27	0.8	949	17	CNS06J08	AL401838
438	27	0.8	500	9	AU087971	C 511	27	0.8	1038	17	CNS06L7M	T7 end of
439	27	0.8	500	9	AU088109	C 512	27	0.8	1101	17	CNS00KON	AL403832
440	27	0.8	500	9	AU088345	C 513	27	0.8	1101	17	CNS05P80	T3 end of
441	27	0.8	500	9	AU088346	C 514	27	0.8	1101	13	BM394561	AL078112
442	27	0.8	500	9	AU088390	C 515	27	0.8	1707	13	BM394561	Drosophil
443	27	0.8	500	9	AU088502	C 516	27	0.8	1878	12	BG845876	AL347649
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	27	0.8	505	9	AI492378	C 517	26	0.7	161	14	BQ633588	50072-2-4
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C 518	26	0.7	167	17	AZ267916	A2267916	RPIC-23-1	C 591	26	0.7	478	10	BE018440
C 519	26	0.7	214	14	BQ596558	BQ596558	RPIC-23-1	C 592	26	0.7	482	14	BQ633203
C 520	26	0.7	214	14	H82340	H82340	YU9H08.r1	C 593	26	0.7	484	12	BF001607
C 521	26	0.7	234	17	AZ882914	AZ882914	RPIC-23-1	C 594	26	0.7	486	13	BQ365318
C 522	26	0.7	236	14	BQ596706	BQ596706	PFEStoab2	C 595	26	0.7	486	14	BQ739708
C 523	26	0.7	247	13	BI815521	BI815521	PFEStoab2	C 596	26	0.7	487	10	BE458384
C 524	26	0.7	257	9	AU086687	AU086687	AU086687	C 597	26	0.7	488	17	AQ120663
C 525	26	0.7	259	9	AI157086	AI157086	ud16a05.r	C 598	26	0.7	489	12	BF513548
C 526	26	0.7	265	13	BM275053	BM275053	PFEStoaa7	C 599	26	0.7	489	17	AQ2060178
C 527	26	0.7	278	10	AV726570	AV726570	AV726570	C 600	26	0.7	490	9	AA800486
C 528	26	0.7	301	14	BQ451048	BQ451048	PFEStoab0	C 601	26	0.7	490	13	BM275231
C 529	26	0.7	301	14	N98106	N98106	2192C3 czap	C 602	26	0.7	490	17	AQ203615
C 530	26	0.7	312	14	N98005	N98005	2026C3 czap	C 603	26	0.7	491	13	BI675562
C 531	26	0.7	312	17	BI822237	BI822237	O20_D_14-	C 604	26	0.7	497	13	BM491430
C 532	26	0.7	312	17	CNS07NOH	AL619187	T2 end of	C 605	26	0.7	497	17	AQ922217
C 533	26	0.7	313	9	AU087609	AU087609	AU087609	C 606	26	0.7	499	17	AQ139954
C 534	26	0.7	319	14	N98074	N98074	2229C3 czap	C 607	26	0.7	500	9	AU086136
C 535	26	0.7	321	14	W16536	W16536	2b10409.r1	C 608	26	0.7	500	9	AU086425
C 536	26	0.7	325	13	BI814312	BI814312	PFEStoaa2	C 609	26	0.7	500	9	AU086748
C 537	26	0.7	325	14	T28727	T28727	EST53404 Hu	C 610	26	0.7	500	9	AU086812
C 538	26	0.7	327	17	AZ257566	AZ257566	RPIC-23-1	C 611	26	0.7	500	9	AU086874
C 539	26	0.7	329	14	BQ392379	BQ392379	NISC mq24	C 612	26	0.7	500	9	AU087021
C 540	26	0.7	330	17	AQ584397	AQ584397	RPIC-11-4	C 613	26	0.7	500	9	AU087155
C 541	26	0.7	342	14	BQ596883	BQ596883	PFEStoab2	C 614	26	0.7	500	9	AU087218
C 542	26	0.7	344	14	BQ451468	BQ451468	PFEStoaa9	C 615	26	0.7	500	9	AU087273
C 543	26	0.7	344	14	BQ452333	BQ452333	PFEStoaa9	C 616	26	0.7	500	9	AU087456
C 544	26	0.7	353	10	AW936480	AW936480	QV4-DT002	C 617	26	0.7	500	9	AU087837
C 545	26	0.7	354	13	BI936191	BI936191	PFEStoaa2	C 618	26	0.7	500	9	AU088026
C 546	26	0.7	358	13	BI936075	BI936075	PFEStoaa2	C 619	26	0.7	500	9	AU088135
C 547	26	0.7	361	9	A409080	AI409080	EST237372	C 620	26	0.7	500	9	AU088483
C 548	26	0.7	361	13	BI814037	BI814037	PFEStoaa0	C 621	26	0.7	500	9	AU088490
C 549	26	0.7	362	10	AV725187	AV725187	AV725187	C 622	26	0.7	501	13	BI814790
C 550	26	0.7	368	13	BI814405	BI814405	PFEStoaa2	C 623	26	0.7	501	13	BI478245
C 551	26	0.7	375	13	BI670658	BI670658	PFEStoaa0	C 624	26	0.7	504	13	BI478245
C 552	26	0.7	378	17	AQ031304	AQ031304	HS-2213_B	C 625	26	0.7	505	13	BI123500
C 553	26	0.7	378	17	AQ106231	AQ106231	HS-3051_B	C 626	26	0.7	508	13	BI514335
C 554	26	0.7	381	10	BB802930	BB802930	BB802930	C 627	26	0.7	510	9	AA893265
C 555	26	0.7	382	13	BI816252	BI816252	PFEStoaa3	C 628	26	0.7	513	10	BE328150
C 556	26	0.7	383	14	N97976	N97976	1739C3 czap	C 629	26	0.7	516	17	BI197671
C 557	26	0.7	388	14	BM854400	BM854400	K-EST0136	C 630	26	0.7	518	13	BM274067
C 558	26	0.7	397	13	BJ078187	BJ078187	BJ078187	C 631	26	0.7	518	17	AZ928055
C 559	26	0.7	398	13	BJ394065	BJ394065	BJ394065	C 632	26	0.7	519	9	AI409079
C 560	26	0.7	398	17	AZ761382	AZ761382	IM0555K10	C 633	26	0.7	520	17	BH843091
C 561	26	0.7	399	14	N97593	N97593	1024C3 czap	C 634	26	0.7	523	13	BM167768
C 562	26	0.7	401	9	BQ739562	BQ739562	PFEStoab4	C 635	26	0.7	524	17	AQ974493
C 563	26	0.7	413	14	AQ702923	AY702923	zi76d04.s	C 636	26	0.7	525	13	BJ426469
C 564	26	0.7	414	13	BI511680	BI511680	BB160006B	C 637	26	0.7	529	17	BI195369
C 565	26	0.7	415	17	AQ150727	AQ150727	HS-3203_A	C 638	26	0.7	529	17	AQ502749
C 566	26	0.7	418	17	AQ216606	AQ216606	HS-2139_A	C 639	26	0.7	530	17	AZ886419
C 567	26	0.7	420	17	AQ533464	AQ533464	RPIC-11-3	C 640	26	0.7	530	17	BI199135
C 568	26	0.7	424	13	BI204186	BI204186	EST522226	C 641	26	0.7	534	17	BI764621
C 569	26	0.7	427	10	AW048128	AW048128	UI-M-BH1-	C 642	26	0.7	535	10	AW638825
C 570	26	0.7	429	17	AQ914351	AQ914351	nbeb00480	C 643	26	0.7	536	17	AQ830438
C 571	26	0.7	429	17	BI195089	BI195089	TC3-68L23	C 644	26	0.7	537	10	AW933537
C 572	26	0.7	431	13	BM275996	BM275996	PFEStoaa8	C 645	26	0.7	537	13	BM275514
C 573	26	0.7	432	14	W37510	W37510	zcl12d04.s1	C 646	26	0.7	537	13	BM275927
C 574	26	0.7	436	10	AW932771	AW932771	EST358614	C 647	26	0.7	537	17	AZ873884
C 575	26	0.7	439	10	AW627569	AW627569	h87h03.x	C 648	26	0.7	538	13	BJ397063
C 576	26	0.7	447	14	BQ452354	BQ452354	PFEStoaa9	C 649	26	0.7	538	13	BJ422055
C 577	26	0.7	453	13	BI411835	BI411835	EST586162	C 650	26	0.7	539	13	BJ396971
C 578	26	0.7	457	13	BI936194	BI936194	PFEStoaa2	C 651	26	0.7	540	13	BI502940
C 579	26	0.7	458	13	BI815758	BI815758	PFEStoaa3	C 652	26	0.7	540	13	BI160703
C 580	26	0.7	460	13	BI675535	BI675535	dac62e06	C 653	26	0.7	543	13	BM275916
C 581	26	0.7	460	17	AQ198638	AQ198638	RPIC11-59	C 654	26	0.7	544	9	AL658903
C 582	26	0.7	461	17	AZ902609	AZ902609	RPIC-24-1	C 655	26	0.7	544	13	BJ392332
C 583	26	0.7	463	9	A1918803	A1918803	ts86g05.x	C 656	26	0.7	545	9	AL781236
C 584	26	0.7	464	13	BM275506	BM275506	PFEStoaa5	C 657	26	0.7	547	13	BJ392160
C 585	26	0.7	465	9	AF244983	AF244983	AF244983	C 658	26	0.7	548	13	BM274922
C 586	26	0.7	465	9	A1410242	A1410242	EST238535	C 659	26	0.7	554	12	BM274497
C 587	26	0.7	465	9	AQ611982	AQ611982	HS-5072_B	C 660	26	0.7	556	12	BG512900
C 588	26	0.7	466	17	BQ451839	BQ451839	PFEStoab0	C 661	26	0.7	556	12	BG512900
C 589	26	0.7	467	14	BI815150	BI815150	PFEStoaa1	C 662	26	0.7	556	13	BI815150
C 590	26	0.7	473	9	AU087951	AU087951	AU087951	C 663	26	0.7	559	13	BI815150

664	26	0.7	560	13	BM653101	BM53101 170006873	C 737	26	0.7	716	13	BM167270
C 665	26	0.7	562	17	AQ998129	RPCI-23-2	C 738	26	0.7	729	17	AZ660406
C 666	26	0.7	566	13	BM275442	PfESToa6	C 739	26	0.7	731	10	AV693920
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C 847	25	0.7	406	13	BI895630	EST5tea94	BI895630	C 920	25	0.7	491	17	AZ215329	Sheared D	AZ215329
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
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ORIGIN
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Qy 855 CCGAGAGTGCAGCAGCAGTGACCCCGCCCTCCAGACAGCCCAAGAGCAGGAG 914
Db 447 CCGGAGAGTGCAGCAGCAGTGACCCCGCCCTCCAGACAGCCCAAGAGCAGGAG 388
Qy 915 CTGAAGCTGGCTGTCTGTGGGCGCTGTACAGCTCCGCGGAACTCCATGTCACG 974
Db 387 CTGAAGCTGGCTGTCTGTGGGCGCTGTACAGCTCCGCGGAACTCCATGTCACG 328
Qy 975 CTGCCCCACACAGCAGCAGCAGTACAGCTGGAGCCCGCTGCTCAGACCCCGTGGGA 1034
Db 327 CTGCCCCACACAGCAGCAGCAGTACAGCTGGAGCCCGCTGCTCAGACCCCGTGGGA 268
Qy 1035 CCCAAGCCGTTTGGGGGTCGCCCCACACATCACCCAGGGCATCGTCTCCAGGAC 1094
Db 267 CCCAAGCCGTTTGGGGGTCGCCCCACACATCACCCAGGGCATCGTCTCCAGGAC 208
Qy 1095 AGCAACATGATGAGCCTGAAGGCTGTCTTCTCCGACGAGGTAGCAAGCTGGGCCAC 1154
Db 207 AGCAACATGATGAGCCTGAAGGCTGTCTTCTCCGACGAGGTAGCAAGCTGGGCCAC 148
Qy 1155 TCGAACAGGAGGACAGAGGGCCCTCGTGTGTGTCGCTCCCCATCTCCAGCGAGGTGC 1214
Db 147 TCGAACAGGAGGACAGAGGGCCCTCGTGTGTGTCGCTCCCCATCTCCAGCGAGGTGC 88
Qy 1215 AGCATCCAGGAGCTGGAAACAGAGCTGTGGAGAGGGAGGGCGCCCTCCAGAGCTCGAG 1274
Db 87 AGCATCCAGGAGCTGGAGCAGAGCTGTGGAGAGGGAGGGCGCCCTCCAGAGCTCGAG 28
Qy 1275 CGCAGCTTTGAGGAGAGGAGCTTGCC 1301
Db 27 CGCAGCTTTGAGGAGAGGAGCTTGCC 1

RESULT 3
LOCUS BF058214/c
DEFINITION 7k28d05.x1 NCI CGAP Ovl8 Homo sapiens cDNA clone IMAGE:3476769 3'
similar to TR:Q9Y5W1 Q9Y5W1 FEZ1. [5] TR:Q9Y5W0 TR:Q9Y5V9 TR:Q9Y5V8
TR:Q9Y5V7 ; contains MER22.t3 TAR1 repetitive element ;, mRNA
sequence.
ACCESSION BF058214
VERSION BF058214.1 GI:10812110
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 668)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.; Ph.D.; Michael
R. Emmert-Buck, M.D.; Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 441.
FEATURES
Location/Qualifiers
1..668
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3476769"
/clone_lib="NCI CGAP Ovl8"
/tissue_type="fibroheoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pTT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGACATTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 105 a 185 c 226 g 150 t 2 others
ORIGIN
Query Match 11.0%; Score 381; DB 12; Length 668;
Best Local Similarity 99.8%; Pred. No. 7.5e-177;
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 776 GGGTCCGAGAGGTCAGTGAGCCACAGCCTTCAAGCCTGTGCTGCCACCGTCAGG 835
Db 514 GGGTCCGAGAGGTCAGTGAGCCACAGCCTTCAAGCCTGTGCTGCCACCGTCAGG 455
Qy 836 AGCCATCTGCATCTCTCCCGGAGAGTGCAGCCACCCGCCCTCCAGAG 895
Db 454 AGCCATCTGCATCTCTCCCGGAGAGTGCAGCCACCCGCCCTCCAGAG 395
Qy 896 CAAGCCCAAGAGCAGAGCTGAAGCCTGTGCTCTGGGGCGCTGTGAGACTCCGG 955
Db 394 CAAGCCCAAGAGCAGAGCTGAAGCCTGTGCTCTGGGGCGCTGTGAGACTCCGG 335
Qy 956 CCGGAATCCATGTCACGCTGCCACACAGCAGCAGCAGCTACAGCTGGAGCC 1015
Db 334 CCGGAATCCATGTCACGCTGCCACACAGCAGCAGCAGCTACAGCTGGAGCC 275

QY 1016 GCTGGTACACCCGCTGGGACCCACAGCCGCTTTTGGGGCTCCGCCACACATCACCA 1075
 |||||
 Db 274 GCTGGTACACCCGCTGGGACCCACAGCCGCTTTTGGGGCTCCGCCACACATCACCA 215
 |||||
 QY 1076 GGGATCTCTCTCCAGGACAGCAACATGATGAGCTTGAAGCTCTGTCTTCTCCGACGG 1135
 |||||
 Db 214 GGGATCTCTCTCCAGGACAGCAACATGATGAGCTTGAAGCTCTGTCTTCTCCGACGG 155
 |||||
 QY 1136 AGGTAGCAAGCTGGGCCACTGCAACAGGACAGCAAGGGCCCTCTGTGTCTCCGCTCCCC 1195
 |||||
 Db 154 AGGTAGCAAGCTGGGCCACTGCAACAGGACAGCAAGGGCCCTCTGTGTCTCCGCTCCCC 95
 |||||
 QY 1196 CATCTCCACGGA 1207
 |||||
 Db 94 CATCTCCACGGA 83
 |||||

RESULT 4
 BF590813/c
 LOCUS BF590813 547 bp mRNA linear EST 12-DEC-2000
 DEFINITION 7h42e07.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:3318660 3' similar to TR:Q9Y5W1 FEZ1. [5] TR:Q9Y5W0 TR:Q9Y5V9 TR:Q9Y5V8 TR:Q9Y5V7 ; contains MER22.t3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION BF590813
 VERSION BF590813.1 GI:11683137
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 547)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 434.

FEATURES
 Location/Qualifiers
 1..547
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3318660"
 /clone_lib="NCI CGAP Col6"
 /tissue_type="colon tumor, RER+"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1057416-1061255, and 1144584-1145351).
 Subtraction by Bento Soares and M. Fatima Ronaldo. "

BASE COUNT 83 a 156 c 189 g 119 t
 ORIGIN
 Query Match 9.6%; Score 333; DB 12; Length 547;
 Best Local Similarity 99.5%; Pred. No. 4.1e-153;
 Matches 433; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 877 TGCACCCCGCCCTCCAGACAGCCCAAGGACGAGCTGAAGCTGGCTGTGCTGTG 936

Db 435 TGACCCCGCCCTCCAGACAGCCCAAGAGAGGAGCTGAAGCTTGGCTGTGCTGTG 376
 |||||
 QY 937 GGGCGTGTTCAGACTCCGGCCGGAATCTCCATGTCTCCAGCTGCCACACACAGCACAGCA 996
 |||||
 Db 375 GGGCGTGTTCAGACTCCGGCCGGAATCTCCATGTCTCCAGCTGCCACACACAGCACAGCA 316
 |||||
 QY 997 GCAGCTACAGCTGGAGCCCGCTGGTACACCCGCTGGGACCCCAAGCCGCTTTTGGGGGCT 1056
 |||||
 Db 315 GCAGCTACAGCTGGAGCCCGCTGGTACACCCGCTGGGACCCCAAGCCGCTTTTGGGGGCT 256
 |||||
 QY 1057 CCGCCCAACAACATCACCCAGGCGATCGTCTCTCCAGGACAGCAACATGATGAGCTGAAGG 1116
 |||||
 Db 255 CCGCCCAACAACATCACCCAGGCGATCGTCTCTCCAGGACAGCAACATGATGAGCTGAAGG 196
 |||||
 QY 1117 CTCTGTCTCTTCGACGAGGCTAGCAAGCTGGGCCACTCGAACAAGGACAGCAAGGGCC 1176
 |||||
 Db 195 CTCTGTCTCTTCGACGAGGCTAGCAAGCTGGGCCACTCGAACAAGGACAGCAAGGGCC 136
 |||||
 QY 1177 CTTCTGTCTCTTCGACGAGGCTAGCAAGCTGGGCCACTCGAACAAGGACAGCAAGGGCC 1236
 |||||
 Db 135 CTTCTGTCTCTTCGACGAGGCTAGCAAGCTGGGCCACTCGAACAAGGACAGCAAGGGCC 76
 |||||
 QY 1237 AGCTGTCTTCGACGAGGCTAGCAAGCTGGGCCACTCGAACAAGGACAGCAAGGGCC 1296
 |||||
 Db 75 AGCTGTCTTCGACGAGGCTAGCAAGCTGGGCCACTCGAACAAGGACAGCAAGGGCC 16
 |||||
 QY 1297 TTGCCTCCAGCTGG 1311
 |||||
 Db 15 TTGCCTCCAGCTGG 1

RESULT 5
 BE276168/c
 LOCUS BE276168 531 bp mRNA linear EST 13-JUL-2000
 DEFINITION 60114424P1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3050716 5', mRNA sequence.

ACCESSION BE276168
 VERSION BE276168.1 GI:9151131
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 531)
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: HLCM96 row: 0 column: 05
 High quality sequence stop: 531.
 Location/Qualifiers
 1..531
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3050716"
 /clone_lib="NIH MGC 20"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit

FEATURES
 source

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 87 a 173 c 156 g 115 t

ORIGIN

Query Match 8.3%; Score 287; DB 10; Length 531;

Best Local Similarity 99.7%; Pred. No. 2.4e-130;

Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1523 GTCTTACGAGAGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 1582

DB 358 GTCTTACGAGAGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 299

QY 1583 GAGGCCACACAGGGCTCATGGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 1642

DB 298 GAGGCCACACAGGGCTCATGGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 239

QY 1643 CTTCTGTGTGTCGCAATAGGTCGCAACACAGACCGCGAGGCAAGCGGGCTAAATGT 1702

DB 238 CTTCTGTGTGTCGCAATAGGTCGCAACACAGACCGCGAGGCAAGCGGGCTAAATGT 179

QY 1703 GCTGGCTTTATCACCACAAAGAGGGCTCCCTGCAAAACCATGTTGGGGGATCGACTTACA 1762

DB 178 GCTGGCTTTATCACCACAAAGAGGGCTCCCTGCAAAACCATGTTGGGGGATCGACTTACA 119

QY 1763 TCTGAGCTTCCTCTGTGTCGCCACCATCACCCTCATGGCTCTAGATTTTCAGTTTCCCAAG 1822

DB 118 TCTGAGCTTCCTCTGTGTCGCCACCATCACCCTCATGGCTCTAGATTTTCAGTTTCCCAAG 59

QY 1823 TGAGCCATTAATCATGAAGCGGAGCCAGATGACCA 1860

DB 58 TGAGCCATTAATCATGAAGCGGAGCCAGATGACCA 21

RESULT 6

BE410921/c

LOCUS BE410921

DEFINITION 601303579F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638203 5',

mRNA sequence.

ACCESSION BE410921

VERSION BE410921.1 GI:9347371

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CNA Library Preparation: Ling Hong/Rubin Laboratory

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

plate: LLC338 row: m column: 20

High quality sequence start: 49

High quality sequence stop: 688.

Location/Qualifiers

1. .743

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3638203"

/clone_lib="NIH_MGC_21"

/tissue_type="choriocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 119 a 229 c 226 g 168 t

ORIGIN

Query Match 8.1%; Score 283; DB 10; Length 743;

Best Local Similarity 99.7%; Pred. No. 2.4e-128;

Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1523 GTCTTACGAGAGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 1582

DB 381 GTCTTACGAGAGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 322

QY 1583 GAGGCCACACAGGGCTCATGGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 1642

DB 321 GAGGCCACACAGGGCTCATGGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 262

QY 1643 CTTCTGTGTGTCGCAATAGGTCGCAACACAGACCGCGAGGCAAGCGGGCTAAATGT 1702

DB 261 CTTCTGTGTGTCGCAATAGGTCGCAACACAGACCGCGAGGCAAGCGGGCTAAATGT 202

QY 1703 GCTGGCTTTATCACCACAAAGAGGGCTCCCTGCAAAACCATGTTGGGGGATCGACTTACA 1762

DB 201 GCTGGCTTTATCACCACAAAGAGGGCTCCCTGCAAAACCATGTTGGGGGATCGACTTACA 142

QY 1763 TCTGAGCTTCCTCTGTGTCGCCACCATCACCCTCATGGCTCTAGATTTTCAGTTTCCCAAG 1822

DB 141 TCTGAGCTTCCTCTGTGTCGCCACCATCACCCTCATGGCTCTAGATTTTCAGTTTCCCAAG 82

QY 1823 TGAGCCATTAATCATGAAGCGGAGCCAGATG 1856

DB 81 TGAGCCATTAATCATGAAGCGGAGCCAGATG 48

RESULT 7

AI984777/c

LOCUS AI984777

DEFINITION wr85b07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:249453 3',

similar to TR:O60299 O60299 KIAA0552 PROTEIN. ; mRNA sequence.

ACCESSION AI984777

VERSION AI984777.1 GI:5812054

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..

NIH-MGC http://mgi.nci.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1307 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 428.

Location/Qualifiers

1. .817

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:249453"

/clone_lib="NCI CGAP Kid11"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Donaldo.

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BASE COUNT      133 a   235 c   266 g   180 t       3 others
ORIGIN

Query Match      6.9%; Score 241; DB 9; Length 817;
Best Local Similarity 99.7%; Pred. No. 1.5e-107; Indels 0; Gaps 0;
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1010 GGACCCGCTGTGCACACCCGCTGGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACAT 1069
Db  292  GGACCCGCTGTGCACACCCGCTGGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACAT 233
Qy  1070 CACCCAGGGCATGCTCTCCAGGACAGCAACATGATGAGCCCTGAAGGCTCTGTCTTCTC 1129
Db  232  CACCCAGGGCATGCTCTCCAGGACAGCAACATGATGAGCCCTGAAGGCTCTGTCTTCTC 173
Qy  1130 CGACGGAGGTAGCAGCTGGGCCACTCGAACAGGCACAGAGGCCCTCTGTGTCTCG 1189
Db  172  CGACGGAGGTAGCAGCTGGGCCACTCGAACAGGCACAGAGGCCCTCTGTGTCTCG 113
Qy  1190 CTCCCCCATCTCCACGAGCGAGTGCAGCATCCAGGAGCTGGAACAGAGCTGTTGGAGAG 1249
Db  112  CTCCCCCATCTCCACGAGCGAGTGCAGCATCCAGGAGCTGGAACAGAGCTGTTGGAGAG 53
Qy  1250 GGAGGGCCCTCCAGAGCTGCAGCGAGCTTTCAGGAGAGGAGCTTGCC 1301
Db  52  GGAGGGCCCTCCAGAGCTGCAGCGAGCTTTCAGGAGAGGAGCTTGCC 1

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RESULT 8
BE384131/c
LOCUS      BE384131      673 bp      mRNA      linear      EST 21-JUL-2000
DEFINITION 601272956F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614076 5',
            mRNA sequence.
ACCESSION  BE384131
VERSION    BE384131.1 GI:9329496
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 673)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTF
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM275 row: P column: 13
            High quality sequence stop: 670.
            Location/Qualifiers
              1..673
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:3614076"
                /clone_lib="NIH_MGC_20"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally

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cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

```

BASE COUNT      110 a   211 c   208 g   144 t
ORIGIN

Query Match      4.8%; Score 165; DB 10; Length 673;
Best Local Similarity 99.5%; Pred. No. 6e-70;
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1523 GTCTTACGAGGGAGAGACCCAGCTTCGGCCCGCTGGAGGAGACCCAGTCGGAGGT 1582
Db  357  GTCTTACGAGGGAGAGACCCAGCTTCGGCCCGCTGGAGGAGACCCAGTCGGAGGT 298
Qy  1583 GAGGCCACACAGGGCTCATGGGTTTGGGTGTTCAGCGGTTTGGCGCCAGTACCCCTCT 1642
Db  297  GAGGCCACACAGGGCTCATGGGTTTGGGTGTTCAGCGGTTTGGCGCCAGTACCCCTCT 238
Qy  1643 CTTTCTGGTGTGCGCCATAGCGTGCAACACAGACCGCGCAGCAAGCGGGGTATATGT 1702
Db  237  CTTTCTGGTGTGCGCCATAGCGTGCAACACAGACCGCGCAGCAAGCGGGGTATATGT 178
Qy  1703 GCTGGCTTTATCAACCAAGAGGGGCTCCCTGCAA 1738
Db  177  GCTGGCTTTATCAACCAAGAGGGGCTCCCTGCAA 142

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RESULT 9
AW016544/c
LOCUS      AW016544      344 bp      mRNA      linear      EST 10-SEP-1999
DEFINITION UI-H-BIOP-abg-g-04-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone
            IMAGE:2711982 3', mRNA sequence.
ACCESSION  AW016544
VERSION    AW016544.1 GI:5865301
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 344)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NCI-CGAP clone distribution
            information can be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA-No.
            Location/Qualifiers
              1..344
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2711982"
                /clone_lib="NCI_CGAP_Sub2"
                /lab_host="DH10B (Life Technologies)"
                /note="vector: pVT3D-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; The
                NCI CGAP Sub2 library is a subtracted library derived from
                BI-Bi constitutes a mixture of 21 normalized or
                subtracted NCI CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22
                , NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16,
                NCI_CGAP_Kid3, NCI_CGAP_Kid12, NCI_CGAP_Kid3,
                NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8,
                NCI_CGAP_CLL1, NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5
                , NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6

```

NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE_Kid3 Clones 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI CGAP Kid3 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clones 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

BASE COUNT 51 a 106 c 112 g 74 t 1 others

ORIGIN
Query Match 4.5%; Score 155; DB 10; Length 344;
Best Local Similarity 99.5%; Pred. No. 4.7e-65;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 327 TACCAGCTGGACCCGCTGGTCCACACCCGTTGGAGCCACCAAGCCGTTTGGGGGCTCCGCC 268
QY 1062 CACAACATCACCCAGGGATGCTCTCCAGACAGCAACATGATGAGCTGAAGGCTCTG 1121
DB 267 CACAACATCACCCAGGGATGCTCTCTNAGGACAGCAACATGATGAGCTGAAGGCTCTG 208
QY 1122 TCCTTCTCCGAGGAGTAGAAGCTGGCCACTCGACAGGACAGCAAGGCCCTCCG 1181
DB 207 TCCTTCTCCGAGGAGTAGAAGCTGGCCACTCGACAGGACAGCAAGGCCCTCCG 148
QY 1182 TGTGTCCGCTCCGCCATCTCCACGGA 1207
DB 147 TGTGTCCGCTCCGCCATCTCCACGGA 122

RESULT 10
AA644373/c
LOCUS
DEFINITION
AA644373
ACCESSION
AA644373.1 GI:2569591
VERSION
KEYWORDS
EST.
SOURCE
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 153)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gaisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wyllie, T., Watson, R., and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE
JOURNAL
COMMENT
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 698 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 146.

FEATURES

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1046802"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pTT3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 24 a 50 c 48 g 31 t

Query Match 3.5%; Score 122; DB 9; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1110 CTGAAGGCTGTCTCTCCGACGAGGTAGCAAGCTGGCCACTCGAACAAAGCAGAC 1169
DB 153 CTGAAGGCTGTCTCTCTCCGACGAGGTAGCAAGCTGGCCACTCGAACAAAGCAGAC 94
QY 1170 AAGGGCCCTCGTGTGTGCTCCGCCATCTCCACGACGAGTGCAGCATCCAGGAGCTG 1229
DB 93 AAGGGCCCTCGTGTGTGCTCCGCCATCTCCACGACGAGTGCAGCATCCAGGAGCTG 34

RESULT 11
AW028197/c
LOCUS
DEFINITION
AW028197
ACCESSION
AW028197.1 GI:5886953
VERSION
KEYWORDS
EST.
SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 397)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1067 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 139.
Location/Qualifiers
1. 397

FEATURES
source

RESULT 15
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DEFINITION
 355 bp DNA linear GSS 19-JUL-2001
RPCI-24-379B9.TV RPCI-24 Mus musculus genomic clone RPCI-24-379B9,
DNA sequence.
ACCESSION
BH105255
VERSION
BH105255.1 GI:14934019
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 355)
AUTHORS
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsengye,G., Geer,K., Krol,M., Shivartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
OTHER GSSES
RPCI-24-379B9.TJ

Search completed: June 17, 2003, 06:22:29
Job time : 3998.84 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 101.346 Seconds
(without alignments)
15794.017 Million cell updates/sec

Title: US-09-513-888c-1_COPY_4365_4419
Perfect score: 55
Sequence: 1 gagcgaggcagacacttgga.....atcagctggcccaacatgag 55

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 1000 summaries

Database :

GenEmbl.:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: gb_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9108	9	AF123653 Homo sapi
2	55	100.0	173264	2	AC025853 Homo sapi
C 3	40	72.7	5321	9	AB037741 Homo sapi
C 4	40	72.7	49999	6	AX015917 Sequence
5	40	72.7	70328	9	AL513472 Human DNA
C 6	40	72.7	100020	9	AC092165 Homo sapi
C 7	40	72.7	105051	2	AC009449 Homo sapi
C 8	40	72.7	124000	9	AP002498 Homo sapi
C 9	40	72.7	143034	9	AC104184 Homo sapi
C 10	40	72.7	146224	9	AC005883 Homo sapi
C 11	40	72.7	152591	2	AC068081 Homo sapi
12	40	72.7	158276	2	AC012033 Homo sapi
C 13	40	72.7	158608	9	CNS05TDJ Human chr
C 14	40	72.7	162190	2	AC020592 Homo sapi
C 15	40	72.7	170330	9	AC097638 Homo sapi
16	40	72.7	172033	9	AL136131 Human DNA
-17	40	72.7	173836	9	AC027125 Homo sapi
18	40	72.7	173889	2	AC013691 Homo sapi
C 19	40	72.7	175250	2	AC069521 Homo sapi
20	40	72.7	179816	2	AC074188 Homo sapi
21	40	72.7	179871	2	AC024602 Homo sapi
22	40	72.7	188126	9	AC087590 Homo sapi
23	40	72.7	190648	9	CNS01DXI Human chr
24	40	72.7	193332	2	AL355349 Homo sapi
C 25	40	72.7	210301	9	AF307337 Homo sapi
26	40	72.7	262951	2	AC124848 Homo sapi
27	39	70.9	129272	9	AL451125 Human DNA
28	39	70.9	167386	2	AL159993 Homo sapi
C 29	39	70.9	180859	2	AC025553 Homo sapi
C 30	38	69.1	78941	9	AC005591 Homo sapi
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32	38	69.1	171123	9	AC020779 Homo sapi
33	38	69.1	174384	2	AC009524 Homo sapi
C 34	38	69.1	179680	9	AC016138 Homo sapi
C 35	38	69.1	196860	2	AC091121 Homo sapi
C 36	37	67.3	95801	9	AC078776 Homo sapi
C 37	37	67.3	149304	9	AC090763 Homo sapi
C 38	37	67.3	150877	2	AC021095 Homo sapi
39	37	67.3	162786	2	AC010783 Homo sapi
40	37	67.3	181777	2	AC068866 Homo sapi
C 41	37	67.3	181980	2	AC011827 Homo sapi
42	37	67.3	187621	2	AC079060 Homo sapi
43	36	65.5	1524	9	AK021770 Homo sapi
44	36	65.5	2901	9	HS0804309 Homo sapi
C 45	36	65.5	10206	9	AL354664 Human DNA
46	36	65.5	72602	2	AC090541 Homo sapi
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65	36	65.5	168602	2	AF271406 Homo sapi

66	36	65.5	169633	9	AC023235	AC023235 Homo sapi	139	31	56.4	151933	2	AC073199	Homo sapi
67	36	65.5	174751	9	AC009137	AC009137 Homo sapi	c 140	31	56.4	159870	9	AC010333	Homo sapi
68	36	65.5	183146	9	AF003778	AF003778 Homo sapi	141	31	56.4	160039	9	AC106804	Homo sapi
69	36	65.5	189994	9	AP002762	AP002762 Homo sapi	142	31	56.4	163846	2	AL513126	Homo sapi
70	36	65.5	193332	2	AL355349	AL355349 Homo sapi	c 143	31	56.4	165653	2	AL138725	Human DNA
71	36	65.5	193989	9	AC015743	AC015743 Homo sapi	c 144	31	56.4	167667	2	AL449064	Homo sapi
72	36	65.5	194799	9	AC006430	AC006430 Homo sapi	145	31	56.4	167671	2	AC090081	Homo sapi
73	36	65.5	195007	2	CNS06C81	AL391749 Human chr	146	31	56.4	173786	2	AC024472	Homo sapi
74	36	65.5	202760	9	AC021987	AC021987 Homo sapi	c 147	31	56.4	174470	2	AC021888	Homo sapi
75	36	65.5	211403	2	AC019093	AC019093 Homo sapi	c 148	31	56.4	179641	9	AC098591	Homo sapi
76	36	65.5	225940	2	AC078799	AC078799 Homo sapi	c 149	31	56.4	180165	9	AC022017	Homo sapi
77	36	65.5	269564	2	AC015564	AC015564 Homo sapi	150	31	56.4	180455	9	AL603926	Human DNA
78	36	65.5	340000	9	AP001719	AP001719 Homo sapi	151	31	56.4	181510	2	AC026338	Homo sapi
79	35	63.6	570	6	AX390391	Sequence	152	31	56.4	185758	2	AC026552	Homo sapi
80	35	63.6	11345	2	AC069023	AC069023 Homo sapi	153	31	56.4	189927	30	AC037439	Homo sapi
81	35	63.6	137473	2	AC015944	AC015944 Homo sapi	154	31	56.4	223955	2	AC073911	Homo sapi
82	35	63.6	168513	2	AC011982	AC011982 Homo sapi	c 155	30	54.5	9449	2	AC106848	Homo sapi
83	35	63.6	173117	2	AL157885	AL157885 Homo sapi	c 156	30	54.5	29759	9	AL133392	Human DNA
84	35	63.6	183491	2	CNS01DU4	AL133163 Human chr	157	30	54.5	86825	9	AC006967	Homo sapi
85	35	63.6	186294	2	AC021108	AC021108 Homo sapi	c 158	30	54.5	96978	9	AC024075	Homo sapi
86	35	63.6	190195	9	AC016954	AC016954 Homo sapi	c 159	30	54.5	125041	2	AC068693	Homo sapi
87	35	63.6	211980	9	AC010735	AC010735 Homo sapi	160	30	54.5	133439	9	AC084438	Homo sapi
88	35	63.6	251124	9	HUAE000660	AB000660 Homo sapi	161	30	54.5	142933	9	AL513102	Human DNA
89	34	61.8	42030	2	AC007565	AC007565 Homo sapi	162	30	54.5	145437	9	HS545L17	Human DNA
90	34	61.8	73845	2	AL356478	AL356478 Homo sapi	163	30	54.5	148521	9	HS1111N9	Human DNA
91	34	61.8	128728	9	AL136179	AL136179 Human DNA	164	30	54.5	159082	9	AC025947	Homo sapi
92	34	61.8	148648	9	AC021713	AC021713 Homo sapi	c 165	30	54.5	168193	9	CNS05TE2	Human chr
93	34	61.8	159424	9	AF064865	AF064865 Homo sapi	c 166	30	54.5	174656	2	AC019249	Homo sapi
94	34	61.8	165531	2	AC023038	AC023038 Homo sapi	c 167	30	54.5	175827	9	AL358472	Human DNA
95	34	61.8	174992	2	AC025422	AC025422 Homo sapi	c 168	30	54.5	184027	2	AL691506	Homo sapi
96	34	61.8	176616	2	AC114489	AC114489 Homo sapi	c 169	30	54.5	215077	9	AC112504	Homo sapi
97	34	61.8	181823	2	AC040167	AC040167 Homo sapi	c 170	30	54.5	233461	9	AC092978	Homo sapi
98	34	61.8	185885	2	AC092122	AC092122 Homo sapi	c 171	29	52.7	293933	9	AC090040	Homo sapi
99	34	61.8	196247	2	HSJ65IN20	AL117346 Homo sapi	172	29	52.7	38046	9	AC092566	Homo sapi
100	34	61.8	340000	9	HSJ2C082	AL163282 Homo sapi	c 173	29	52.7	40146	2	AC092307	Homo sapi
101	33	60.0	38565	9	HS433G19	AL008735 Human DNA	c 174	29	52.7	46127	2	AC093230	Homo sapi
102	33	60.0	184989	2	AC113392	AC113392 Homo sapi	175	29	52.7	68420	2	AC130285	Homo sapi
103	33	60.0	191035	9	AC093527	AC093527 Homo sapi	176	29	52.7	140151	9	AC009804	Homo sapi
104	33	60.0	217328	2	AC007513	AC007513 Homo sapi	177	29	52.7	144046	2	AC068334	Homo sapi
105	33	60.0	223606	2	AC013479	AC013479 Homo sapi	c 178	29	52.7	152594	9	AL158196	Human DNA
106	32	58.2	77702	9	AC034241	AC034241 Homo sapi	c 179	29	52.7	163167	9	AC011347	Homo sapi
107	32	58.2	80506	9	AC098857	AC098857 Homo sapi	180	29	52.7	166016	9	AL591378	Human DNA
108	32	58.2	106465	9	HSJ765F13	AL109853 Human DNA	c 181	29	52.7	179056	9	AC068936	Homo sapi
109	32	58.2	113778	2	AC109438	AC109438 Homo sapi	c 182	29	52.7	182051	9	AC007638	Homo sapi
110	32	58.2	133042	9	AC011354	AC011354 Homo sapi	183	29	52.7	184896	2	AC012616	Homo sapi
111	32	58.2	135545	2	AC025184	AC025184 Homo sapi	184	29	52.7	189312	2	AC126406	Homo sapi
112	32	58.2	140628	2	AC016468	AC016468 Homo sapi	185	29	52.7	198141	9	AL355499	Human DNA
113	32	58.2	145161	2	AC012640	AC012640 Homo sapi	c 186	29	52.7	296483	2	AC069258	Homo sapi
114	32	58.2	151262	9	AC093824	AC093824 Homo sapi	c 187	28	50.9	3337	9	AB038344	Homo sapi
115	32	58.2	160822	2	AC020920	AC020920 Homo sapi	188	28	50.9	35414	9	AC005328	Homo sapi
116	32	58.2	161777	2	AC119056	AC119056 Papio cyn	c 189	28	50.9	70851	9	AC002540	Human BAC
117	32	58.2	162739	9	AL353788	AL353788 Human DNA	190	28	50.9	71123	2	AC130350	Homo sapi
118	32	58.2	169921	2	AC008913	AC008913 Homo sapi	c 191	28	50.9	73565	9	AC007962	Homo sapi
119	32	58.2	171148	9	AL359195	AL359195 Human DNA	c 192	28	50.9	97749	9	AC004906	Homo sapi
120	32	58.2	172309	9	AC018553	AC018553 Homo sapi	193	28	50.9	98069	9	AC011496	Homo sapi
121	32	58.2	176109	9	AC003992	AC003992 Homo sapi	194	28	50.9	109101	9	AL136446	Human DNA
122	32	58.2	182902	9	AC092405	AC092405 Papio cyn	195	28	50.9	119395	9	AL139189	Human DNA
123	32	58.2	184012	9	AC017080	AC017080 Homo sapi	c 196	28	50.9	119760	9	AC025458	Homo sapi
124	32	58.2	184092	2	AC124858	AC124858 Homo sapi	c 197	28	50.9	121460	2	AC027330	Homo sapi
125	32	58.2	186740	9	AC007343	AC007343 Homo sapi	c 198	28	50.9	126929	9	AC093801	Homo sapi
126	32	58.2	210230	9	AC103409	AC103409 Homo sapi	199	28	50.9	128289	9	AC007972	Homo sapi
127	32	58.2	218444	2	AL365256	AL365256 Homo sapi	c 200	28	50.9	131839	9	AC112166	Homo sapi
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130	31	56.4	51479	9	AL596137	AL596137 Human DNA	c 203	28	50.9	144165	9	AC002127	Human BAC
131	31	56.4	72245	9	HS93C23	AL008713 Human DNA	c 204	28	50.9	146741	9	AC011452	Homo sapi
132	31	56.4	79111	2	AC010257	Continuation (4 of	205	28	50.9	150728	2	AL158034	Homo sapi
133	31	56.4	79555	9	AL583856	AL583856 Human DNA	c 206	28	50.9	158560	9	AC098969	Homo sapi
134	31	56.4	85543	9	AC010553	AC010553 Homo sapi	c 207	28	50.9	159691	9	AC025160	Homo sapi
135	31	56.4	96678	9	AC108104	AC108104 Homo sapi	c 208	28	50.9	161449	9	AC005341	Homo sapi
136	31	56.4	120510	9	AL356457	AL356457 Human DNA	209	28	50.9	162043	2	AC018803	Homo sapi
137	31	56.4	127539	9	CNS01DSN	AL121821 Human chr	210	28	50.9	165458	2	AC090587	Homo sapi
138	31	56.4	140233	2	AC009422	AC009422 Homo sapi	c 211	28	50.9	168230	2	AC010624	Homo sapi

212	28	50.9	172893	2	AC024596	AC024596 Homo sapi
213	28	50.9	174396	2	AC021645	AC021645 Homo sapi
214	28	50.9	174535	2	AC106872	AC106872 Homo sapi
215	28	50.9	175756	2	AC034296	AC034296 Homo sapi
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218	28	50.9	178256	2	AC009027	AC009027 Homo sapi
219	28	50.9	181188	2	AC067983	AC067983 Homo sapi
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221	28	50.9	183901	2	AL356425	AL356425 Human DNA
222	28	50.9	186199	2	AC093708	AC093708 Pan trogl
223	28	50.9	189672	2	AL133480	AL133480 Homo sapi
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226	28	50.9	194385	2	CNS00001	AL049776 Human chr
227	28	50.9	205886	2	AC012504	AC012504 Homo sapi
228	28	50.9	215645	2	AC109329	AC109329 Homo sapi
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230	28	50.9	224292	2	AC026873	AC026873 Homo sapi
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235	27	49.1	125378	2	AL391416	AL391416 Human DNA
236	27	49.1	125429	2	AC084291	AC084291 Homo sapi
237	27	49.1	128728	2	AL136179	AL136179 Human DNA
238	27	49.1	146410	2	AC079002	AC079002 Homo sapi
239	27	49.1	146810	2	AL159170	AL159170 Human DNA
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254	27	49.1	196247	2	HS0651N20	HS0651N20 Homo sapi
255	27	49.1	201545	2	AC103967	AC103967 Homo sapi
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257	27	49.1	212030	2	AC019148	AC019148 Homo sapi
258	27	49.1	223879	2	AC008735	AC008735 Homo sapi
259	27	49.1	281662	2	AC117374	AC117374 Homo sapi
260	26	47.3	68589	2	HS237J2	AL021394 Human DNA
261	26	47.3	110000	2	AC117465_2	Continuation (3 of
262	26	47.3	120821	2	AC004702	AC004702 Homo sapi
263	26	47.3	129389	2	HS526114	Z82214 Human DNA s
264	26	47.3	132937	2	AC115097	AC115097 Homo sapi
265	26	47.3	136943	2	AL359842	AL359842 Human DNA
266	26	47.3	146811	2	AC084706	AC084706 Homo sapi
267	26	47.3	148973	2	CNS01DUZ	AL133374 Homo sapi
268	26	47.3	158779	2	AL713851	AL713851 Human DNA
269	26	47.3	162996	2	AC027682	AC027682 Homo sapi
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279	26	47.3	183807	2	AC091778	AC091778 Papio cyn
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282	26	47.3	193234	2	AC024293	AC024293 Homo sapi
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299	25	45.5	26128	2	HSJ885H15	AL049793 Human DNA
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301	25	45.5	33666	2	AC027214	AC027214 Homo sapi
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322	25	45.5	79470	2	AL391000	AL391000 Homo sapi
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326	25	45.5	84388	2	AL589984	AL589984 Human DNA
327	25	45.5	85836	2	AC108384	AC108384 Pan trogl
328	25	45.5	87616	2	AL133540	AL133540 Homo sapi
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333	25	45.5	95597	2	AC012555	AC012555 Homo sapi
334	25	45.5	97082	2	AC103888	AC103888 Homo sapi
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337	25	45.5	100152	2	AC000085	AC000085 Homo sapi
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345	25	45.5	108893	2	AC079169	AC079169 Homo sapi
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351	25	45.5	121050	2	AC074135	AC074135 Homo sapi
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354	25	45.5	124034	2	HS416J7	AL035696 Human DNA
355	25	45.5	124048	2	HUAC002045	AC002045 Human Chr
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C 372	25	45.5	140053	2	AC007873	Homo sapi	AC026896	Homo sapi
C 373	25	45.5	140179	2	AC084688	Homo sapi	AL161728	Human DNA
C 374	25	45.5	141963	2	AC121253	Homo sapi	AC004127	Homo sapi
C 375	25	45.5	142723	9	HS1039K5	Human DNA	AC027537	Homo sapi
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C 379	25	45.5	145329	2	AC055850	Homo sapi	AC074200	Homo sapi
C 380	25	45.5	145495	2	AC093273	Homo sapi	AC007216	Homo sapi
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C 396	25	45.5	152224	2	AC007933	Homo sapi	AC024357	Mus muscu
C 397	25	45.5	152626	2	AL357252	Homo sapi	AC016611	Homo sapi
C 398	25	45.5	153444	2	AC040948	Homo sapi	AF000501	Homo sapi
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C 405	25	45.5	156300	9	AC005919	Homo sapi	AC009161	Homo sapi
C 406	25	45.5	156399	9	AC002456	Homo sapi	AC016025	Homo sapi
C 407	25	45.5	156801	9	AC104740	Homo sapi	AC117181	Homo sapi
C 408	25	45.5	157324	9	AC013643	Homo sapi	AC027011	Homo sapi
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C 417	25	45.5	161696	2	AC093250	Homo sapi	AC093207	Homo sapi
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C 559	24	43.6	700	6	AX183424	AX183424 Sequence
C 560	24	43.6	731	9	HS607060	Z96665 H. sapiens t
C 561	24	43.6	897	9	AF278736	AF278736 Pygathrix
C 562	24	43.6	915	6	AX188339	AX188339 Sequence
C 563	24	43.6	1572	9	HSN040482	AX1404852 Homo sapi
C 564	24	43.6	1693	9	AK055893	AK055893 Homo sapi
C 565	24	43.6	1728	9	AK021930	AK021930 Homo sapi
C 566	24	43.6	1813	9	AK024205	AK024205 Homo sapi
C 567	24	43.6	1868	9	AK025326	AK025326 Homo sapi
C 568	24	43.6	1880	9	AB072764	AB072764 Macaca fa
C 569	24	43.6	1889	9	HSJ474M20	AL110117 Human DNA
C 570	24	43.6	1896	9	AK092411	AK092411 Homo sapi
C 571	24	43.6	2086	9	AK091792	AK091792 Homo sapi
C 572	24	43.6	2128	9	AK098787	AK098787 Homo sapi
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C 574	24	43.6	2167	9	AK095488	AK095488 Homo sapi
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C 576	24	43.6	2235	9	AK022396	AK022396 Homo sapi

C 577	24	43.6	2272	9	HSU34054	U34054 Human Down
C 578	24	43.6	2342	9	AK097130	AK097130 Homo sapi
C 579	24	43.6	2357	9	HSM805079	AL837366 Homo sapi
C 580	24	43.6	2360	9	AK074353	AK074353 Homo sapi
C 581	24	43.6	2476	9	AK097927	AK097927 Homo sapi
C 582	24	43.6	2603	9	HSM802565	AL162045 Homo sapi
C 583	24	43.6	2646	9	BC005142	BC005142 Homo sapi
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C 585	24	43.6	3019	9	AK056809	AK056809 Homo sapi
C 586	24	43.6	3069	9	HSRAP	X67123 H. sapiens T
C 587	24	43.6	3079	9	AB058709	AB058709 Homo sapi
C 588	24	43.6	3270	9	HSM803853	AL832544 Homo sapi
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C 590	24	43.6	3447	9	AL1390014	AL1390014 Human DNA
C 591	24	43.6	3492	9	HSAPDEVPL3	U72845 Homo sapien
C 592	24	43.6	3498	9	AC0931072	AC0931072 Homo sapi
C 593	24	43.6	3896	9	HSU50434	U50434 Human Down
C 594	24	43.6	3994	9	AC118058	AL18058 Homo sapi
C 595	24	43.6	4178	9	BC036445	BC036445 Homo sapi
C 596	24	43.6	4434	9	AK024494	AK024494 Homo sapi
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C 602	24	43.6	6023	9	HSMTGRIE13	AF076461 Homo sapi
C 603	24	43.6	6135	9	AF060972S1	AF060972 Homo sapi
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C 605	24	43.6	6977	9	HSMCRP2	AF073485 Homo sapi
C 606	24	43.6	7004	9	HSPDEEX13	X90589 H. sapiens D
C 607	24	43.6	7161	9	AB011168	AB011168 Homo sapi
C 608	24	43.6	7174	9	HSM804580	AL833267 Homo sapi
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C 611	24	43.6	10988	9	AL592286	AL592286 Human DNA
C 612	24	43.6	12053	9	AL590722	AL590722 Human DNA
C 613	24	43.6	12253	9	AL450285	AL450285 Human DNA
C 614	24	43.6	12610	9	HS30A23	AL022156 Human DNA
C 615	24	43.6	13133	9	HS30A23	X87579 H. sapiens C
C 616	24	43.6	13135	9	AL589908	AL589908 Human DNA
C 617	24	43.6	13208	9	AB028893	AB028893 Homo sapi
C 618	24	43.6	13271	9	AL365231	AL365231 Human DNA
C 619	24	43.6	13472	9	AF020057	AF020057 Homo sapi
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C 621	24	43.6	14140	9	HS24F8	Z69666 Human DNA s
C 622	24	43.6	17072	9	HUMFDHAL	D90084 Human pyruv
C 623	24	43.6	17586	9	AL591507	AL591507 Human DNA
C 624	24	43.6	18285	9	HS437022	AL035496 Human DNA
C 625	24	43.6	18922	9	AC108208	AC108208 Homo sapi
C 626	24	43.6	19654	9	D86566	D86566 Human DNA f
C 627	24	43.6	20267	9	AB000877	AB000877 Homo sapi
C 628	24	43.6	22038	9	HSPMFG2	AF141309 Homo sapi
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C 631	24	43.6	24420	9	AC0353585	AL353585 Human DNA
C 632	24	43.6	25183	9	AC073079	AC073079 Homo sapi
C 633	24	43.6	25605	9	AC023280	AC023280 Homo sapi
C 634	24	43.6	26078	9	AF376770	AF376770 Homo sapi
C 635	24	43.6	27084	9	AL133297	AL133297 Human DNA
C 636	24	43.6	27745	9	AC112915	AC112915 Homo sapi
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C 638	24	43.6	28945	9	AF048729	AF048729 Homo sapi
C 639	24	43.6	29145	9	AL138771	AL138771 Human DNA
C 640	24	43.6	29186	9	AL357560	AL357560 Human DNA
C 641	24	43.6	29359	2	AP001083	AP001083 Homo sapi
C 642	24	43.6	29507	9	AL391064	AL391064 Human DNA
C 643	24	43.6	29518	9	AL136361	AL136361 Human DNA
C 644	24	43.6	29862	9	AL662798	AL662798 Human DNA
C 645	24	43.6	30110	9	HSU124H12	Z49918 Human DNA s
C 646	24	43.6	30190	9	AC108010	AC108010 Homo sapi
C 647	24	43.6	30625	6	AX491281	AX491281 Sequence
C 648	24	43.6	30676	6	AX491284	AX491284 Sequence
C 649	24	43.6	30980	9	AC003102	AC003102 Homo sapi

c 650	24	43.6	31325	9	AP000274	Homo sapi	723	24	43.6	46460	2	AC113248	Homo sapi
c 651	24	43.6	31679	9	AL772330	Human DNA	c 724	24	43.6	46894	9	AC114729	Homo sapi
c 652	24	43.6	31720	9	HS19663	Human DNA	c 725	24	43.6	47084	9	AC011515	Homo sapi
c 653	24	43.6	31874	9	HSB44467	Human DNA	c 726	24	43.6	47152	9	AP001542	Homo sapi
c 654	24	43.6	32360	9	AL607067	Human DNA	c 727	24	43.6	47159	9	AL160011	Human DNA
c 655	24	43.6	32633	9	AC009402	Homo sapi	c 728	24	43.6	47972	9	AL391843	Human DNA
c 656	24	43.6	33963	9	AB065669	Homo sapi	c 729	24	43.6	48036	9	HS633019	Human DNA
c 657	24	43.6	34335	9	AC126776	Homo sapi	c 730	24	43.6	48606	2	AC025671	Homo sapi
c 658	24	43.6	34336	9	AC000094	Homo sapi	c 731	24	43.6	48730	9	AL136301	Human DNA
c 659	24	43.6	34680	9	AC023159	Homo sapi	c 732	24	43.6	49049	9	AL108023	Homo sapi
c 660	24	43.6	34864	9	U73649	Human Chrom	c 733	24	43.6	49217	9	HS179D3	Human DNA
c 661	24	43.6	35116	9	AC004151	Homo sapi	c 734	24	43.6	49322	9	AC112788	Homo sapi
c 662	24	43.6	36037	9	AC003966	Homo sapi	c 735	24	43.6	49936	9	HSJ816K9	Human DNA
c 663	24	43.6	36787	9	AC108072	Homo sapi	c 736	24	43.6	50675	2	AC087448	Homo sapi
c 664	24	43.6	36838	9	AC020947	Homo sapi	c 737	24	43.6	50675	2	AC087448	Homo sapi
c 665	24	43.6	36892	9	AC099797	Homo sapi	c 738	24	43.6	51190	9	AC091637	Human DNA
c 666	24	43.6	37000	9	AL663061	Human DNA	c 739	24	43.6	51859	9	HSJ1193N1	Human DNA
c 667	24	43.6	37001	9	AC005513	Homo sapi	c 740	24	43.6	51874	2	AC129511	Homo sapi
c 668	24	43.6	37107	9	AC009000	Homo sapi	c 741	24	43.6	52193	9	AL139011	Human DNA
c 669	24	43.6	37107	9	AC009000	Homo sapi	c 742	24	43.6	52884	2	AC068018	Homo sapi
c 670	24	43.6	37392	9	AC005946	Homo sapi	c 743	24	43.6	53000	2	AC003656	Continuation (8 of
c 671	24	43.6	37425	9	AP000308	Homo sapi	c 744	24	43.6	53402	9	AL158844	Human DNA
c 672	24	43.6	37535	9	AC113341	Homo sapi	c 745	24	43.6	53430	2	AC116166	Homo sapi
c 673	24	43.6	37552	9	AL391993	Human DNA	c 746	24	43.6	53448	2	AC103682	Homo sapi
c 674	24	43.6	38055	2	AC006190	Homo sapi	c 747	24	43.6	53773	9	AL355342	Human DNA
c 675	24	43.6	38149	9	AC022154	Homo sapi	c 748	24	43.6	53805	9	AC109360	Homo sapi
c 676	24	43.6	38411	9	AC005257	Homo sapi	c 749	24	43.6	54054	2	AC013600	Homo sapi
c 677	24	43.6	38476	9	U73034	Homo sapi	c 750	24	43.6	54058	2	AL611965	Continuation (4 of
c 678	24	43.6	38649	9	AC004391	Homo sapi	c 751	24	43.6	54184	9	AL713889	Human DNA
c 679	24	43.6	38888	9	AC092301	Homo sapi	c 752	24	43.6	55001	9	AL133507	Human DNA
c 680	24	43.6	38939	9	AC004678	Homo sapi	c 753	24	43.6	55469	9	AL445490	Human DNA
c 681	24	43.6	39196	9	AB023060	Homo sapi	c 754	24	43.6	55860	9	AC112505	Homo sapi
c 682	24	43.6	39198	6	AX078379	Sequence	c 755	24	43.6	56295	9	AC004011	Human BAC
c 683	24	43.6	39383	9	AC022149	Homo sapi	c 756	24	43.6	56295	9	AC004011	Human DNA
c 684	24	43.6	39426	9	AC008983	Homo sapi	c 757	24	43.6	56611	2	AC111183	Human DNA
c 685	24	43.6	39443	9	AC010505	Homo sapi	c 758	24	43.6	56813	9	AL390955	Human DNA
c 686	24	43.6	39594	9	AC005624	Homo sapi	c 759	24	43.6	56827	9	HSMHCA35	U93335 Homo sapien
c 687	24	43.6	39744	9	AC068296	Homo sapi	c 760	24	43.6	57316	9	AL353796	Human DNA
c 688	24	43.6	40111	9	AL603833	Human DNA	c 761	24	43.6	57408	9	AL670471	Human DNA
c 689	24	43.6	40352	9	AF272142	Homo sapi	c 762	24	43.6	57688	9	AP000048	Homo sapi
c 690	24	43.6	40583	9	AC005621	Homo sapi	c 763	24	43.6	57722	2	HSCB33B10	282175 Homo sapien
c 691	24	43.6	41459	9	AC004637	Homo sapi	c 764	24	43.6	57759	9	AL137162	Human DNA
c 692	24	43.6	41503	9	AL137185	Human DNA	c 765	24	43.6	57966	2	AC027692	Homo sapi
c 693	24	43.6	41618	9	AL355473	Human DNA	c 766	24	43.6	58274	2	AC084092	Homo sapi
c 694	24	43.6	41907	9	AC009001	Homo sapi	c 767	24	43.6	58345	9	AC011999	Homo sapi
c 695	24	43.6	41918	9	AC114765	Homo sapi	c 768	24	43.6	59105	9	AC004013	Human BAC
c 696	24	43.6	42019	9	AC000082	Homo sapi	c 769	24	43.6	59505	2	AC130706	Human DNA
c 697	24	43.6	42213	9	AC010527	Homo sapi	c 770	24	43.6	59506	2	AC060787	Homo sapi
c 698	24	43.6	42213	9	AC010527	Homo sapi	c 771	24	43.6	59510	2	AC126384	Homo sapi
c 699	24	43.6	42265	9	AC010504	Homo sapi	c 772	24	43.6	59596	9	HS449017	298749 Human DNA s
c 700	24	43.6	42393	9	AC005400	Homo sapi	c 773	24	43.6	59634	9	AC062028	Homo sapi
c 701	24	43.6	42949	9	AC104665	Homo sapi	c 774	24	43.6	59657	9	AC074013	Homo sapi
c 702	24	43.6	42987	9	AC005576	Homo sapi	c 775	24	43.6	59731	9	AC068442	Homo sapi
c 703	24	43.6	43018	9	AL356142	Human DNA	c 776	24	43.6	59776	9	AC098831	Homo sapi
c 704	24	43.6	43034	9	HSN5H6	293024 Human DNA s	c 777	24	43.6	60385	2	AC009511	Homo sapi
c 705	24	43.6	43456	9	AL353113	Human DNA	c 778	24	43.6	60481	2	AC099844	Homo sapi
c 706	24	43.6	43473	9	AF022141	Homo sapi	c 779	24	43.6	60857	2	AC039800	Homo sapi
c 707	24	43.6	43632	9	AC108358	Homo sapi	c 780	24	43.6	61101	2	AC083975	Homo sapi
c 708	24	43.6	44073	2	AC110293	Homo sapi	c 781	24	43.6	61169	2	AC129487	Homo sapi
c 709	24	43.6	44185	9	AP000701	Homo sapi	c 782	24	43.6	61209	9	AP000220	Homo sapi
c 710	24	43.6	44348	9	AC006046	Homo sapi	c 783	24	43.6	61541	9	AC005232	Homo sapi
c 711	24	43.6	44379	9	AC006163	Homo sapi	c 784	24	43.6	61633	2	AC084075	Homo sapi
c 712	24	43.6	44544	9	AC004262	Homo sapi	c 785	24	43.6	62138	2	AC100831	Homo sapi
c 713	24	43.6	44767	9	AL669893	Human DNA	c 786	24	43.6	62147	2	AC026510	Homo sapi
c 714	24	43.6	44830	9	HSJ738A13	Human DNA	c 787	24	43.6	62186	2	AC110604	Homo sapi
c 715	24	43.6	44868	9	AL353892	Human DNA	c 788	24	43.6	62249	2	AC091592	Homo sapi
c 716	24	43.6	45333	9	HS10618A	Human DNA	c 789	24	43.6	62825	2	AC090452	Homo sapi
c 717	24	43.6	45381	2	AC018585	Homo sapi	c 790	24	43.6	62825	2	AC090452	Homo sapi
c 718	24	43.6	45572	9	AC011530	Homo sapi	c 791	24	43.6	62906	2	AL391628	Human DNA
c 719	24	43.6	45858	9	AC006123	Homo sapi	c 792	24	43.6	63367	2	AC090915	Homo sapi
c 720	24	43.6	45980	6	AX473125	Sequence	c 793	24	43.6	63629	2	AC091187	Homo sapi
c 721	24	43.6	46225	9	AC069305	Homo sapi	c 794	24	43.6	63650	2	AC084342	Homo sapi
c 722	24	43.6	46239	9	AP003391	Homo sapi	c 795	24	43.6	63905	2	AC022515	Homo sapi

C 796	24	43.6	63930	2	AC106017	Homo sapi
C 797	24	43.6	64196	9	AC110804	Homo sapi
C 798	24	43.6	64329	9	AL449188	Human DNA
C 799	24	43.6	64359	9	AC005233	Homo sapi
C 800	24	43.6	64544	2	AC117551	Mus muscu
C 801	24	43.6	64693	9	AL662907	Human DNA
C 802	24	43.6	64789	2	AC083839	Homo sapi
C 803	24	43.6	65111	2	AC055857	Homo sapi
C 804	24	43.6	65111	2	AC055857	Homo sapi
C 805	24	43.6	65138	9	AL590812	Human DNA
C 806	24	43.6	65694	2	AC091065	Homo sapi
C 807	24	43.6	65777	2	AC124299	Homo sapi
C 808	24	43.6	65961	2	AC090266	Homo sapi
C 809	24	43.6	66058	2	AC090065	Homo sapi
C 810	24	43.6	66353	2	AC095348	Homo sapi
C 811	24	43.6	66403	9	AC074295	Homo sapi
C 812	24	43.6	66477	9	AL591133	Human DNA
C 813	24	43.6	66497	2	AC073026	Homo sapi
C 814	24	43.6	66660	9	AC013270	Homo sapi
C 815	24	43.6	66761	2	AC044823	Homo sapi
C 816	24	43.6	66768	2	AC126389	Homo sapi
C 817	24	43.6	66788	9	AL353653	Human DNA
C 818	24	43.6	66817	9	AC005201	Homo sapi
C 819	24	43.6	66867	2	AC073170	Homo sapi
C 820	24	43.6	66933	6	AX277532	Sequence
C 821	24	43.6	66933	6	AX418096	Sequence
C 822	24	43.6	67120	2	AC130331	Homo sapi
C 823	24	43.6	67289	2	AC040994	Homo sapi
C 824	24	43.6	67434	2	AC090801	Homo sapi
C 825	24	43.6	67529	2	AC069312	Homo sapi
C 826	24	43.6	67610	2	AC084344	Homo sapi
C 827	24	43.6	68001	9	AP001442	Homo sapi
C 828	24	43.6	68048	9	AC004764	Homo sapi
C 829	24	43.6	68049	9	AL513322	Human DNA
C 830	24	43.6	68049	9	AL513322	Human DNA
C 831	24	43.6	68065	2	AC110285	Homo sapi
C 832	24	43.6	68273	9	AL138695	Human DNA
C 833	24	43.6	68468	9	HM9651	Human DNA
C 834	24	43.6	68589	2	AC087682	Homo sapi
C 835	24	43.6	68651	9	AC027343	Homo sapi
C 836	24	43.6	68692	2	AP003163	Homo sapi
C 837	24	43.6	69012	2	AC023849	Homo sapi
C 838	24	43.6	69097	9	AL356235	Human DNA
C 839	24	43.6	69113	9	AL359960	Human DNA
C 840	24	43.6	69291	2	AC107957	Homo sapi
C 841	24	43.6	69373	9	AL513331	Human DNA
C 842	24	43.6	69397	2	AC036233	Homo sapi
C 843	24	43.6	69413	9	AL136172	Human DNA
C 844	24	43.6	69570	2	AC021246	Homo sapi
C 845	24	43.6	69570	2	AC055831	Homo sapi
C 846	24	43.6	69637	9	AL138745	Human DNA
C 847	24	43.6	69656	9	AL390729	Human DNA
C 848	24	43.6	69684	9	AC006475	Homo sapi
C 849	24	43.6	69967	2	AC126337	Homo sapi
C 850	24	43.6	70128	9	AC007536	Homo sapi
C 851	24	43.6	70193	9	AL627303	Human DNA
C 852	24	43.6	70203	2	AC024012	Homo sapi
C 853	24	43.6	70288	9	AL662867	Human DNA
C 854	24	43.6	70299	9	AL161945	Human DNA
C 855	24	43.6	70638	9	AC079306	Homo sapi
C 856	24	43.6	70975	2	AP000579	Homo sapi
C 857	24	43.6	71132	2	AC130383	Homo sapi
C 858	24	43.6	71132	9	AC092184	Homo sapi
C 859	24	43.6	71206	2	AC027744	Homo sapi
C 860	24	43.6	71353	9	AF104455	Homo sapi
C 861	24	43.6	71418	9	AL732442	Human DNA
C 862	24	43.6	71438	9	AC026754	Homo sapi
C 863	24	43.6	72049	6	AX277530	Sequence
C 864	24	43.6	72049	6	AX418094	Sequence
C 865	24	43.6	72302	2	AC090995	Homo sapi
C 866	24	43.6	72356	9	AL583861	Human DNA
C 867	24	43.6	72383	2	AC027746	Homo sapi
C 868	24	43.6	72417	2	AC087497	Homo sapi

C 869	24	43.6	72568	9	AC106762	Homo sapi
C 870	24	43.6	72826	9	AL391539	Human DNA
C 871	24	43.6	73087	9	HS147M19	Homo sapi
C 872	24	43.6	73141	2	AC025123	Homo sapi
C 873	24	43.6	73149	9	AL590642	Human DNA
C 874	24	43.6	73246	2	AC089463	Homo sapi
C 875	24	43.6	73246	2	AC066592	Homo sapi
C 876	24	43.6	73899	9	AC005156	Homo sapi
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C 888	24	43.6	76875	2	AC018419	Homo sapi
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C 890	24	43.6	77313	9	AC110757	Homo sapi
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C 892	24	43.6	77808	9	AL512634	Human DNA
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C 896	24	43.6	79470	2	AL391000	Homo sapi
C 897	24	43.6	79509	9	AL353769	Human DNA
C 898	24	43.6	79516	9	AC004834	Homo sapi
C 899	24	43.6	80010	9	AC005995	Homo sapi
C 900	24	43.6	80119	9	AC111152	Homo sapi
C 901	24	43.6	80146	9	AL583963	Human DNA
C 902	24	43.6	80198	9	AP003040	Homo sapi
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C 912	24	43.6	81896	9	AL663123	Human DNA
C 913	24	43.6	81914	9	HS0J63M2	Human DNA
C 914	24	43.6	82329	9	AL160162	Human DNA
C 915	24	43.6	82494	9	AL357146	Human DNA
C 916	24	43.6	82771	2	AC011953	Homo sapi
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C 920	24	43.6	83306	9	AC062021	Homo sapi
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C 922	24	43.6	83709	9	HSJ403A15	Human DNA
C 923	24	43.6	83727	9	AL356120	Human DNA
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C 928	24	43.6	84364	9	HS522J7	Human DNA
C 929	24	43.6	84759	9	AC100838	Homo sapi
C 930	24	43.6	84841	9	AL391813	Human DNA
C 931	24	43.6	84997	9	AL583832	Human DNA
C 932	24	43.6	85086	9	AL589946	Human DNA
C 933	24	43.6	85275	9	AC092180	Homo sapi
C 934	24	43.6	85322	9	AL138923	Human DNA
C 935	24	43.6	85543	2	AC010553	Homo sapi
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ALIGNMENTS

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LOCUS Homo sapiens FEZ1 (FEZ1) gene, complete cds.
ACCESSION AF123653
VERSION AF123653.1 GI:4572463
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9108)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
99199287
MEDLINE
10097140.
REFERENCE
2 (bases 1 to 9108)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2338 10th street, Philadelphia, PA 19107, USA
FEATURES
Location/Qualifiers
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/genes="FEZ1"
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/protein_id="FEZ1"
/db_xref="GI:4572464"
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LQDNNMSLKALSFSDGSKLGHSHKADKSPCVSPISSTDECSIQELQKLEREGA
LQKQSRPEKLESLMKQDLLETLRKSRERKTSFGPALEETQWECVQSGSEIS
LQKQKESQTEVNKASLELQKQKDLTRKLEGLRQDLEGLARTRKQLELEVC
ENLQKQKNEALLREKVNALLQELQKQALALARDMGPTTFEDVPALQRLERLR
AELRBRQGHQDMSGFGHERLVWKEEKVIQYQKQSQSYVAMYQNRQRLKALQQ
LARGDSAGSPELVLDLEGADIPYDIATETI"
BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others
ORIGIN
Query Match 100.0%; Score 55; DB 9; Length 9108;
Best Local Similarity 100.0%; Pred. No. 2.5e-21;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCGAGGAGACACTTGAGGTCAGGATTCAGATCAGCCTGGCCACATGAG 55
Db 4425 GAGCGAGGAGACACTTGAGGTCAGGATTCAGATCAGCCTGGCCACATGAG 4479
RESULT 2
AC025853 AC025853 173264 bp DNA linear HTG 17-JUN-2002
LOCUS Homo sapiens chromosome 8 clone RP11-353K12 map 8, *** SEQUENCING
DEFINITION IN PROGRESS ***, 3 unordered pieces.
ACCESSION AC025853
VERSION AC025853.13 GI:21431202
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173264)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-353K12
Unpublished
REFERENCE
2 (bases 1 to 173264)
```

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPeters, R., Meldrim, J., Meneus, B., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 173264)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, B., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Robert, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 17, 2002 this sequence version replaced gi:21321864.

All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Smith, A.F.A. & Green, P. (1996-1997)

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7454

Center clone name: 353_K_12

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 39461: contig of 39461 bp in length

* 39462 39561: gap of 100 bp

FEATURES

source

* 39562 108347: contig of 68786 bp in length
* 108348 108447: gap of 100 bp
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 2.3e-21;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

AB037741/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

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VSDWIKNTEVSGVEREDPVIOMFWVEVVEDITQSERVLLLOFVTGSRVRPHGCFANIM
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ORIGIN

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Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS

DEFINITION Sequence 20 from Patent WO9950284.

ACCESSION AX015917

VERSION AX015917.1 GI:10041660

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 49999)

Aigner, T., Hess, J., Rosenthal, A., Rump, A. and Wirth, T.

Nucleic acid molecules which code proteins influencing bone

development

Patient: WO 950284-A 20 OCT-1999;

AIGNER THOMAS (DE); HESS JOCHEN (DE); ROSENTHAL ANDRE (DE); RUMP

ANDREAS (DE); WIRTH THOMAS (DE)

FEATURES

source

1. 49999

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 10382 a 14932 c 14107 g 10578 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 40; DB 6; Length 49999;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 24864 CACTTGAGTTCAGGAATTCGAGATCAGCTGCCCAACATG 24825

RESULT 5

AL513472

LOCUS

DEFINITION Human DNA sequence from clone RP11-271J19 on chromosome 6, complete

sequence.

ACCESSION AL513472

VERSION AL513472.9 GI:14031111

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 70328)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

LAIRD, G.

Direct Submission

Submitted (10-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On May 14, 2001 this sequence version replaced gi:13751550.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given in the feature table with their source databases: En:, EMBL; Sw:,

SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6

RP11-271J19 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-271J19 it may be shorter because we sequence overlapping

sections only once, except for a 100 base overlap.

The true left end of clone RP11-271J19 is at 1 in this sequence.

The true left end of clone RP11-809N15 is at 70229 in this sequence.

FEATURES

source

1. 70328

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="RP11-271J19"

/clone_lib="RPCI-11.1"

/notes="L1ME3A repeat: matches 5280. 6153 of consensus"

2379. 2984

/note="L2 repeat: matches 1844. 2412 of consensus"

2979. 3100

/note="L2 repeat: matches 2617. 2750 of consensus"

3272. 3428

/note="FRAM repeat: matches 4. 157 of consensus"

3714. 3777

/note="32 copies 2 mer aa 78% conserved"

5007. 7916

/note="L1PA7 repeat: matches -567. 3339 of consensus"

7918. 8213

/note="ALUSg repeat: matches 2. 296 of consensus"

8363. 14484

/note="L1PA7 repeat: matches 11. 6141 of consensus"

14495. 14800

/note="ALUy repeat: matches 1. 306 of consensus"

15089. 15553

/note="Tiger4 (Zombi) repeat: matches 2274. 2731 of

consensus"

15554. 15853

/note="ALUSx repeat: matches 1. 303 of consensus"

15854. 15864

/note="Tiger4 (Zombi) repeat: matches 2265. 2274 of

consensus"

15865. 16163

/note="ALUSx repeat: matches 1. 296 of consensus"

16164. 18241

/note="Tiger4 (Zombi) repeat: matches 1. 2265 of

consensus"

18608. 18677

/note="U6 repeat: matches 1. 71 of consensus"

18680. 18839

/note="MIR repeat: matches 63. 251 of consensus"

19021. 19555

/note="L2 repeat: matches 1850. 2371 of consensus"

20821. 21093

repeat_region /notes="AluJo repeat: matches 28. .298 of consensus"
21779. .21848 /notes="LIPa6 repeat: matches 11. .6143 of consensus"
repeat_region /notes="MIR repeat: matches 119. .191 of consensus"
2223. .22522 /notes="AluJo repeat: matches 1. .288 of consensus"
repeat_region /notes="AluSc repeat: matches 1. .300 of consensus"
24173. .24214 /notes="AluSc repeat: matches 1. .304 of consensus"
repeat_region /notes="AluSc repeat: matches 1. .300 of consensus"
24555. .24825 /notes="AluSc repeat: matches 1. .300 of consensus"
repeat_region /notes="LIPa6 repeat: matches 5909. .6184 of consensus"
24951. .25016 /notes="LIPa6 repeat: matches 5909. .6184 of consensus"
repeat_region /notes="L2 repeat: matches 2641. .2710 of consensus"
25752. .25837 /notes="L2 repeat: matches 2641. .2710 of consensus"
repeat_region /notes="MIR repeat: matches 173. .262 of consensus"
25867. .26175 /notes="MIR repeat: matches 173. .262 of consensus"
repeat_region /notes="AluYa5 repeat: matches 1. .308 of consensus"
26180. .26465 /notes="AluYa5 repeat: matches 1. .308 of consensus"
repeat_region /notes="AluSc repeat: matches 5. .289 of consensus"
26846. .27189 /notes="AluSc repeat: matches 5. .289 of consensus"
repeat_region /notes="AluYb8 repeat: matches 1. .308 of consensus"
28316. .28454 /notes="AluYb8 repeat: matches 1. .308 of consensus"
repeat_region /notes="MIR repeat: matches 38. .188 of consensus"
29560. .29844 /notes="MIR repeat: matches 38. .188 of consensus"
repeat_region /notes="AluX repeat: matches 1. .286 of consensus"
30299. .30607 /notes="AluX repeat: matches 1. .286 of consensus"
repeat_region /notes="AluJo repeat: matches 1. .295 of consensus"
31460. .31626 /notes="AluJo repeat: matches 1. .295 of consensus"
repeat_region /notes="MIR repeat: matches 23. .196 of consensus"
31665. .31799 /notes="MIR repeat: matches 23. .196 of consensus"
repeat_region /notes="MIR repeat: matches 124. .262 of consensus"
32065. .32098 /notes="MIR repeat: matches 124. .262 of consensus"
repeat_region /notes="L2 repeat: matches 17. .85% conserved"
32368. .32965 /notes="L2 repeat: matches 17. .85% conserved"
repeat_region /notes="LIMC4 repeat: matches 7167. .7837 of consensus"
32975. .33268 /notes="LIMC4 repeat: matches 7167. .7837 of consensus"
repeat_region /notes="LIMC4 repeat: matches 5335. .6939 of consensus"
33309. .33415 /notes="LIMC4 repeat: matches 5335. .6939 of consensus"
repeat_region /notes="LIMC4 repeat: matches 6445. .6574 of consensus"
33779. .33886 /notes="LIMC4 repeat: matches 6445. .6574 of consensus"
repeat_region /notes="MADE1 repeat: matches 2. .80 of consensus"
33956. .33993 /notes="MADE1 repeat: matches 2. .80 of consensus"
repeat_region /notes="MIR repeat: matches 1. .36 of consensus"
33994. .34297 /notes="MIR repeat: matches 1. .36 of consensus"
repeat_region /notes="AluYb repeat: matches 3. .311 of consensus"
34298. .34438 /notes="AluYb repeat: matches 3. .311 of consensus"
repeat_region /notes="MIR repeat: matches 36. .189 of consensus"
35192. .35360 /notes="MIR repeat: matches 36. .189 of consensus"
repeat_region /notes="MIR repeat: matches 64. .259 of consensus"
35678. .35727 /notes="MIR repeat: matches 64. .259 of consensus"
repeat_region /notes="L2 repeat: matches 2656. .2705 of consensus"
37839. .38143 /notes="L2 repeat: matches 2656. .2705 of consensus"
repeat_region /notes="AluX repeat: matches 1. .299 of consensus"
38242. .38418 /notes="AluX repeat: matches 1. .299 of consensus"
repeat_region /notes="AluYb repeat: matches 135. .311 of consensus"
42257. .42569 /notes="AluYb repeat: matches 135. .311 of consensus"
repeat_region /notes="AluYb repeat: matches 1. .311 of consensus"
44398. .44773 /notes="AluYb repeat: matches 1. .311 of consensus"
repeat_region /notes="LTR3 repeat: matches 1. .369 of consensus"
44774. .45072 /notes="LTR3 repeat: matches 1. .369 of consensus"
repeat_region /notes="AluY repeat: matches 2. .301 of consensus"
45896. .46024 /notes="AluY repeat: matches 2. .301 of consensus"
repeat_region /notes="MIR repeat: matches 94. .239 of consensus"
46408. .46698 /notes="MIR repeat: matches 94. .239 of consensus"
repeat_region /notes="AluX repeat: matches 1. .295 of consensus"
47883. .48195 /notes="AluX repeat: matches 1. .295 of consensus"
repeat_region /notes="AluYb repeat: matches 1. .307 of consensus"
49573. .49884 /notes="AluYb repeat: matches 1. .307 of consensus"
repeat_region /notes="AluSc repeat: matches 1. .313 of consensus"
50973. .51063 /notes="AluSc repeat: matches 1. .313 of consensus"
repeat_region /notes="MER93 repeat: matches 1. .91 of consensus"
51111. .51331 /notes="MER93 repeat: matches 1. .91 of consensus"
repeat_region /note="MER93 repeat: matches 179. .397 of consensus"
51333. .51451 /note="MER93 repeat: matches 179. .397 of consensus"
/notes="MIR repeat: matches 28. .151 of consensus"

51549. .57643 /notes="LIPa6 repeat: matches 11. .6143 of consensus"
repeat_region /notes="AluJo repeat: matches 1. .288 of consensus"
57966. .58253 /notes="AluJo repeat: matches 1. .288 of consensus"
repeat_region /notes="AluSc repeat: matches 1. .304 of consensus"
58803. .59107 /notes="AluSc repeat: matches 1. .304 of consensus"
repeat_region /notes="AluSc repeat: matches 1. .300 of consensus"
59691. .59991 /notes="AluSc repeat: matches 1. .300 of consensus"
repeat_region /notes="MIR repeat: matches 79. .249 of consensus"
60098. .60266 /notes="MIR repeat: matches 79. .249 of consensus"
repeat_region /notes="L2 repeat: matches 1685. .2710 of consensus"
60903. .61893 /notes="L2 repeat: matches 1685. .2710 of consensus"
repeat_region /notes="L2 repeat: matches 2628. .2710 of consensus"
62439. .62517 /notes="L2 repeat: matches 2628. .2710 of consensus"
repeat_region /notes="L2 repeat: matches 2628. .2710 of consensus"
62995. .63070 /notes="L2 repeat: matches 2628. .2710 of consensus"
repeat_region /notes="38 copies 2 mer ta 81% conserved"
63395. .63587 /notes="38 copies 2 mer ta 81% conserved"
repeat_region /notes="MER3 repeat: matches 8. .199 of consensus"
63995. .64246 /notes="MER3 repeat: matches 8. .199 of consensus"
repeat_region /notes="AluJo repeat: matches 49. .296 of consensus"
64994. .65149 /notes="AluJo repeat: matches 49. .296 of consensus"
repeat_region /notes="AluJo repeat: matches 3. .157 of consensus"
65242. .65443 /notes="AluJo repeat: matches 3. .157 of consensus"
repeat_region /notes="MER20 repeat: matches 1. .214 of consensus"
65583. .65802 /notes="MER20 repeat: matches 1. .214 of consensus"
repeat_region /notes="110 copies 2 mer aa 57% conserved"
65831. .66432 /notes="110 copies 2 mer aa 57% conserved"
repeat_region /notes="HAL1 repeat: matches 325. .988 of consensus"
66442. .66786 /notes="HAL1 repeat: matches 325. .988 of consensus"
repeat_region /notes="MSTR repeat: matches 40. .426 of consensus"
66789. .67156 /notes="MSTR repeat: matches 40. .426 of consensus"
repeat_region /notes="MSTR-internal repeat: matches 3. .382 of consensus"
67157. .67446 /notes="MSTR-internal repeat: matches 3. .382 of consensus"

Query Match 72.7%; Score 40; DB 9; Length 70328;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTCAGGTTCAGGAATTCAGATCAGCTGCGCCACATG 53
|||||
DB 37900 CACTTCAGGTTCAGGAATTCAGATCAGCTGCGCCACATG 37939
|||||

RESULT 6
AC092165/c 100020 bp DNA linear PRI 21-FEB-2002
LOCUS Homo sapiens BAC clone RP11-753F4 from 2, complete sequence.
DEFINITION AC092165
ACCESSION AC092165.4 GI:18056750
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 100020)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 98063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 100020)
AUTHORS Abbott, S. and Haglund, K.
TITLE The sequence of Homo sapiens BAC clone RP11-753F4
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 100020)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 100020)
AUTHORS Waterston, R.H.
TITLE Direct Submission

JOURNAL Submitted (04-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 100020)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Jan 4, 2002 this sequence version replaced gi:117981677.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@wustl.wustl.edu

----- Summary Statistics

Center project name: H_NH0753F04

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oseogawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-762N20, 2000 bp overlap; the clone sequenced to the right is RP11-485D7. Actual start of this clone is at base position 98039 of RP11-762N20; actual end is at base position 100020 of RP11-753F4.

Data from AC09338 and AC074188 was used to finish this clone, AC092165. Polymorphisms have been identified between AC074188 and AC092165.

FEATURES	source	Location/Qualifiers
	1. .100020	/organism="Homo sapiens"
		/db xref="taxon:9606"
		/chromosome="2"
		/map="2"
		/clone="RP11-753F4"
		/clone_lib="RPCI-11"
repeat_region	31. .176	/rpt_family="L1"
repeat_region	177. .459	/rpt_family="Alu"
repeat_region	456. .501	/rpt_family="CA)n"
repeat_region	501. .3543	/rpt_family="L1"
repeat_region	4004. .4114	
repeat_region	4631. .4933	/rpt_family="CR1"
repeat_region	6357. .6664	/rpt_family="Alu"
misc_feature	6459. .6464	/note="similar to Homo sapiens EST BI830777 (NID:G15942327)"
misc_feature	8893. .9252	/note="similar to Sus scrofa EST B1346780 (NID:G15040069)"
misc_feature	8894. .9319	/note="match to EST A1625488 (NID:G4650419) ty56a01.x1"
misc_feature	8894. .9258	/note="match to EST AW247923 (NID:G6591011)"
misc_feature	8896. .9178	/note="match to EST BE782599 (NID:G10203797)"
misc_feature	8897. .9319	/note="similar to Rattus norvegicus EST AW523743 (NID:G156128)"
misc_feature	8907. .9319	/note="similar to Mus musculus EST BB187253 (NID:G16270533)"
misc_feature	8908. .9319	/note="match to EST BF663245 (NID:G11937127)"
misc_feature	8920. .9319	/note="match to EST AA523527 (NID:G2264239) ni45g12.s1"
misc_feature	9187. .9319	/note="similar to Rattus norvegicus EST BF562978 (NID:G11672708)"
misc_feature	9274. .9319	/note="similar to EST BG803768 (NID:G17950677)"
misc_feature	9323	/note="match to EST AW247923 (NID:G6591011)"
misc_feature	9466. .9547	/note="match to EST AA523527 (NID:G2264239) ni45g12.s1"
misc_feature	9466. .9545	/note="similar to Mus musculus EST BB187253 (NID:G16270533)"
misc_feature	9466. .9542	/note="match to EST BF663245 (NID:G11937127)"
misc_feature	9466. .9542	/note="similar to EST BG803768 (NID:G17950677)"
misc_feature	9466. .9542	/note="similar to Rattus norvegicus EST BF562978 (NID:G11672708)"
misc_feature	9466. .9523	/note="similar to Rattus norvegicus EST AW523743 (NID:G156128)"
misc_feature	9785. .9880	/note="match to EST BF663245 (NID:G11937127)"
misc_feature	9785. .9880	/note="similar to EST BG803768 (NID:G17950677)"
misc_feature	9785. .9880	/note="similar to Mus musculus EST A1608187 (NID:G4617354) vc84dl2.y1"
misc_feature	9785. .9880	/note="similar to Rattus norvegicus EST BF562978 (NID:G11672708)"
misc_feature	9785. .9856	/note="match to EST A1625488 (NID:G4650419) ty56a01.x1"
misc_feature	10158. .10223	/note="match to EST BF663245 (NID:G11937127)"
misc_feature	10158. .10223	/note="similar to EST BG803768 (NID:G17950677)"
misc_feature	10158. .10223	/note="similar to Mus musculus EST A1608187 (NID:G4617354) vc84dl2.y1"
misc_feature	10158. .10223	/note="similar to Rattus norvegicus EST BF562978 (NID:G11672708)"
misc_feature	10170. .10223	

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misc_feature /note="match to EST R61440 (NID:g832135) yh1sh02.r1"
10573. .10698
/note="similar to Mus musculus EST A1608187 (NID:g4617354)
vc84d12.Y1"
10573. .10697
/note="match to EST BF663245 (NID:g11937127)"
10573. .10697
/note="match to EST R61440 (NID:g832135) yh1sh02.r1"
10573. .10697
/note="similar to EST BG803768 (NID:g17950677)"
10573. .10697
/note="similar to Rattus norvegicus EST BF562978
(NID:g11672708)"
10608. .10697
/note="similar to Bos taurus EST AV588944 (NID:g9699937)"
10849. .10916
/note="match to EST R61440 (NID:g832135) yh1sh02.r1"
10849. .10916
/note="similar to Bos taurus EST AV588944 (NID:g9699937)"
10849. .10916
/note="similar to EST BG803768 (NID:g17950677)"
10849. .10897
/note="match to EST BF663245 (NID:g11937127)"
10849. .10877
/note="similar to Rattus norvegicus EST BF562978
(NID:g11672708)"

```

```

Query Match 72.7%; Score 40; DB 9; Length 100020;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 14 CACTTGAGGTGAGGATTCGAGATTCGAGCTGGCCCAACATG 53
|||||
Db 38849 CACTTGAGGTGAGGATTCGAGATTCGAGCTGGCCCAACATG 38810
|||||

```

```

RESULT 7
AC009449/c
LOCUS
DEFINITION Homo sapiens chromosome 17 clone CTD-2291H15 map 17, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
AC009449
AC009449.5 GI:15291073
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArrellano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
Karatas,A., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P.,
Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
Meldrim,J., Mollia,M., Morris,W., Morrow,J., Mychaleckyj,J.,
Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
Peterson,K., Pollara,V., Rilev,R., Roberts,D., Roy,A., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
Tesiaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
Direct Submission
Submitted (22-AUG-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 26, 2001 this sequence version replaced gi:14626922.
All repeats were identified using RepeatMasker:

```

```

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L775
Center clone name: 2291.H.15
----- Summary Statistics
Sequencing vector: M13; M7815; 19% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 102893 bases at least Q40
Consensus quality: 103343 bases at least Q30
Consensus quality: 103573 bases at least Q20
Insert size: 104651; sum-of-contigs
Quality coverage: 16.2 in Q20 bases; sum-of-contigs

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 617: contig of 617 bp in length
* 618 717: gap of 100 bp
* 718 1791: contig of 1074 bp in length
* 1792 1891: gap of 100 bp
* 1892 11154: contig of 9263 bp in length
* 11155 11254: gap of 100 bp
* 11255 47275: contig of 36021 bp in length
* 47276 47375: gap of 100 bp
* 47376 105051: contig of 57676 bp in length.

```

FEATURES

```

source
1. .105051
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="CTD-2291H15"
/clone_lib="CITD Human BAC"
1. .617
/misc_feature /note="assembly_fragment"
718. .1791
/misc_feature /note="assembly_fragment"
1892. .11154
/misc_feature /note="assembly_fragment"
11255. .47275
/misc_feature /note="assembly_fragment"
47376. .105051
/misc_feature /note="assembly_fragment"
BASE COUNT 29638 a 22552 c 21751 g 30707 t 403 others
ORIGIN

```

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Query Match 72.7%; Score 40; DB 2; Length 105051;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 14 CACTTGAGGTGAGGATTCGAGATTCGAGCTGGCCCAACATG 53
|||||
Db 64397 CACTTGAGGTGAGGATTCGAGATTCGAGCTGGCCCAACATG 64358
|||||

```

```

RESULT 8
AP002498/c
LOCUS
DEFINITION Homo sapiens genomic DNA, chromosome 11q, clone:CTD-2547H16,

```

```

complete sequence.
ACCESSION AF002498 GI:14861115
VERSION AF002498.3 GI:14861115
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:CTD-2547H18.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2000)
REFERENCE 2
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@psc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Jul 17, 2001 this sequence version replaced gi:11320563.
FEATURES
source
Location/Qualifiers
1..124000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clones="CTD-2547H18"
BASE COUNT 36237 a 23655 c 24287 g 39821 t
ORIGIN
Query Match 72.7%; Score 40; DB 9; Length 124000;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 14 CACTTGAGTTCAGGAATTCGAGATCAGCTGGCCAAATG 53
|||||
Db 8217 CACTTGAGTTCAGGAATTCGAGATCAGCTGGCCAAATG 8178

RESULT 9
AC104184
LOCUS AC104184 143034 bp DNA linear PRI 23-MAR-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-188P20, complete sequence.
ACCESSION AC104184 AC027581
VERSION AC104184.2 GI:19697457
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Mar 23, 2002 this sequence version replaced gi:17386316.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC

```

Web site: <http://www.genome.washington.edu>
 Contact: uwgchgs@u.washington.edu
 Drafting Center: BCM

----- Project Information

Center project name: chr-3
 Center clone name: RP11-188P20 (bc0291)
 ----- Summary Statistics
 Sequencing vector: unknown; 58% of reads
 Sequencing vector: plasmid; L08752; 42% of reads
 Chemistry: Dye-terminator ET; 67% of reads
 Chemistry: Dye-terminator Big Dye; 33% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 142918 bases at least Q40
 Consensus quality: 143028 bases at least Q30
 Consensus quality: 143034 bases at least Q20
 Insert size: 142838; sum-of-contigs
 Quality coverage: 8.0x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:

5': Mapping in progress
 3': RP11-258N2 (UWGC:bc0637) AC024378

----- Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI		HindIII		BglII	
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
8696	8704	1129	1114	10270	10243
6	<800	6382	6515	2067	2063
2882	2945	512	<800	5480	5668
2540	2530	449	<800	3606	3574
3643	3781	2552	2517	928	930
1514	1486	3416	3369	365	<800
631	<800	7168	7307	7579	7709
865	847	1854	1889	782	<800

2055	2049	1696	1655	4596	4559
909	897	397	<800	2776	2784
3796	3781	2926	2977	184	<800
5481	5462	4712	4619	2132	2156
1935	1951	45	<800	856	867
507	<800	825	895	659	<800
120	<800	5281	5260	1899	1874
1153	1139	4614	4619	1261	1259
2641	2663	2273	2249	2817	2784
2145	2184	2075	2065	6712	6648
1526	1486	14383	14415	128	<800
1000	997	10039	9940	4209	4192
1126	1139	8620	8673	46	<800
1649	1651	501	<800	2157	2156
637	<800	11469	11355	6593	6648
788	<800	1883	1889	6080	6248
18870	19027	4982	4848	3363	3421
1312	1314	1943	1889	5134	5104
172	<800	886	895	5754	5668
3298	3303	881	895	4281	4192
1332	1314	85	<800	4197	4192
5959	5917	4281	4178	3177	3210
10560	10431	593	<800	9088	9070
7179	7208	66	<800	150	<800
3985	4046	3551	3581	2704	2784
9799	9561	488	<800	3282	3210
4653	4680	5651	5589	708	<800
1150	1139	2443	2517	8040	8083
7764	7701	1249	1229	3827	3766
5866	5917	4839	4848	228	<800
1182	1139	1244	1229	662	<800
1154	1139	185	<800	4221	4192
973	997	1386	1353	9761	9678
2345	2368	2602	2517	1167	1161
225	<800	1492	1453	7807	7709
326	<800	2460	2517	---	---
2508	2530	72	<800	---	---

FEATURES

source Location/Qualifiers

1. 143034
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-188P20"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 41310 a 29565 c 30285 g 41874 t
ORIGIN

Query Match 72.7%; Score 40; DB 9; Length 143034;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTGAGGTTCAGAAATTCAGATCAGCTGCGCCACATG 53

Db 132437 CACTTGAGGTTCAGAAATTCAGATCAGCTGCGCCACATG 132476

RESULT 10

AC005883/c

LOCUS AC005883 146224 bp DNA linear PRI 10-FEB-2001
DEFINITION Homo sapiens chromosome 17, clone RP11-958E11, complete sequence.

AC005883

AC005883

AC005883.14 GI:12740259

HTG.

KEYWORDS

HTG.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 146224)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C.,

Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K.,

Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R.,

Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagos, B., Heaford, A.,

Herena, A., Horton, L., Howland, J. C., Jacotot, L., Jones, C., Kann, L.,

Karatas, A., Leloczky, J., Macdonald, P., Marquis, N., McEwan, P.,

McGurk, A., McKernan, K., Meldrum, J., Molla, M., Morris, W., Morrow, J.,

Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T.,

O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A.,

Severy, P., Stange-Thomann, N., Stillwell, J., Stojanovic, N., Stone, C.,

Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I.,

Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D.,

Ye, W. J., Zhao, J. and Zody, M.

Direct Submission

Submitted (28-OCT-1998) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 146224)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B., Brown, A.,

Camranta, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S.,

Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, P., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Soungez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

Direct Submission

JOURNAL

Submitted (10-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Feb 10, 2001 this sequence version replaced gi:11991319.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L439

Center clone name: 958_E_11

Only 146.2 kilobases from the middle of this clone are being submitted. The remainder overlaps either accession number AC002090 (WICGR project L106) or accession number AC005823 (WICGR project L448).

FEATURES

Source

Location/Qualifiers

1..146224

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="17"

/map="17"

/clone="RP11-958E11"

/clone_lib="RC1-11 Human Male BAC"

310..346

/rpt_family="(CA)n"

618..958

/rpt_family="(CA)n"

988..1054

/rpt_family="(TATC)n"

complement(1345...1590)

/rpt_family="(CA)n"

complement(1591..1891)

/rpt_family="(CA)n"

complement(1892..2119)

/rpt_family="(CA)n"

2283..2419

/rpt_family="(MER103)"

2466..2628

/rpt_family="(MIR3)"

complement(3127..3269)

/rpt_family="(MIR3)"

3846..3874

/rpt_family="(TAGG)n"

3874..3896

/rpt_family="(TAGG)n"

4390..4493

/rpt_family="(MIR)"

complement(4898..5109)

/rpt_family="(MERS9A)"

5119..5337

/rpt_family="(MIR3)"

/rpt_family="(MIR3)"

repeat_region 5718..5796
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repeat_region 7459..7618
/rpt_family="(MIR)"

repeat_region 7796..7972
/rpt_family="(MIR3)"

repeat_region 8395..8481
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repeat_region 8652..8687
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repeat_region 8747..8997
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repeat_region complement(9493..9674)
/rpt_family="(MIR)"

repeat_region 9692..9863
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repeat_region complement(9935..10080)
/rpt_family="(LIMB1)"

repeat_region complement(10081..13303)
/rpt_family="(LIPA3)"

repeat_region complement(13304..13749)
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repeat_region 13755..14196
/rpt_family="(LIMA10)"

repeat_region 14243..14285
/rpt_family="(AT-rich)"

repeat_region 14286..14432
/rpt_family="(MERSB)"

repeat_region 14852..14993
/rpt_family="(L2)"

repeat_region 15583..15690
/rpt_family="(L2)"

repeat_region complement(16367..16668)
/rpt_family="(AluJo)"

repeat_region 16869..17020
/rpt_family="(MLT1A1)"

repeat_region 17042..17147
/rpt_family="(MERSB)"

repeat_region complement(17373..17596)
/rpt_family="(MER46A)"

repeat_region complement(18044..18085)
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repeat_region complement(18512..18608)
/rpt_family="(L2)"

repeat_region 18704..18852
/rpt_family="(MER91A)"

repeat_region complement(18911..19065)
/rpt_family="(L2)"

repeat_region 19200..19296
/rpt_family="(MIR)"

repeat_region complement(19826..19973)
/rpt_family="(MIR)"

repeat_region 20083..20592
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repeat_region complement(20593..20889)
/rpt_family="(AluSx)"

repeat_region complement(21104..21304)
/rpt_family="(MIR)"

repeat_region 22515..22621
/rpt_family="(MIR)"

repeat_region 22836..22993
/rpt_family="(MIR)"

repeat_region complement(23220..23360)
/rpt_family="(MLT1J2)"

repeat_region complement(23398..23447)
/rpt_family="(MLT2B3)"

repeat_region 23471..23653
/rpt_family="(GA-rich)"

repeat_region 23584
/note="Probably G"

repeat_region 23632..23720
/note="Less than 30 qual SNGL region"

repeat_region 23667..23857

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/rpt_family="GA-rich"
23721..23722
/note="Fingerprint digest shows there are 200 base pairs
of missing sequence here"
23723..23803
/note="Less than 30 qual SNGL region"
23892..23933
/rpt_family="Ricksha"
complement(23934..24110)
/rpt_family="MLT2B3"
complement(24140..24338)
/rpt_family="MLT1J2"
24453..24497
/rpt_family="TTCA)n"
complement(24499..24642)

Query Match 72.7%; Score 40; DB 9; Length 146224;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCTGCCCAACATG 53
|||||
Db 102073 CACTTGAGGTCAGGAATTCGAGATCAGCTGCCCAACATG 102034

RESULT 11
AC068081/c 152591 bp DNA linear HTG 04-MAY-2001
LOCUS Homo sapiens chromosome 11 clone RP11-259H21 map 11, WORKING DRAFT
DEFINITION SEQUENCE, 10 unordered pieces.
AC068081
VERSION AC068081.2 GI:8576212
HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152591)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thumann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teafaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
Submitted (28-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 21, 2000 this sequence version replaced gi:7658355.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

```

```

Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10094
Center clone name: 259_H_21
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145477 bases at least Q40
Consensus quality: 149315 bases at least Q30
Consensus quality: 150842 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 151691; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1378: contig of 1378 bp in length
* 1379 1478: gap of 100 bp
* 1479 3504: contig of 2026 bp in length
* 3505 3604: gap of 100 bp
* 3605 3778: contig of 174 bp in length
* 3779 3878: gap of 100 bp
* 3879 13991: contig of 10113 bp in length
* 13992 14091: gap of 100 bp
* 14092 22007: contig of 7916 bp in length
* 22008 22107: gap of 100 bp
* 22108 31212: contig of 9105 bp in length
* 31213 31312: gap of 100 bp
* 31313 44192: contig of 12880 bp in length
* 44193 44292: gap of 100 bp
* 44293 57334: contig of 13042 bp in length
* 57335 57434: gap of 100 bp
* 57435 86879: contig of 29445 bp in length
* 86880 86979: gap of 100 bp
* 86980 152591: contig of 65612 bp in length.
FEATURES
Source
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/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-259H21"
/clone_lib="RPC1-11 Human Male BAC"
1..1378
/note="assembly_fragment"
1479..3504
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3605..3778
/note="assembly_fragment"
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vector_side:left
3879..13991
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14092..22007
/note="assembly_fragment"
22108..31212
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31313..44192
/note="assembly_fragment"
vector_end:T7
44293..57334
/note="assembly_fragment"
57435..86879
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1479..3504
misc_feature
3605..3778
misc_feature
86880..86979
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14092..22007
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44293..57334
misc_feature
57435..86879

```

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86980..152591
/note="assembly_fragment"
BASE COUNT 43817 a 29008 c 29123 g 49535 t 908 others
ORIGIN
Query Match 72.7%; Score 40; DB 2; Length 152591;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 CACTTGAGGTCAGGAATTCGAGATTCAGCTGGCCCAACATG 53
Db 43245 CACTTGAGGTCAGGAATTCGAGATTCAGCTGGCCCAACATG 43206
AC012033 158276 bp DNA linear HTG 04-SEP-2000
LOCUS Homo sapiens clone RP11-91N19, WORKING DRAFT SEQUENCE, 15 unordered
DEFINITION pieces.
AC012033
VERSION AC012033.20 GI:9966196
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158276)
Muzny,D.M., Adams,C., Bailey,M., Barberia,J., Blankenburg,K.,
Bodony,D.M., Bock,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
David,R., Delgado,O., Deshazo,D., Ding,Y., Donah-Rashid,N.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Forcuna-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,
Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
Lichter,O., Liu,J., Liu,W., Logan,O., Lozano,R.J., Lu,J.,
Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,C., Morgan,M.,
Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,
Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,
Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sugrue,R.,
Taber,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M.,
Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A.,
Worley,K., Wren,J., Wrenford,G., Yu,W., Zhou,X., Nelson,D., and
Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 158276)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 4, 2000 this sequence version replaced gi:9929521.
COMMENT ----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMOR
Center clone name: RP11-91N19
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 135987 bases at least Q40
Consensus quality: 145984 bases at least Q30
Consensus quality: 149762 bases at least Q20
Estimated insert size: 149948; sum-of-contigs estimation
Estimated insert size: 249006; agarose-ep estimation
Quality coverage: 2.8x in Q20 bases; agarose-ep estimation
Quality coverage: 4.6x in Q20 bases; sum-of-contigs estimation
----- NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 15 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 44367: contig of 44367 bp in length
* 44368: gap of unknown length
* 44467: contig of 28611 bp in length
* 73078: gap of unknown length
* 73079: gap of unknown length
* 73179: contig of 21028 bp in length
* 94206: contig of 21028 bp in length
* 94207: gap of unknown length
* 94306: gap of unknown length
* 112788: contig of 18482 bp in length
* 112789: gap of unknown length
* 120323: contig of 7435 bp in length
* 120324: gap of unknown length
* 120424: contig of 10017 bp in length
* 130441: gap of unknown length
* 130541: contig of 5278 bp in length
* 135819: gap of unknown length
* 135919: contig of 5316 bp in length
* 141234: gap of unknown length
* 141235: gap of unknown length
* 141335: contig of 3898 bp in length
* 145232: gap of unknown length
* 145233: gap of unknown length
* 145333: contig of 4328 bp in length
* 149661: gap of unknown length
* 149760: gap of unknown length
* 150931: contig of 1171 bp in length
* 150932: gap of unknown length
* 151032: contig of 1726 bp in length
* 152757: gap of unknown length
* 152758: contig of 2076 bp in length
* 152858: gap of unknown length
* 154933: contig of 2076 bp in length
* 155034: gap of unknown length
* 155034: contig of 1684 bp in length
* 156718: gap of unknown length
* 156818: contig of 1459 bp in length.
FEATURES
Location/Qualifiers
source
1..158276
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone="RP11-91N19"
BASE COUNT 36546 a 42190 c 43059 g 35064 t 1417 others
ORIGIN
Query Match 72.7%; Score 40; DB 2; Length 158276;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 CACTTGAGGTCAGGAATTCGAGATTCAGCTGGCCCAACATG 53
Db 22780 CACTTGAGGTCAGGAATTCGAGATTCAGCTGGCCCAACATG 22819
AC012033 158276 bp DNA linear PRI 08-JUN-2001
LOCUS Human chromosome 14 DNA sequence BAC R-45419 of library RPI-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
AC012033
VERSION AL356801.5 GI:14347105
KEYWORDS HTG; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158608)
Heilig,R., Pettit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
```


TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Gvayay,G., Saurin,W. and Weissenbach,J.
 Sequencing of the human chromosome 14
 Unpublished
 2 (bases 1 to 158608)
 Genoscope.
 Direct Submission
 Submitted (07-JUN-2001) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 On Jun 11, 2001 this sequence version replaced gi:12657330.

----- Genome Center
 Center: Genoscope / Centre National de Sequencage
 Center code: GS
 Web site: http://www.genoscope.cns.fr/
 Contact: SeqRef@genoscope.cns.fr

 The following BAC sequence is oriented from the T7 to the SP6 end.
 Upstream BAC (overlapping the T7 end) : R-132J14 (AC=AL138499)
 Downstream BAC (overlapping the SP6 end) : R-665C16 -----
 Summary Statistics
 Assembly program: Phrap; version 2.0
 Quality coverage: 8.46x in Q20 bases; sum-of-contigs

 Overall quality chart :
 Range : bases
 0 :
 1 - 9 :
 10 - 19 : 3
 20 - 29 : 31
 30 - 39 : 90
 40 - 49 : 1490
 50 - 59 : 3664
 60 - 69 : 5342
 70 - 79 : 14751
 80 - 89 : 42882
 90 - 99 : 90555

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES source

Location/Qualifiers
 1..158608
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="14"
 /clone="R-454L9"
 /clone_lib="RPC1-11"
 16635..16756
 /note="matching EMBL:N62946
 RHdb:RH69643
 STS
 dbSTS:STS49521
 Identified using the e-PCR software (G. Schuler)"
 16717..16941
 /note="matching EMBL:N62939
 RHdb:RH46155
 STS
 dbSTS:STS39223
 Identified using the e-PCR software (G. Schuler)"
 127255..127385
 /note="matching EMBL:G33247
 RHdb:RH100175
 STS
 dbSTS:STS36291
 Identified using the e-PCR software (G. Schuler)"
 132342..132540
 /note="matching EMBL:T96658
 RHdb:RH64855
 STS
 dbSTS:STS44788
 Identified using the e-PCR software (G. Schuler)"
 132444..132591
 /note="matching EMBL:H73005
 RHdb:RH68681
 STS
 dbSTS:STS48588
 Identified using the e-PCR software (G. Schuler)"
 46768 a 32989 c 33903 g 44948 t

ORIGIN

Query Match 72.7%; Score 40; DB 9; Length 158608;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 14 CACTTGAGGTGAGGAATTCGAGATCAGCCTTGCCCAACATG 53
 Db 130174 CACTTGAGGTGAGGAATTCGAGATCAGCCTTGCCCAACATG 130135

 RESULT 14
 AC020592/c
 LOCUS
 DEFINITION
 Homo sapiens chromosome 6 clone RP11-159G14, WORKING DRAFT
 SEQUENCE, 21 unordered pieces.
 AC020592
 AC020592.4 GI:8954237
 HTG; HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE
 Homo sapiens
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1. (bases 1 to 162190)
 Waterston,R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 162190)
 Waterston,R.H.
 Direct Submission
 Submitted (05-JAN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 COMMENT
 On Jul 7, 2000 this sequence version replaced gi:8569833.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0159G14
 ----- Summary Statistics -----
 Sequencing vector: M13; 78%
 Chemistry: Dye-primer ET; 78% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 152536 bases at least Q40
 Consensus quality: 155427 bases at least Q30
 Consensus quality: 157179 bases at least Q20
 Insert size: 151000; agarose-fp
 Insert size: 160190; sum-of-contigs
 Quality coverage: 4.51 in Q20 bases; agarose-fp
 Quality coverage: 4.09 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 21 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 1039: contig of 1038 bp in length
 * 1139: gap of unknown length
 * 1139: contig of 1401 bp in length
 * 2540: gap of unknown length
 * 2639: contig of 1565 bp in length
 * 4204: gap of unknown length
 * 4304: contig of 1598 bp in length
 * 4205: gap of unknown length
 * 5902: contig of 1598 bp in length
 * 5903: gap of unknown length
 * 6002: contig of 3032 bp in length
 * 6003: gap of unknown length
 * 9134: contig of 3032 bp in length
 * 9035: gap of unknown length

* 9135 12275: contig of 3141 bp in length
 * 12276 12375: gap of unknown length
 * 12376 16345: contig of 3970 bp in length
 * 16346 16445: gap of unknown length
 * 16446 19575: contig of 3130 bp in length
 * 19576 19675: gap of unknown length
 * 19676 24774: contig of 5099 bp in length
 * 24775 24874: gap of unknown length
 * 24875 29734: contig of 4859 bp in length
 * 29734 29833: gap of unknown length
 * 29834 35071: contig of 5238 bp in length
 * 35072 35171: gap of unknown length
 * 35172 42515: contig of 7344 bp in length
 * 42516 42615: gap of unknown length
 * 42616 51228: contig of 8613 bp in length
 * 51229 51328: gap of unknown length
 * 51329 60180: contig of 8852 bp in length
 * 60181 60280: gap of unknown length
 * 60281 68856: contig of 8576 bp in length
 * 68857 68956: gap of unknown length
 * 68957 79903: contig of 10947 bp in length
 * 79904 80003: gap of unknown length
 * 80004 93922: contig of 13919 bp in length
 * 93923 94022: gap of unknown length
 * 94023 109396: contig of 15374 bp in length
 * 109397 109496: gap of unknown length
 * 109497 127193: contig of 17697 bp in length
 * 127194 127293: gap of unknown length
 * 127294 145291: contig of 17998 bp in length
 * 145292 145391: gap of unknown length
 * 145392 162190: contig of 16799 bp in length.

FEATURES

Location/Qualifiers
 1..162190
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RP11-159G14"

BASE COUNT 48548 a 29894 c 30463 g 51262 t 2023 others

Query Match 72.7%; Score 40; DB 2; Length 162190;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTCAGTCAGGAATTCGAGATCAGCTGCCCAACATG 53
 DB 149897 CACTTCAGTCAGGAATTCGAGATCAGCTGCCCAACATG 149858

RESULT 15
 AC097638/c AC097638 170330 bp DNA linear PRI 25-FEB-2002
 LOCUS Homo sapiens chromosome 3 clone RP11-353H3, complete sequence.
 DEFINITION
 AC097638
 VERSION AC097638.2 GI:18874944

KEYWORDS

HTG

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 170330)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.

Direct Submission

Unpublished

2 (bases 1 to 170330)

Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (20-OCT-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 170330)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.

TITLE

JOURNAL

COMMENT

Direct Submission
 Submitted (25-FEB-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 On Feb 25, 2002 this sequence version replaced gi:16303437.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: http://www.genome.washington.edu

Contact: uwgchgs@u.washington.edu

----- Project Information

Center project name: chr-3

Center clone name: RP11-353H3 (bc0380)

----- Summary Statistics

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator ET; 92% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 170013 bases at least Q40

Consensus quality: 170315 bases at least Q30

Consensus quality: 170330 bases at least Q20

Insert size: 170227; sum-of-contigs

Quality coverage: 8.0x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-316123 AC027592

3': RP11-258N2 (UMGC:bc0637) AC024378

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

Genbank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an

alternate chemistry or covered by high quality data (i.e., Phred

quality >= 30); an attempt was made to resolve all sequencing

problems, such as compressions and repeats; all regions were

covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest

fingerprinting. Comparison of the experimentally derived digest

fragments with sequence-predicted fragments is given below.

The electronically-digested sequence consists of both insert and

vector in order to accurately represent the entire circular BAC.

Small fragments below a variable cutoff (approximately 400-800 bp)

are not resolved in the fingerprint and hence do not appear

in the table. There are no significant remaining discrepancies

between the experimental and predicted values. Uniquely ordered

fragments are separated by dashed lines.

BgIII EcoRI HindIII

SeqDerMap FngPrnt SeqDerMap FngPrnt SeqDerMap FngPrnt

2325 2289 8696 8822 3039 3001

2067 2139 6 6382 6486

5402 5514 18870 19040 512 <800

6080 6227 788 <800 449 <800

6593 6638 637 <800 6244 6256

2157 2139 1649 1609 14383 14433

46	<800	1126	1124	2075	2223	884	859	123	<800	776	806
4209	4178	1000	1062	2273	2223	4792	4710	2395	2485	3300	3264
128	<800	1526	1560	4614	4602	1108	1081	12934	12772	2236	2223
6712	6638	2145	2154	5281	5253	1765	1728	3843	3825	2223	2223
2817	2790	2641	2746	825	806	4110	4045	893	884	5130	5079
1261	1242	1153	1124	45	<800	728	<800	1605	1560	1835	1778
1899	2045	120	<800	4712	4602	9197	9115	4253	4220	1748	1778
659	<800	507	<800	2926	3001	14971	15022	2249	2234	280	<800
856	859	1935	1928	397	<800	1638	1593	10057	9933	217	<800
2132	2139	5481	5476	1696	1778	7966	7911	701	<800	711	<800
184	<800	3796	3825	1854	1930	3016	2950	2354	2358	1966	2040
2776	2950	909	956	7168	7232	2607	2552	2269	2234	412	<800
4596	4541	2055	2014	3416	3339	852	859	4013	3825	4296	4251
782	859	865	884	2984	3001	3016	2950	2707	2851	3499	3503
7579	7639	631	<800	5188	5079	2607	2552	3594	3606	5348	5253
365	<800	1514	1462	1512	1482	852	859	3248	3225	2558	2540
928	859	3643	3606	8533	8484	7966	7911	701	<800	711	<800
3606	3555	2540	2642	2796	2816	3016	2950	2354	2358	1966	2040
2976	2950	2882	3085	3181	3264	2607	2552	2269	2234	412	<800
865	859	3629	3606	1215	1166	2607	2552	2269	2234	412	<800
4748	4710	907	884	2989	3173	852	859	4013	3825	4296	4251
1729	1728	50	<800	3082	3001	3016	2950	2707	2851	3499	3503
1081	1081	1560	1560	1521	1482	2607	2552	3594	3606	5348	5253
7175	7093	10518	10409	6228	6256	2607	2552	3248	3225	2558	2540
1039	1081	824	813	616	<800	2607	2552	3248	3225	2558	2540
3147	3128	9	<800	5676	5551	2607	2552	3248	3225	2558	2540
3249	3252	1076	1124	4665	4602	2607	2552	3248	3225	2558	2540
814	859	1192	1124	338	<800	2607	2552	3248	3225	2558	2540
1897	1861	2257	2234	163	<800	2607	2552	3248	3225	2558	2540
2556	2552	141	<800	1398	1368	2607	2552	3248	3225	2558	2540
7888	7911	45	<800	1610	1610	2607	2552	3248	3225	2558	2540
2906	2950	1405	1357	2848	2816	2607	2552	3248	3225	2558	2540
2588	2552	3066	3225	693	<800	2607	2552	3248	3225	2558	2540
13936	13906	6126	6037	3695	3625	2607	2552	3248	3225	2558	2540
123	<800	6335	6352	1627	1610	2607	2552	3248	3225	2558	2540
519	<800	2820	2930	2666	2666	2607	2552	3248	3225	2558	2540

Query Match 72.7% Score 40: DB 9: Length 170330;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCCTGGCCACATG 53

Db 122509 CACTTGAGGTCAGGAATTCGAGATCAGCCTGGCCACATG 122470

Search completed: June 17, 2003, 03:56:16

Job time : 155.346 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 9.70963 Seconds
(without alignments)

12756.396 Million cell updates/sec

Title: US-09-513-888c-1_COPY_4365_4419

Perfect score: 55

Sequence: 1 gagcgaggcagacacttga.....atcagctgccaacatgag 55

Scoring table: Oligo NUC

Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_101002.*

1: /SID22/gcgdata/geneq/geneq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneq/geneq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneq/geneq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneq/geneq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneq/geneq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneq/geneq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneq/geneq-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneq/geneq-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneq/geneq-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneq/geneq-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneq/geneq-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneq/geneq-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneq/geneq-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneq/geneq-emb1/NA1993.DAT.*
15: /SID22/gcgdata/geneq/geneq-emb1/NA1994.DAT.*
16: /SID22/gcgdata/geneq/geneq-emb1/NA1995.DAT.*
17: /SID22/gcgdata/geneq/geneq-emb1/NA1996.DAT.*
18: /SID22/gcgdata/geneq/geneq-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneq/geneq-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneq/geneq-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneq/geneq-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneq/geneq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneq/geneq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneq/geneq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9048	21	AA64507
2	40	72.7	49999	20	AA223904
3	36	65.5	824	22	AAH03907
4	36	65.5	1524	22	AAH17143
5	35	63.6	570	24	ABN65352
6	35	63.6	10740	22	AAK64788
7	25	45.5	218	24	ABL77817
8	25	45.5	250	22	ABA16332
9	25	45.5	320	21	AAC05198

DNA encoding novel
Human cDNA sequenc
Human transporter
Human nervous syst
Human immune/haema
Human immune/haema
Human immune/haema
Human genomic DNA
Human immune/haema
Human immune/haema
Human immune/haema
Human immune/haema
Human immune/haema
Human 3-hydroxy-3-
Human HMGCL gene,
Human cDNA differe
Genomic sequence #
Genomic sequence #
Human excretory re
Human kidney relat
Human immune/haema
Human secreted pro
Human immune/haema
Human immune/haema
Human secreted pro
Human polynucleoti
Human prostate exp
Human reproductive
Human testicular a
Human secreted pro
Human nervous syst
Human ovarian canc
DNA encoding novel
Human ovarian canc
Human prostate exp
Human cancer relat
Human prostate exp
Human nervous syst
Human nervous syst
Human prostate exp
Human cDNA clone (
Human cDNA clone (
Human cDNA clone (
Human prostate exp
Human prostate exp
Human prostate exp
Human immune/haema
Human inflammatory
Human neuroblastom
Human EST-derived
Human gene express
Human gene express
Human prostate exp
Human secreted pro
Human cervical can
Human immune/haema
Human full-length
Human reproductive
Human testicular a
Human cDNA encodin
Human musculoskele
Human immune/haema
Human cDNA sequenc
Human cDNA sequenc
Human secreted pro
Human cDNA sequenc
Human AD4 gene gen
Human genomic DNA
Genomic sequence #
Human immune/haema

C	83	24	43.6	2884	22	AA160494	Human polynucleoti	156	24	43.6	121162	21	AAC66548	Human kinesin-like	
C	84	24	43.6	3089	22	AAK72379	Human immune/haema	157	24	43.6	122888	24	ABQ83569	Human cDNA differ	
C	85	24	43.6	3223	22	AA136276	Human musculoskele	C	158	24	43.6	125439	24	ABQ88177	Human osteoblast d
C	86	24	43.6	3223	22	AA136277	Human musculoskele	C	159	24	43.6	138169	21	AAQ34791	Human adenosine re
C	87	24	43.6	3224	22	AA136278	Human musculoskele	C	160	24	43.6	141589	21	AAQ34791	Human ELAM-1 polyn
C	88	24	43.6	4015	22	AA501490	Human secreted,pro	C	161	24	43.6	141589	21	AAQ34791	Human low adenosin
C	89	24	43.6	5075	22	ABAI6701	Human nervous syst	C	162	24	43.6	141589	21	AAQ34791	Human low adenosin
C	90	24	43.6	5076	22	ABAI6702	Human nervous syst	C	163	24	43.6	141589	21	AAQ34791	Human adenosine re
C	91	24	43.6	5526	23	AA576845	DNA encoding novel	C	164	24	43.6	141589	21	AAQ34791	Human adenosine re
C	92	24	43.6	5734	22	AAK67406	Human immune/haema	C	165	24	43.6	145831	24	ABL62309	Colon adenocarcino
C	93	24	43.6	5778	22	AAK53086	Human polynucleoti	C	166	24	43.6	145831	24	ABL62309	Colon adenocarcino
C	94	24	43.6	5801	22	AAK52102	Human polynucleoti	C	167	24	43.6	145831	24	ABL62309	Lung cancer relate
C	95	24	43.6	5984	23	AAK23461	Human lung tumour-	C	168	24	43.6	145831	24	ABL62309	Kidney cancer rela
C	96	24	43.6	6135	24	ABQ88237	Human osteoblast d	C	169	24	43.6	145831	24	ABL62309	Prostate cancer re
C	97	24	43.6	6598	22	AAQ46660	Human reproductive	C	170	24	43.6	145831	24	ABL62309	Human ELAM-1 polyn
C	98	24	43.6	6598	23	AB197567	Human testicular a	C	171	24	43.6	145831	24	ABL62309	Human osteoblast d
C	99	24	43.6	7686	22	ABAI4580	Human nervous syst	C	172	24	43.6	145831	24	ABL62309	Human cDNA differ
C	100	24	43.6	8288	22	ABAI4581	Human nervous syst	C	173	24	43.6	145831	24	ABL62309	Human factor-relat
C	101	24	43.6	9160	24	ABK69900	Human secreted pro	C	174	24	43.6	145831	24	ABL62309	Human cDNA differ
C	102	24	43.6	9266	24	ABK69899	Human secreted pro	C	175	24	43.6	145831	24	ABL62309	Human chromosome
C	103	24	43.6	9268	24	ABK69898	Human secreted pro	C	176	24	43.6	145831	24	ABL62309	Human chromosom
C	104	24	43.6	11026	22	AAK72958	Human immune/haema	C	177	24	43.6	145831	24	ABL62309	Human schizophre
C	105	24	43.6	11096	22	ABAI18278	Human nervous syst	C	178	24	43.6	145831	24	ABL62309	Human Oestrogen re
C	106	24	43.6	11762	22	AAK81037	Human immune/haema	C	179	24	43.6	145831	24	ABL62309	Human prostate exp
C	107	24	43.6	11762	22	AAK81038	Human immune/haema	C	180	24	43.6	145831	24	ABL62309	Human prostate exp
C	108	24	43.6	12712	22	AA527765	DNA encoding novel	C	181	24	43.6	145831	24	ABL62309	Human prostate exp
C	109	24	43.6	13287	22	ABAI4431	Human nervous syst	C	182	24	43.6	145831	24	ABL62309	Human prostate exp
C	110	24	43.6	14175	22	AA527814	DNA encoding novel	C	183	24	43.6	145831	24	ABL62309	Human polynucleoti
C	111	24	43.6	14175	22	AAK78859	Human immune/haema	C	184	24	43.6	145831	24	ABL62309	Human immune/haema
C	112	24	43.6	14209	22	AAK89137	Human digestive sy	C	185	24	43.6	145831	24	ABL62309	Human immune/haema
C	113	24	43.6	17357	22	AAK86680	Human immune/haema	C	186	24	43.6	145831	24	ABL62309	Human immune/haema
C	114	24	43.6	17363	22	AAK86681	Human immune/haema	C	187	24	43.6	145831	24	ABL62309	Human ovarian can
C	115	24	43.6	17462	22	ABAI5655	Human nervous syst	C	188	24	43.6	145831	24	ABL62309	Human cancer relat
C	116	24	43.6	17816	22	AAK33417	DNA encoding human	C	189	24	43.6	145831	24	ABL62309	Human cancer relat
C	117	24	43.6	19596	22	AAK73967	Human immune/haema	C	190	24	43.6	145831	24	ABL62309	Human prostate exp
C	118	24	43.6	19596	22	AAK73968	Human immune/haema	C	191	24	43.6	145831	24	ABL62309	Human prostate exp
C	119	24	43.6	21989	22	ABAI15942	Human nervous syst	C	192	24	43.6	145831	24	ABL62309	Human cancer relat
C	120	24	43.6	22893	24	ABK12810	Human tumour suppr	C	193	24	43.6	145831	24	ABL62309	Human cancer relat
C	121	24	43.6	24999	22	AAK56282	Human immune/haema	C	194	24	43.6	145831	24	ABL62309	Human prostate exp
C	122	24	43.6	25003	22	ABAI9679	Human nervous syst	C	195	24	43.6	145831	24	ABL62309	Human prostate exp
C	123	24	43.6	25235	22	AAK45310	Human nervous syst	C	196	24	43.6	145831	24	ABL62309	Human cDNA clone (
C	124	24	43.6	27733	22	ABAI19324	Human nervous syst	C	197	24	43.6	145831	24	ABL62309	Human prostate exp
C	125	24	43.6	30625	24	ABK12808	Human tumour suppr	C	198	24	43.6	145831	24	ABL62309	Human prostate exp
C	126	24	43.6	30676	24	ABK12811	Human tumour suppr	C	199	24	43.6	145831	24	ABL62309	Human neuroblastom
C	127	24	43.6	30826	22	ABAI07345	Human pancreatic c	C	200	24	43.6	145831	24	ABL62309	Human secreted pro
C	128	24	43.6	30826	22	AAK32772	Human genomic DNA	C	201	24	43.6	145831	24	ABL62309	Human reproductive
C	129	24	43.6	31584	22	AAK81054	Human immune/haema	C	202	24	43.6	145831	24	ABL62309	Human full-length
C	130	24	43.6	31749	22	AAK72959	Human immune/haema	C	203	24	43.6	145831	24	ABL62309	Human beta-glucuro
C	131	24	43.6	34917	22	AAK70686	Human immune/haema	C	204	24	43.6	145831	24	ABL62309	Human zinc finger
C	132	24	43.6	32199	22	AAK90296	Human digestive sy	C	205	24	43.6	145831	24	ABL62309	Human conjugated p
C	133	24	43.6	32199	22	AAI57673	Human colorectal c	C	206	24	43.6	145831	24	ABL62309	Human cDNA sequenc
C	134	24	43.6	32216	22	ABAI6118	Human nervous syst	C	207	24	43.6	145831	24	ABL62309	Human cDNA sequenc
C	135	24	43.6	33747	22	AAK69279	Human immune/haema	C	208	24	43.6	145831	24	ABL62309	Human immune/haema
C	136	24	43.6	34917	22	AAK73093	Human immune/haema	C	209	24	43.6	145831	24	ABL62309	Human immune/haema
C	137	24	43.6	38771	22	AAK81036	Human immune/haema	C	210	24	43.6	145831	24	ABL62309	Human nervous syst
C	138	24	43.6	39198	22	AAK58067	Human immune/haema	C	211	24	43.6	145831	24	ABL62309	Human nervous syst
C	139	24	43.6	41684	21	AAK28150	Human polyamine-mo	C	212	24	43.6	145831	24	ABL62309	Human immune/haema
C	140	24	43.6	44861	24	AAK20000	Human purh gene ge	C	213	24	43.6	145831	24	ABL62309	Human immune/haema
C	141	24	43.6	45993	24	AAK36070	DNA encoding pyrid	C	214	24	43.6	145831	24	ABL62309	Human immune/haema
C	142	24	43.6	46553	22	AAK67926	Human liver glucok	C	215	24	43.6	145831	24	ABL62309	Human immune/haema
C	143	24	43.6	46553	22	AAK81745	Human immune/haema	C	216	24	43.6	145831	24	ABL62309	Human immune/haema
C	144	24	43.6	47090	22	AAK68725	Human immune/haema	C	217	24	43.6	145831	24	ABL62309	Human immune/haema
C	145	24	43.6	47090	22	AAK78219	Human immune/haema	C	218	24	43.6	145831	24	ABL62309	Human immune/haema
C	146	24	43.6	51474	22	AAK97846	Human neuroblastom	C	219	24	43.6	145831	24	ABL62309	Human immune/haema
C	147	24	43.6	54108	24	ABK22782	Human high bone ma	C	220	24	43.6	145831	24	ABL62309	Human testicular a
C	148	24	43.6	57273	24	ABK22784	Human high bone ma	C	221	24	43.6	145831	24	ABL62309	Human immune/haema
C	149	24	43.6	58837	24	ABK52612	Human Claspin geno	C	222	24	43.6	145831	24	ABL62309	Human immune/haema
C	150	24	43.6	66933	22	ABK82625	Human HBM gene reg	C	223	24	43.6	145831	24	ABL62309	Human immune/haema
C	151	24	43.6	72049	22	ABK82623	Human HBM gene reg	C	224	24	43.6	145831	24	ABL62309	Human ovarian and
C	152	24	43.6	74037	24	ABK94412	DNA encoding endot	C	225	24	43.6	145831	24	ABL62309	Human reproductive
C	153	24	43.6	78925	21	ABK98988	Human FN gene. Ho	C	226	24	43.6	145831	24	ABL62309	Human genomic DNA
C	154	24	43.6	109906	24	ABK94411	DNA encoding endot	C	227	24	43.6	145831	24	ABL62309	Human neuroblastom
C	155	24	43.6	110096	24	ABN95044	Gene #1542 used to	C	228	24	43.6	145831	24	ABL62309	Gene #2387 used to

c 375	21	38.2	403	23	ABV34058	Human prostate exp	c 448	21	38.2	559	23	ABV43378	Human prostate exp
c 376	21	38.2	406	22	AAI91420	Human polynucleoti	449	21	38.2	565	24	ABN63987	Human cancer relat
c 377	21	38.2	406	23	ABV34520	Human prostate exp	c 450	21	38.2	570	23	ABV40598	Human prostate exp
c 378	21	38.2	407	23	ABV31285	Human prostate exp	c 451	21	38.2	570	23	ABV43230	Human prostate exp
c 379	21	38.2	407	23	ABV34365	Human prostate exp	c 452	21	38.2	570	23	ABV43562	Human prostate exp
c 380	21	38.2	408	23	ABV34338	Human prostate exp	c 453	21	38.2	570	23	ABV43844	Human prostate exp
c 381	21	38.2	409	23	ABV35813	Human prostate exp	c 454	21	38.2	570	23	ABV43847	Human prostate exp
c 382	21	38.2	409	23	ABV43199	Human prostate exp	455	21	38.2	571	24	ABN62519	Human cancer relat
c 383	21	38.2	410	23	ABV00877	Human prostate exp	456	21	38.2	572	22	AAK69488	Human immune/haema
c 384	21	38.2	416	23	ABV34963	Human prostate exp	457	21	38.2	583	22	AAI192237	Human polynucleoti
c 385	21	38.2	417	22	AAK84004	Human immune/haema	458	21	38.2	583	24	ABN64637	Human cancer relat
c 386	21	38.2	419	23	ABV13473	Human prostate exp	459	21	38.2	589	23	ABV45492	Human prostate exp
c 387	21	38.2	419	23	ABV30889	Human prostate exp	460	21	38.2	609	22	AAH31418	Human secreted pro
c 388	21	38.2	419	23	ABV43408	Human prostate exp	461	21	38.2	613	23	ABV58362	Human prostate exp
c 389	21	38.2	420	23	ABV04077	Human prostate exp	462	21	38.2	619	24	ABN60465	Human cancer relat
c 390	21	38.2	420	23	ABV31317	Human prostate exp	c 463	21	38.2	627	23	ABV40286	Human prostate exp
c 391	21	38.2	421	23	ABV34935	Human prostate exp	c 464	21	38.2	627	23	ABV43800	Human prostate exp
c 392	21	38.2	421	23	ABV45205	Human prostate exp	c 465	21	38.2	655	23	ABV39857	Human prostate exp
c 393	21	38.2	422	23	ABV04050	Human prostate exp	c 466	21	38.2	667	22	AAI09720	Human breast cance
c 394	21	38.2	422	23	ABV05567	Human prostate exp	c 467	21	38.2	719	22	AAI96912	Human neuroblastom
c 395	21	38.2	422	23	ABV31218	Human prostate exp	c 468	21	38.2	732	22	AAI18392	Human breast cance
c 396	21	38.2	424	23	ABV04081	Human prostate exp	469	21	38.2	745	22	AAI04175	Human reproductive
c 397	21	38.2	425	23	ABV04233	Human prostate exp	470	21	38.2	812	24	ABQ89826	Human prostate exp
c 398	21	38.2	427	23	ABV34369	Human prostate exp	471	21	38.2	937	22	AAK73117	Human immune/haema
c 399	21	38.2	427	23	ABV43220	Human prostate exp	472	21	38.2	937	22	AAK87588	Human immune/haema
c 400	21	38.2	431	23	ABV10460	Human prostate exp	473	21	38.2	968	22	AAK62687	Human immune/haema
c 401	21	38.2	431	23	ABV35839	Human prostate exp	474	21	38.2	1002	22	AAK82253	Human immune/haema
c 402	21	38.2	432	22	AAI93171	Human polynucleoti	c 475	21	38.2	1061	22	ABA08722	Human secreted pro
c 403	21	38.2	432	23	ABV13887	Human prostate exp	c 476	21	38.2	1128	22	AAH72873	Human cervical can
c 404	21	38.2	435	23	ABV15355	Human prostate exp	c 477	21	38.2	1173	20	AAZ24883	Human secreted pro
c 405	21	38.2	437	23	ABV04654	Human prostate exp	478	21	38.2	1195	24	AAZ62498	cDNA sequence #285
c 406	21	38.2	437	23	ABV37582	Human prostate exp	479	21	38.2	1361	23	ABK42147	Genomic sequence #
c 407	21	38.2	437	23	ABV43226	Human prostate exp	c 480	21	38.2	1391	22	AAZ32591	Human genomic DNA
c 408	21	38.2	438	23	ABV13839	Human prostate exp	481	21	38.2	1808	23	ABK42148	Genomic sequence #
c 409	21	38.2	438	23	ABV34707	Human prostate exp	482	21	38.2	1808	23	ABK42149	Genomic sequence #
c 410	21	38.2	439	23	ABV13884	Human prostate exp	483	21	38.2	1906	21	AAZ26302	Human secreted pro
c 411	21	38.2	439	23	ABV42925	Human prostate exp	484	21	38.2	1954	22	AAK73112	Human immune/haema
c 412	21	38.2	440	23	ABV13246	Human prostate exp	485	21	38.2	1954	22	AAK73118	Human immune/haema
c 413	21	38.2	441	23	ABV04670	Human prostate exp	486	21	38.2	1954	22	AAK87581	Human immune/haema
c 414	21	38.2	441	23	ABV31630	Human prostate exp	487	21	38.2	1954	22	AAK87589	Human immune/haema
c 415	21	38.2	441	23	ABV43681	Human prostate exp	488	21	38.2	1963	22	AAK65736	Human immune/haema
c 416	21	38.2	441	23	ABV44907	Human prostate exp	489	21	38.2	1963	22	AAK65738	Human immune/haema
c 417	21	38.2	442	23	ABV04423	Human prostate exp	490	21	38.2	1963	22	AAK70033	Human immune/haema
c 418	21	38.2	442	23	ABV55150	Human prostate exp	491	21	38.2	1963	22	AAK70034	Human immune/haema
c 419	21	38.2	444	23	ABV35978	Human prostate exp	492	21	38.2	2349	22	AAI04170	Human reproductive
c 420	21	38.2	446	22	AAZ32414	Human cDNA encodin	c 493	21	38.2	2349	22	AAI04171	Human reproductive
c 421	21	38.2	446	23	ABV07674	Human prostate exp	494	21	38.2	2361	22	AAH14258	Human cDNA sequenc
c 422	21	38.2	446	23	ABV43445	Human prostate exp	495	21	38.2	2455	22	AAZ64162	Human cDNA P776P s
c 423	21	38.2	446	23	ABV43480	Human prostate exp	496	21	38.2	2455	22	AAZ64163	Human cDNA P776P s
c 424	21	38.2	448	23	ABV36436	Human prostate exp	497	21	38.2	2455	22	AAH93926	P776P full length
c 425	21	38.2	450	23	ABV34996	Human prostate exp	498	21	38.2	2455	22	AAH93927	P776P full length
c 426	21	38.2	450	23	ABV40552	Human prostate exp	499	21	38.2	2455	24	ABI95533	Human P776P splice
c 427	21	38.2	450	23	ABV45041	Human prostate exp	500	21	38.2	2455	24	ABI95534	Human P776P splice
c 428	21	38.2	451	23	ABV36710	Human prostate exp	501	21	38.2	2470	22	AAH31369	Human secreted pro
c 429	21	38.2	451	23	ABV44016	Human prostate exp	c 502	21	38.2	2610	22	AAK69595	Human immune/haema
c 430	21	38.2	451	23	ABV44902	Human prostate exp	503	21	38.2	2956	22	AAH18381	Human cDNA sequenc
c 431	21	38.2	451	23	ABK41641	cDNA encoding nove	504	21	38.2	3032	22	AAH47883	Human Polyisopreny
c 432	21	38.2	452	23	ABV04718	Human prostate exp	505	21	38.2	3287	22	ABK92140	Prostate cancer-as
c 433	21	38.2	470	22	AAI91794	Human polynucleoti	c 506	21	38.2	3350	21	AAZ40700	Human EGFR poly
c 434	21	38.2	471	23	ABV40188	Human prostate exp	507	21	38.2	3350	22	AAK83868	Human immune/haema
c 435	21	38.2	471	23	ABV40254	Human prostate exp	508	21	38.2	3422	22	AAK67565	Human immune/haema
c 436	21	38.2	471	23	ABV43460	Human prostate exp	509	21	38.2	4958	22	AAK68610	Human immune/haema
c 437	21	38.2	471	23	ABV43812	Human prostate exp	510	21	38.2	4958	22	AAK68610	Human immune/haema
c 438	21	38.2	471	23	ABV44613	Human prostate exp	c 511	21	38.2	5421	22	AAZ30523	DNA encoding novel
c 439	21	38.2	479	23	ABV34999	Human prostate exp	512	21	38.2	5421	22	AAI06301	Human reproductive
c 440	21	38.2	487	23	ABV33001	Human prostate exp	c 513	21	38.2	6422	22	ABA07692	Human ovarian and
c 441	21	38.2	498	23	ABV12933	Human prostate exp	c 514	21	38.2	6422	22	AAI02726	Human reproductive
c 442	21	38.2	505	23	ABV13823	Human prostate exp	c 515	21	38.2	6437	22	AAK82889	Human immune/haema
c 443	21	38.2	505	24	ABN65626	Human cancer relat	516	21	38.2	8394	22	AAK68243	Human immune/haema
c 444	21	38.2	522	24	ABN64650	Human cancer relat	517	21	38.2	8394	22	AAK68245	Human immune/haema
c 445	21	38.2	524	23	ABV03832	Human prostate exp	518	21	38.2	8394	22	AAK68246	Human immune/haema
c 446	21	38.2	541	24	ABN60569	Human cancer relat	519	21	38.2	8396	21	AAZ59353	Human STP2 (phenol
c 447	21	38.2	558	24	ABQ56499	Human colon cancer	c 520	21	38.2	8406	22	AAK68244	Human immune/haema
										8923	22	AAK87591	Human immune/haema

C 521	21	38.2	9236	22	AAS03689	Rhesus gene locus:	594	21	38.2	34658	22	AAK69489	Human immune/haema
C 522	21	38.2	9241	22	AAS03690	Rhesus gene locus:	C 595	21	38.2	34831	22	ABK82518	Human immune/haema
C 523	21	38.2	9246	22	AAS03688	Rhesus gene locus:	C 596	21	38.2	35973	22	ABK13076	Human amyloid beta
C 524	21	38.2	10221	21	AAF58417	Human oligonucleot	597	21	38.2	37736	22	AAK86139	Human immune/haema
C 525	21	38.2	10545	21	AAC59132	Human ABC1 gene ex	C 598	21	38.2	39068	22	AAK71820	Human immune/haema
C 526	21	38.2	11244	22	AAK74606	Human immune/haema	C 599	21	38.2	39068	22	AAK73078	Human immune/haema
C 527	21	38.2	11655	22	AAK71335	Human immune/haema	C 600	21	38.2	39068	22	AAK85294	Human immune/haema
C 528	21	38.2	11860	22	ABA21528	Human nervous syst	C 601	21	38.2	39068	22	AAK87544	Human immune/haema
C 529	21	38.2	12221	22	AAK71585	Human immune/haema	C 602	21	38.2	39110	22	AAK71825	Human immune/haema
C 530	21	38.2	12542	22	AAS26800	Human genomic DNA	C 603	21	38.2	39110	22	AAK73087	Human immune/haema
C 531	21	38.2	12718	24	ABK52229	CDNA encoding huma	C 604	21	38.2	39110	22	AAK73087	Human immune/haema
C 532	21	38.2	13216	22	AAK73092	Human immune/haema	C 605	21	38.2	39110	22	AAK87555	Human immune/haema
C 533	21	38.2	13216	22	AAK87561	Human immune/haema	C 606	21	38.2	39887	22	AAK79153	Human immune/haema
C 534	21	38.2	13333	22	AAK79541	Human immune/haema	C 607	21	38.2	39887	22	AAK81263	Human immune/haema
C 535	21	38.2	14282	22	AAK68418	Human immune/haema	C 608	21	38.2	40308	22	AAK68184	Human immune/haema
C 536	21	38.2	15090	22	AAK72319	Human immune/haema	C 609	21	38.2	40668	22	ABO88150	Human osteoblast d
C 537	21	38.2	15090	22	ABK69842	Human immune/haema	C 610	21	38.2	44100	21	ABN97975	Human retroviral s
C 538	21	38.2	15090	24	ABK69842	Human secreted pro	C 611	21	38.2	44354	22	AAK77833	Human immune/haema
C 539	21	38.2	15296	22	AAK74605	Human secreted pro	C 612	21	38.2	44354	22	AAK77836	Human immune/haema
C 540	21	38.2	15783	22	AAS39803	Human immune/haema	C 613	21	38.2	44354	22	AAK77837	Human immune/haema
C 541	21	38.2	15783	22	AAK90159	Genomic sequence #	C 614	21	38.2	45300	22	AAK73079	Human immune/haema
C 542	21	38.2	16281	22	AAK70314	Human digestive sy	C 615	21	38.2	45300	22	AAK87547	Human immune/haema
C 543	21	38.2	16281	22	AAK70314	Human immune/haema	C 616	21	38.2	56093	24	ABL61744	Colon adenocarcino
C 544	21	38.2	16285	22	ABK42480	Genomic sequence #	C 617	21	38.2	68804	24	ABK67050	Human transporter
C 545	21	38.2	16285	22	AAK70316	Human immune/haema	C 618	21	38.2	81001	22	AAF30035	Human apolipoprote
C 546	21	38.2	16285	22	ABK42481	Human immune/haema	C 619	21	38.2	84495	24	AAS20588	Human methionine a
C 547	21	38.2	16285	23	ABK42482	Genomic sequence #	C 620	21	38.2	106746	21	AAA10225	Human PCTA-1 genom
C 548	21	38.2	16285	23	ABK42482	Genomic sequence #	C 621	21	38.2	109201	24	ABO88125	Human osteoblast d
C 549	21	38.2	16579	22	ABA20363	Human nervous syst	C 622	21	38.2	110096	24	ABN95044	Gene #1542 used to
C 550	21	38.2	16579	22	AAK05755	Human reproductive	C 623	21	38.2	126512	24	ABN83429	Human transporter
C 551	21	38.2	16817	22	AAK87099	Human immune/haema	C 624	21	38.2	128978	24	ABK83459	Human cDNA differe
C 552	21	38.2	17154	22	AAS46803	Human immune/haema	C 625	21	38.2	138169	21	AAA34791	Human adenosine re
C 553	21	38.2	17687	22	AAS42069	Genomic sequence #	C 626	21	38.2	139904	24	ABK83562	Human cDNA differe
C 554	21	38.2	18636	22	AAS12088	Human tumour necro	C 627	21	38.2	139904	24	ABK83562	Human cDNA differe
C 555	21	38.2	19815	22	AAS42064	Genomic sequence #	C 628	21	38.2	141589	21	AAK20913	Human ELAM-1 polyn
C 556	21	38.2	20991	22	AAK87545	Human immune/haema	C 629	21	38.2	141589	21	AAK21127	Human low adenosin
C 557	21	38.2	21576	22	AAK71582	Human immune/haema	C 630	21	38.2	141589	21	AAA31552	Human low adenosin
C 558	21	38.2	21747	22	AAK76413	Human immune/haema	C 631	21	38.2	141589	21	AAA35005	Human adenosine re
C 559	21	38.2	23934	22	ABA19145	Human nervous syst	C 632	21	38.2	141589	21	AAA35030	Human adenosine re
C 560	21	38.2	23934	22	AAK36171	Human musculoskele	C 633	21	38.2	146981	21	AAK21442	Human ELAM-1 polyn
C 561	21	38.2	23934	22	AAK36179	Human musculoskele	C 634	21	38.2	165199	24	ABK83460	Human cDNA differe
C 562	21	38.2	23934	22	AAK04522	Human reproductive	C 635	21	38.2	189739	24	ABQ88186	Human osteoblast d
C 563	21	38.2	23934	22	AAS28343	Genomic sequence #	C 636	21	38.2	178896	24	ABQ88186	Human osteoblast d
C 564	21	38.2	23934	22	ABL71442	Human immune/haema	C 637	21	38.2	183999	22	AAK92831	Human ABC1 genomic
C 565	21	38.2	25231	22	AAK03112	Human testicular a	C 638	21	38.2	201143	24	ABK83568	Human DNA differen
C 566	21	38.2	26225	22	AAS35776	Human reproductive	C 639	21	38.2	209273	21	AAK21437	Human factor-relat
C 567	21	38.2	26277	22	AAK70428	Human cardiovascular	C 640	21	38.2	227968	24	ABK83497	Human cDNA differe
C 568	21	38.2	26372	22	AAK77103	Human immune/haema	C 641	21	38.2	240825	22	AAK24497	Human PS-3 gene.
C 569	21	38.2	26928	20	AAK232184	Human immune/haema	C 642	21	38.2	302250	24	ABL67703	Oesophagus cancer
C 570	21	38.2	26928	24	ABN95780	Gene #2278 used to	C 643	21	38.2	302250	24	ABL67703	Oesophagus cancer
C 571	21	38.2	27118	22	ABA08223	Human ovarian and	C 644	21	38.2	302250	24	ABL67703	Human neuroregulin-1
C 572	21	38.2	27118	22	AAK07542	Human reproductive	C 645	21	38.2	1503900	22	AAK96733	Human neuroregulin-1
C 573	21	38.2	27681	22	AAS36497	Human cardiovascular	C 646	21	38.2	1503900	22	AAK96733	Human nonconservat
C 574	21	38.2	27681	22	AAS36498	Human cardiovascular	C 647	21	38.2	1503900	22	AAK96733	Human digestive sy
C 575	21	38.2	27681	22	AAK58543	Human immune/haema	C 648	21	38.2	1503900	22	AAK96733	Human liver associ
C 576	21	38.2	27960	22	AAK69779	Human immune/haema	C 649	21	38.2	1503900	22	AAK96733	Human liver antige
C 577	21	38.2	27960	22	AAK73320	Human immune/haema	C 650	21	38.2	1503900	22	AAK96733	Human immune/haema
C 578	21	38.2	32169	22	ABA14358	Human nervous syst	C 651	21	38.2	1503900	22	AAK96733	Human immune/haema
C 579	21	38.2	32169	22	ABA19573	Human nervous syst	C 652	21	38.2	1503900	22	AAK96733	Human immune/haema
C 580	21	38.2	32169	22	AAK05917	Human nervous syst	C 653	21	38.2	1503900	22	AAK96733	Human gene signatu
C 581	21	38.2	32169	23	ABL98481	Human reproductive	C 654	21	38.2	1503900	22	AAK96733	Human immune/haema
C 582	21	38.2	32169	23	ABK43076	Human testicular a	C 655	21	38.2	1503900	22	AAK96733	Human immune/haema
C 583	21	38.2	32189	22	ABA16341	Genomic sequence #	C 656	21	38.2	1503900	22	AAK96733	Human secreted pro
C 584	21	38.2	32189	22	ABA17492	Human nervous syst	C 657	21	38.2	1503900	22	AAK96733	Human secreted pro
C 585	21	38.2	32189	22	ABA17790	Human nervous syst	C 658	21	38.2	1503900	22	AAK96733	Human excretory re
C 586	21	38.2	32189	22	ABA19572	Human nervous syst	C 659	21	38.2	1503900	22	AAK96733	Human kidney relat
C 587	21	38.2	32189	22	AAK36926	Human nervous syst	C 660	21	38.2	1503900	22	AAK96733	Human ovarian cunc
C 588	21	38.2	32189	22	AAK05916	Human musculoskele	C 661	21	38.2	1503900	22	AAK96733	Human immune/haema
C 589	21	38.2	32189	23	ABL98480	Human reproductive	C 662	21	38.2	1503900	22	AAK96733	Human secreted pro
C 590	21	38.2	32190	22	AAK62927	Human testicular a	C 663	21	38.2	1503900	22	AAK96733	Human nervous syst
C 591	21	38.2	32191	22	AAS32492	Human genomic DNA	C 664	21	38.2	1503900	22	AAK96733	Gene #129 used to
C 592	21	38.2	32249	22	AAK62932	Human genomic DNA	C 665	21	38.2	1503900	22	AAK96733	Oesophagus cancer
C 593	21	38.2	33971	22	AAK69257	Human immune/haema	C 666	21	38.2	1503900	22	AAK96733	Human ovarian cunc

667	20	36.4	379	22	AAI87138	Human polynucleoti
668	20	36.4	392	22	AAI86178	Human polynucleoti
669	20	36.4	394	22	AAK67893	Human immune/haema
670	20	36.4	394	22	AAK67893	Human immune/haema
671	20	36.4	395	22	AAK67895	Human immune/haema
672	20	36.4	395	22	ABV16854	Human prostate exp
673	20	36.4	401	22	AAK64793	Novel human polynu
674	20	36.4	404	22	ABV10116	Human prostate exp
675	20	36.4	405	22	AAI83828	Human polynucleoti
676	20	36.4	406	22	AAI83828	Human prostate cance
677	20	36.4	408	22	AAI11863	Human breast cance
678	20	36.4	410	22	ABV16846	Human prostate exp
679	20	36.4	415	22	AAI17159	Human breast cance
680	20	36.4	419	22	AAI17164	Human breast cance
681	20	36.4	421	22	AAK78678	Human immune/haema
682	20	36.4	421	22	ABV00947	Human immune/haema
683	20	36.4	423	22	ABV00947	Human prostate exp
684	20	36.4	424	21	AAK63796	Human ovarian cance
685	20	36.4	425	24	ABL87604	Human ovarian cance
686	20	36.4	432	22	AAI09270	Human breast cance
687	20	36.4	433	23	ABV16862	Human prostate exp
688	20	36.4	437	22	ABV16769	Human nervous syst
689	20	36.4	439	22	ABV16768	Human nervous syst
690	20	36.4	439	22	ABV16770	Human nervous syst
691	20	36.4	445	22	AAI04524	Human reproductive
692	20	36.4	445	23	ABL97448	Human testicular a
693	20	36.4	450	24	ABN62921	Human cancer relat
694	20	36.4	455	23	ABV31288	Human prostate exp
695	20	36.4	455	23	ABV40257	Human prostate exp
696	20	36.4	464	22	AAI09275	Human breast cance
697	20	36.4	466	22	AAK63934	Human immune/haema
698	20	36.4	468	23	ABV46659	Human prostate exp
699	20	36.4	475	23	ABV46651	Human prostate exp
700	20	36.4	477	22	AAI88593	Human polynucleoti
701	20	36.4	481	23	ABV46643	Human prostate exp
702	20	36.4	491	22	AAI05281	Human reproductive
703	20	36.4	491	23	ABL98165	Human testicular a
704	20	36.4	493	22	AAI44750	Human breast cance
705	20	36.4	509	22	AAH09751	Human cDNA clone (
706	20	36.4	517	23	ABV51695	Human prostate exp
707	20	36.4	519	24	ABN62837	Human cancer relat
708	20	36.4	533	22	AAH13155	Human cDNA clone (
709	20	36.4	535	22	ABL12785	Human breast cance
710	20	36.4	556	22	ABN65570	Human cancer relat
711	20	36.4	562	22	AAH10364	Human cDNA clone (
712	20	36.4	565	24	ABN64610	Human cancer relat
713	20	36.4	570	22	AAH09368	Human cDNA clone (
714	20	36.4	572	23	ABV58617	Human prostate exp
715	20	36.4	581	22	AAK64519	Human immune/haema
716	20	36.4	583	24	ABN61233	Human cancer relat
717	20	36.4	599	22	AAI21656	Human breast cance
718	20	36.4	599	22	AAI21656	Human breast cance
719	20	36.4	614	24	ABN65960	Human cancer relat
720	20	36.4	615	23	ABV52452	Human prostate exp
721	20	36.4	623	22	AAI12256	Human breast cance
722	20	36.4	742	22	AAI96647	Human neuroblastom
723	20	36.4	758	23	ABV20606	Human prostate exp
724	20	36.4	758	23	ABV20624	Human prostate exp
725	20	36.4	758	23	ABV20706	Human prostate exp
726	20	36.4	758	23	ABV26446	Human prostate exp
727	20	36.4	758	23	ABV26465	Human prostate exp
728	20	36.4	758	23	ABV26548	Human prostate exp
729	20	36.4	777	22	AAK93642	Human immune/haema
730	20	36.4	826	22	AAK78909	Human immune/haema
731	20	36.4	839	22	AAI97451	Human neuroblastom
732	20	36.4	846	24	ABT04077	Human ovary specif
733	20	36.4	898	22	AAK71188	Human immune/haema
734	20	36.4	908	22	AAK78673	Human immune/haema
735	20	36.4	911	22	AAI21133	Human breast cance
736	20	36.4	927	23	AAK69262	DNA encoding novel
737	20	36.4	1005	22	AAK79470	Human immune/haema
738	20	36.4	1005	22	AAK79471	Human immune/haema
739	20	36.4	1129	22	ABV19926	Human nervous syst
740	20	36.4	1159	22	AAH13849	Human cDNA sequenc
741	20	36.4	1237	21	AAK59111	Human secreted pro
742	20	36.4	1397	22	ABV14291	Human nervous syst
743	20	36.4	1535	21	AAK60999	Human vesicle asso
744	20	36.4	1628	22	ABV13358	Human nervous syst
745	20	36.4	1639	22	AAK33044	Human secreted pro
746	20	36.4	1826	22	AAH16610	Human cDNA sequenc
747	20	36.4	1904	21	AAK81106	Human secreted pro
748	20	36.4	2135	24	ABV55770	Human TNFR/NGFR pr
749	20	36.4	2233	22	AAK72556	Human immune/haema
750	20	36.4	2240	22	AAH43612	Human uroplakin II
751	20	36.4	2240	22	AAI70144	Human uroplakin II
752	20	36.4	2240	23	AAK87241	Uroplakin II-TRE f
753	20	36.4	2304	22	AAK89139	Human digestive sy
754	20	36.4	2304	22	AAK31887	Human liver associ
755	20	36.4	2304	24	ABN90242	Human liver antige
756	20	36.4	2405	22	AAH17253	Human cDNA sequenc
757	20	36.4	2581	24	AAK62492	cDNA sequence #279
758	20	36.4	2696	22	AAI07233	Human reproductive
759	20	36.4	2696	22	AAI07235	Human reproductive
760	20	36.4	2696	23	ABV98781	Human testicular a
761	20	36.4	2696	23	ABV98783	Human testicular a
762	20	36.4	3419	22	ABV15562	Human nervous syst
763	20	36.4	3420	22	ABV15563	Human nervous syst
764	20	36.4	3441	24	ABV53963	Leukaemia-associat
765	20	36.4	4593	22	AAK94929	Human full-length
766	20	36.4	4608	22	AAK74675	Human immune/haema
767	20	36.4	4610	22	AAK74677	Human immune/haema
768	20	36.4	4747	22	ABV07815	Human ovarian and
769	20	36.4	4747	22	AAI03617	Human reproductive
770	20	36.4	5564	22	AAK81104	Human immune/haema
771	20	36.4	6073	22	AAK82558	Human immune/haema
772	20	36.4	6074	22	AAK82558	Human immune/haema
773	20	36.4	6159	22	AAK75604	Human immune/haema
774	20	36.4	6164	22	AAK75613	Human immune/haema
775	20	36.4	6165	22	AAK75603	Human immune/haema
776	20	36.4	6167	22	AAK75609	Human immune/haema
777	20	36.4	6248	22	AAI98941	Human excretory re
778	20	36.4	6248	22	AAI63291	Human kidney relat
779	20	36.4	6252	22	AAI98940	Human excretory re
780	20	36.4	6252	22	AAI63290	Human kidney relat
781	20	36.4	6259	22	AAK83975	Human immune/haema
782	20	36.4	6426	22	ABA20567	Human nervous syst
783	20	36.4	6618	22	ABA18101	Human nervous syst
784	20	36.4	6960	22	AAK85579	Human immune/haema
785	20	36.4	7703	22	AAK90904	Human digestive sy
786	20	36.4	7703	22	AAK90945	Human digestive sy
787	20	36.4	7703	22	AAK31939	Human liver associ
788	20	36.4	7703	22	AAK31980	Human liver associ
789	20	36.4	7703	24	ABN90294	Human liver antige
790	20	36.4	7703	24	ABN90335	Human immune/haema
791	20	36.4	7760	22	AAK74676	Human immune/haema
792	20	36.4	7849	16	AAK94109	DNA encoding novel
793	20	36.4	7970	22	AAK27697	Human immune/haema
794	20	36.4	8308	22	AAK68091	Human immune/haema
795	20	36.4	8308	22	AAK79820	Human immune/haema
796	20	36.4	8514	22	AAK81530	Human immune/haema
797	20	36.4	9324	22	AAK75610	Human immune/haema
798	20	36.4	9329	22	AAI02697	Human reproductive
799	20	36.4	10093	22	ABV07820	Human ovarian and
800	20	36.4	10093	22	AAI03622	Human reproductive
801	20	36.4	10093	22	AAK68011	Human immune/haema
802	20	36.4	10515	24	ABK10772	Human small induci
803	20	36.4	10515	24	ABK10772	Human small induci
804	20	36.4	10612	22	AAI36946	Human musculoskele
805	20	36.4	10614	22	AAI36948	Human musculoskele
806	20	36.4	10842	21	AAK51381	Chromosome 16q tum
807	20	36.4	10901	22	AAI03236	Human reproductive
808	20	36.4	12026	22	AAK67211	Human immune/haema
809	20	36.4	12169	22	AAK61443	Human immune/haema
810	20	36.4	12309	22	AAK89483	Human digestive sy
811	20	36.4	12309	22	AAK90834	Human digestive sy
812	20	36.4	13204	20	AAK232189	Human platelet gly

C 813	20	36.4	13694	22	ABA20301	Human nervous syst	886	19	34.5	102	22	AAK71109	Human immune/haema
C 814	20	36.4	13694	22	ABA20302	Human nervous syst	C 887	19	34.5	102	22	AAK91029	Human digestive sy
C 815	20	36.4	13694	22	AAK9696	Human digestive sy	C 888	19	34.5	102	22	AAK32064	Human liver asocci
C 816	20	36.4	13694	22	AAK9697	Human digestive sy	C 889	19	34.5	102	24	ABN90419	Human liver antige
C 817	20	36.4	14483	22	AAH45311	Human HCR DNA. Ho	C 890	19	34.5	141	21	AAK12033	Human secreted pro
C 818	20	36.4	14543	24	ABK15798	Human von Hippel-L	C 891	19	34.5	165	22	AAK64234	Human immune/haema
C 819	20	36.4	14574	22	AAK70205	Human immune/haema	C 892	19	34.5	216	22	AAK37149	Human musculoskele
C 820	20	36.4	15765	24	AAK32179	Human NFkB gene.	C 893	19	34.5	222	22	ABA17143	Human nervous syst
C 821	20	36.4	15765	22	AAK32327	Human NFkB gene.	C 894	19	34.5	222	22	ABA17143	Human nervous syst
C 822	20	36.4	16525	22	AAK73303	Human immune/haema	C 895	19	34.5	223	22	ABA17142	Human nervous syst
C 823	20	36.4	17154	22	AAK64803	Human immune/haema	C 896	19	34.5	233	22	ABA12237	Human nervous syst
C 824	20	36.4	17249	22	AAK71137	Human immune/haema	C 897	19	34.5	240	18	AAK65660	Polymorphic repeat
C 825	20	36.4	17327	14	AAQ44278	Serglycin - proteo	C 898	19	34.5	293	22	AAK66812	Human immune/haema
C 826	20	36.4	18664	22	AAK65421	Human immune/haema	C 899	19	34.5	298	22	ABA18823	Human nervous syst
C 827	20	36.4	18664	22	AAK64438	Human immune/haema	C 900	19	34.5	300	20	AAK12553	Human gene express
C 828	20	36.4	18772	22	AAK16561	Human novel protei	C 901	19	34.5	309	22	AAK78074	Human immune/haema
C 829	20	36.4	18820	22	ABA07938	Human ovarian and	C 902	19	34.5	320	24	ABL66854	Human ovarian can
C 830	20	36.4	18820	22	AAK03764	Human reproductive	C 903	19	34.5	342	22	ABF67472	Novel human polynu
C 831	20	36.4	19846	22	AAK36182	Human cardiovascular	C 904	19	34.5	343	22	AAK60899	Human polynucleoti
C 832	20	36.4	19846	22	AAK36183	Human cardiovascular	C 905	19	34.5	352	23	AAK90899	Human polynucleoti
C 833	20	36.4	19851	22	AAK85642	Human immune/haema	C 906	19	34.5	353	24	ABL80599	Human immune/haema
C 834	20	36.4	20029	23	ABK42737	Genomic sequence #	C 907	19	34.5	353	24	ABL80599	Human ovarian can
C 835	20	36.4	20050	24	ABL53875	Human immunoglobul	C 908	19	34.5	357	22	AAK62529	Human cancer relat
C 836	20	36.4	20835	22	AAK86765	Human immune/haema	C 909	19	34.5	360	22	AAK62534	Human immune/haema
C 837	20	36.4	21721	20	AAK83427	Human immune/haema	C 910	19	34.5	368	22	AAK191579	Human polynucleoti
C 838	20	36.4	22976	20	AAK83426	Human lipolysis st	C 911	19	34.5	368	22	AAK191579	Human polynucleoti
C 839	20	36.4	23109	22	AAK82298	Genomic region con	C 912	19	34.5	370	22	AAK186851	Human polynucleoti
C 840	20	36.4	23187	21	AAK50273	Human immune/haema	C 913	19	34.5	370	22	AAK66761	Human immune/haema
C 841	20	36.4	23187	21	AAK50273	Human lipolysis st	C 914	19	34.5	384	22	AAK55782	Human immune/haema
C 842	20	36.4	25541	22	AAK76231	Human leptin fragm	C 915	19	34.5	390	22	AAK30332	Human immune/haema
C 843	20	36.4	25806	22	AAK86766	Human immune/haema	C 916	19	34.5	390	22	AAK30332	Human encoding novel
C 844	20	36.4	26747	24	AAI67784	Human immune/haema	C 917	19	34.5	401	24	ABL87065	Human reproductive
C 845	20	36.4	30676	24	ABK12811	Nucleotide sequenc	C 918	19	34.5	402	22	AAK87959	Human ovarian can
C 846	20	36.4	32146	22	AAK28363	Human tumour suppr	C 919	19	34.5	407	22	AAK58774	Human polynucleoti
C 847	20	36.4	32148	22	AAK04218	Genomic sequence #	C 920	19	34.5	410	22	AAK37051	Human immune/haema
C 848	20	36.4	32196	22	AAK18857	Human reproductive	C 921	19	34.5	411	21	AAK99911	Human secreted pro
C 849	20	36.4	32248	22	AAK28368	Human nervous syst	C 922	19	34.5	411	21	AAK182311	Human polynucleoti
C 850	20	36.4	32476	22	AAK85314	Genomic sequence #	C 923	19	34.5	418	24	ABL80692	Human ovarian can
C 851	20	36.4	32816	24	ABK49701	Human immune/haema	C 924	19	34.5	420	22	AAK35347	Human musculoskele
C 852	20	36.4	34435	22	AAK76172	Human transporter	C 925	19	34.5	424	23	AAK84250	Human immune/haema
C 853	20	36.4	35959	22	AAK78275	Human immune/haema	C 926	19	34.5	424	23	ABV08353	Human immune/haema
C 854	20	36.4	39287	24	ABN80533	Human immune/haema	C 927	19	34.5	430	23	ABV53894	Human prostate exp
C 855	20	36.4	40023	24	ABL51954	Human P450(cytochr	C 928	19	34.5	432	22	AAI90102	Human prostate exp
C 856	20	36.4	41936	24	ABL67924	Ovary cancer relat	C 929	19	34.5	437	24	ABL81650	Human polynucleoti
C 857	20	36.4	42881	22	AAK97868	Human cancer relat	C 930	19	34.5	440	22	AAK56443	Human ovarian can
C 858	20	36.4	44848	21	AAK75080	Human neuroblastom	C 931	19	34.5	461	23	ABV38162	Human immune/haema
C 859	20	36.4	45845	24	ABK12809	Nucleotide sequenc	C 932	19	34.5	462	22	AAK88476	Human prostate exp
C 860	20	36.4	46340	21	ABN97978	Human tumour suppr	C 933	19	34.5	469	22	ABA07308	Human digestive c
C 861	20	36.4	49744	24	ABK12807	Human retroviral s	C 934	19	34.5	469	22	AAK90467	Human digestive c
C 862	20	36.4	49999	20	AAK23900	Human tumour suppr	C 935	19	34.5	471	22	AAK90466	Human digestive c
C 863	20	36.4	49999	20	AAK23903	Human LOBO homolog	C 936	19	34.5	471	22	AAK90466	Human digestive c
C 864	20	36.4	52354	24	AAK35032	Human transporter	C 937	19	34.5	474	21	AAK22710	Human secreted pro
C 865	20	36.4	54863	22	AAK86026	Human immune/haema	C 938	19	34.5	477	24	ABN62831	Human cancer relat
C 866	20	36.4	54877	22	AAK86026	Human immune/haema	C 939	19	34.5	483	24	ABN62748	Human cancer relat
C 867	20	36.4	57248	24	ABK83563	Human immune/haema	C 940	19	34.5	486	22	AAH13358	Human CDNA clone (
C 868	20	36.4	56608	24	ABL62910	Breast cancer differe	C 941	19	34.5	491	24	ABN61604	Human cancer relat
C 869	20	36.4	56608	24	ABL64414	Stomach cancer rela	C 942	19	34.5	501	24	ABN62125	Human cancer relat
C 870	20	36.4	56608	24	ABL67668	Oesophagus cancer	C 943	19	34.5	532	24	ABN61804	Human cancer relat
C 871	20	36.4	66685	22	AAK07380	Human genomic DNA	C 944	19	34.5	540	22	AAH10467	Human CDNA clone (
C 872	20	36.4	73465	24	ABQ88161	Human osteoblast d	C 945	19	34.5	552	22	AAK92807	Human CDNA 3'-end
C 873	20	36.4	84607	22	AAK90847	Human osteoblast d	C 946	19	34.5	552	22	AAK94069	Human CDNA clone (
C 874	20	36.4	107820	22	AAK16230	Human ATP-binding	C 947	19	34.5	555	23	ABV49410	Human prostate exp
C 875	20	36.4	110000	22	AAK84800	Nucleotide sequenc	C 948	19	34.5	555	23	ABV49410	Human prostate exp
C 876	20	36.4	110000	22	AAK84800	Nucleotide sequenc	C 949	19	34.5	572	22	AAH08830	Human CDNA clone (
C 877	20	36.4	114793	22	AAK08215	Human genome from	C 950	19	34.5	580	22	AAK59667	Human immune/haema
C 878	20	36.4	110263	24	ABK83573	Human CDNA differe	C 951	19	34.5	580	23	ABV53320	Human prostate exp
C 879	20	36.4	136284	24	ABK83575	Human CDNA differe	C 952	19	34.5	589	24	AAK62220	Human cancer relat
C 880	20	36.4	160552	22	AAK02697	Human glycosyl sul	C 953	19	34.5	592	22	AAK80560	Human immune/haema
C 881	20	36.4	162450	21	AAK286967	Retinoblastoma bin	C 954	19	34.5	593	23	ABV51781	Human prostate exp
C 882	20	36.4	175737	24	ABK83571	Human CDNA differe	C 955	19	34.5	606	23	ABV57484	Human prostate exp
C 883	20	36.4	178896	24	ABQ88146	Human osteoblast d	C 956	19	34.5	608	23	ABV53637	Human prostate exp
C 884	19	34.5	97	22	AAK05926	Human reproductive	C 957	19	34.5	610	22	AAK80559	Human immune/haema
C 885	19	34.5	97	23	ABL98490	Human testicular a	C 958	19	34.5	612	22	AAK39407	CDNA encoding nove

C 959	19	34.5	612	22	AAK88255	Human digestive sy
C 960	19	34.5	614	22	ABA12806	Human nervous syst
C 961	19	34.5	653	24	ABQ57345	Human colon cancer
C 962	19	34.5	705	22	AAK68041	Human immune/haema
C 963	19	34.5	725	20	AAZ15035	Human gene express
C 964	19	34.5	783	22	ABA18325	Human nervous syst
C 965	19	34.5	811	20	AAK20485	Human secreted pro
C 966	19	34.5	814	22	AAH03306	Human cDNA clone (
C 967	19	34.5	817	24	ABQ89220	Human prostate exp
C 968	19	34.5	823	22	AAH06772	Human cDNA clone (
C 969	19	34.5	839	22	AAK82054	Human immune/haema
C 970	19	34.5	858	22	AAI19791	Human neuroblastom
C 971	19	34.5	867	23	ABV28810	Human prostate exp
C 972	19	34.5	904	24	ABL53184	Nucleotide sequenc
C 973	19	34.5	954	22	AAK73640	Human immune/haema
C 974	19	34.5	954	22	AAK73641	Human immune/haema
C 975	19	34.5	1027	22	AAK39719	Human immune/haema
C 976	19	34.5	1027	22	AAK39720	Genomic sequence #
C 977	19	34.5	1027	22	AAK90061	Genomic sequence #
C 978	19	34.5	1027	22	AAK90062	Human digestive sy
C 979	19	34.5	1071	22	AAK78073	Human immune/haema
C 980	19	34.5	1071	22	AAK78075	Human immune/haema
C 981	19	34.5	1071	22	AAK78077	Human immune/haema
C 982	19	34.5	1121	22	AAK75957	Human immune/haema
C 983	19	34.5	1121	22	AAK86278	Human immune/haema
C 984	19	34.5	1179	22	AAH16951	Human immune/haema
C 985	19	34.5	1209	22	AAK82755	Human cDNA sequenc
C 986	19	34.5	1225	22	AAH99064	Human immune/haema
C 987	19	34.5	1313	24	ABK12347	Human EST-derived
C 988	19	34.5	1325	22	AAK63203	Human nonerythroid
C 989	19	34.5	1349	24	AAK55585	Human immune/haema
C 990	19	34.5	1383	22	AAAL05637	DNA encoding human
C 991	19	34.5	1420	18	AAAT72167	Human reproductive
C 992	19	34.5	1482	22	AAK33428	Alzheimer's disease
C 993	19	34.5	1492	21	AAAS1403	DNA encoding human
C 994	19	34.5	1505	22	AAH99119	Chromosome 16q tum
C 995	19	34.5	1590	22	AAH13675	Human EST-derived
C 996	19	34.5	1727	22	AAH18282	Human cDNA sequenc
C 997	19	34.5	1734	22	AAH16375	Human cDNA sequenc
C 998	19	34.5	1740	22	ABA18100	Human nervous syst
C 999	19	34.5	1776	22	AAH31393	Human secreted pro
C1000	19	34.5	2120	22	AAK21280	Human cDNA sequenc

ALIGNMENTS

RESULT 1
AAA64507
ID AAA64507 standard; DNA; 9048 BP.

DT 02-JAN-2001 (first entry)

DE Nucleotide sequence comprising the human FEZ1 gene.

Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth; tumour proliferation; tubulin; microtubule; protein EPI-gamma; tubulin polymerisation disorder; mitosis initiation; cell proliferation; cell growth; cell shape; cell rigidity; cell motility; DNA replication; tumorigenesis; tumour survival; metastasis; ss.

AA Homo sapiens.
OS

AA
PN
WO200050565-A2.

XX
PD 31-AUG-2000.

XX
PF 25-FEB-2000: 2000WO-US04950.

XX
PR 25-FEB-1999: 99US-0121537.

XX

(UYJE-) UNIV JEFFERSON THOMAS.

Croce CM, Ishii H;

WPI: 2000-558396/51.

New polynucleotide homologous with a portion of one strand of the human FEZ1 gene, useful for alleviating abnormal cell proliferation such as cancer -

Claim 2: Fig 5A: 255pp: English.

The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour suppressor gene, located at chromosome location 8p22. Decreased or no expression of FEZ1 is detected in a variety of cancer cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts with tubulin, with microtubules, and with protein EPI-gamma.

initiation of mitosis, modulation of the initiation and rate of polymerization reactions, such as those associated with the formation of microtubules.

Query Match 100.0%; Score 55; DB 21; Length 9048;

Query Match	100.0%;	Score 33;	DB 21;
Best Local Similarity	100.0%;	Pred. No. 3.1e-19;	

Best Local Similarity 100.0%; Freq. NO: 3.1e-19;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGGCAGGCAGGCACCTTGAGGTCAGGAATTCGAGATCAGCCTGGCCACATGAG 55

4365 GAGGCAGGCAGAGCACTTGAGGTCAGGAA^{TT}CCAGATCAGCCCTGGCCAA^{CAT}GAG 4419

RESULT 2

RESULT 2
AAZ23904/C

AAZ23904/C
ID AAZ23904 standard: DNA: 49999 BP.

XX
AC AAZ23904:

XX
DT 25-JAN-2000 (first entry)

XX DE Human LOBO homo]ome genomic DNA fragment 6

xx
KW LOBO; long bones; bone development; bone extension; skull; osteopathic;
KW diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;
KW spondyloepiphyseal dysplasia; achondroplasia; human; ds.

XX Homo sapiens.

XX
PN W09950284-A2XX
07-OCT-1999

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DE 26-MAR-1988. 0000-00000000

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37 MAY 1966
0000 1013700

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1555-001320/JT.

PT useful for treating and studying bone disorders -

PS Example 3; Page 356-384; 391pp; German.
 CC This invention describes novel nucleic acids (I; designated LOBO (long
 CC bones)) encoding proteins influencing bone development in mammals. The
 CC proteins of the invention reduce and/or inactivate bone extension (i.e.
 CC development), with exception of the skull and have osteopathic activity.
 CC The nucleic acid molecules, proteins and antibodies can be used in
 CC diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods
 CC and nucleic acid molecules, etc. are useful for production of transgenic
 CC animals, especially a transgenic mouse for the study of diseases
 CC associated with bone development, e.g. spondyloepiphyseal dysplasia and
 CC achondroplasia. This sequence encodes a human LOBO protein described
 CC in the method of the invention.
 XX
 SQ Sequence 49999 BP; 10382 A; 14932 C; 14107 G; 10578 T; 0 other;

Query Match 72.7%; Score 40; DB 20; Length 49999;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
 Db 24864 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 24825

RESULT 3
 AAH03907
 ID AAH03907 standard; cDNA; 824 BP.
 AC AAH03907;
 XX
 XX
 DT 26-JUN-2001 (first entry)
 DE Human cDNA clone (5'-primer) SEQ ID NO:742.
 XX
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX Homo sapiens.
 XX EPI074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 XX 27-AUG-1999; 99JP-0300253.
 XX 11-JAN-2000; 2000JP-0118776.
 XX 02-MAY-2000; 2000JP-0183767.
 XX 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 DR
 XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -

PS Claim 1; SEQ ID 742; 2537pp + CD ROM; English.
 XX
 XX The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 824 BP; 227 A; 185 C; 226 G; 183 T; 3 other;

Query Match 65.5%; Score 36; DB 22; Length 824;
 Best Local Similarity 100.0%; Pred. No. 2.5e-09;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
 Db 583 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 618

RESULT 4
 AAH17143
 ID AAH17143 standard; cDNA; 1524 BP.
 AC AAH17143;
 XX
 XX
 DT 26-JUN-2001 (first entry)
 DE Human cDNA sequence SEQ ID NO:16486.
 XX
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX Homo sapiens.
 XX EPI074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 XX 27-AUG-1999; 99JP-0300253.
 XX 11-JAN-2000; 2000JP-0118776.
 XX 02-MAY-2000; 2000JP-0183767.
 XX 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 DR
 XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -

PS Claim 8; SEQ ID 16486; 2537pp + CD ROM; English.
 XX
 XX The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX SQ Sequence 1524 BP; 451 A; 339 C; 409 G; 325 T; 0 other;

Query Match 65.5%; Score 36; DB 22; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TGAGGTCAGGAATTCGAGATCAGCCTGGCCCAACATG 53
|||||
DB 583 TGAGGTCAGGAATTCGAGATCAGCCTGGCCCAACATG 618

RESULT 5
ABN65352
ID ABN65352 standard; cDNA; 570 BP.

XX AC ABN65352;

XX DT 28-JUN-2002 (first entry)

XX DE Human cancer related polynucleotide SEQ ID NO 5319.

XX KW Human; cytostatic; gene expression; gene mapping; tissue profiling;
XX gene therapy; cancer; tumour; gene; ss.

XX OS Homo sapiens.

XX FN WO200214500-A2.

XX PD 21-FEB-2002.

XX PF 16-AUG-2001; 2001WO-US25840.

XX PR 16-AUG-2000; 2000US-226326P.

XX PA (CHIR) CHIRON CORP.

XX PA (HYSE-) HYSEQ INC.

XX PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F;

XX PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I; .

XX DR WPI; 2002-241905/29.

XX PT New nucleic acid for producing a polypeptide, detecting differentially
XX expressed genes correlated with a cancerous state of a mammalian cell,
XX and inhibiting tumor growth -

XX PS Claim 1; SEQ ID NO 5319; 883pp + Sequence Listing; English.

XX CC The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
XX with cytostatic activity. The polynucleotide is used to produce a
XX polypeptide, to detect differentially expressed genes correlated with a
XX cancerous state of a mammalian cell and to inhibit tumour growth. The
XX polynucleotide is used as a probe in mapping and tissue profiling. The
XX encoded polypeptide and antibodies to the polypeptide can also be used
XX for therapeutic and diagnostic purposes. The polynucleotide is useful for

CC gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 570 BP; 158 A; 116 C; 156 G; 140 T; 0 other;

Query Match 63.6%; Score 35; DB 24; Length 570;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTCAGGTCAGGAATTCGAGATCAGCCTGGCCA 48
|||||
DB 348 CACTTCAGGTCAGGAATTCGAGATCAGCCTGGCCA 382

RESULT 6
AAK64788
ID AAK64788 standard; DNA; 10740 BP.

XX AC AAK64788;

XX DT 06-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19600.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.

XX OS Homo sapiens.

XX FN WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 14-JUL-2000; 2000US-0218290.

XX PR 26-JUL-2000; 2000US-0220963.

XX PR 26-JUL-2000; 2000US-0220964.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0224519.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225214.

XX PR 14-AUG-2000; 2000US-0225266.

XX PR 14-AUG-2000; 2000US-0225267.

XX PR 14-AUG-2000; 2000US-0225268.

XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

XX PR 14-AUG-2000; 2000US-0225757.

XX PR 14-AUG-2000; 2000US-0225758.

XX PR 14-AUG-2000; 2000US-0225759.

XX PR 18-AUG-2000; 2000US-0226279.

XX PR 22-AUG-2000; 2000US-0226681.

XX PR 22-AUG-2000; 2000US-0226686.

XX PR 22-AUG-2000; 2000US-0227182.

XX PR 23-AUG-2000; 2000US-0227009.

XX PR 30-AUG-2000; 2000US-0228924.

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PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233085.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236389.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 19600; 3071pp + Sequence Listing; English.
XX
XX AA54951 to AA64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AA82170 to AA82191. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AA64703
XX to AA87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AA54942 to AA54950 and AA82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 10740 BP; 3239 A; 1965 C; 2229 G; 3307 T; 0 other;
XX
Query Match 63.6%; Score 35; DB 22; Length 10740;
Best Local Similarity 100.0%; Pred. No. 7.3e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 CACTTGAGGTCAGGAATTCGAGATCAGCTCGGCCA 48
Db 1580 CACTTGAGGTCAGGAATTCGAGATCAGCTCGGCCA 1614
RESULT 7
ABL77817
ID ABL77817 standard; cDNA; 218 BP.
XX
```

AC ABL77817;
 XX
 XX 17-MAY-2002 (first entry)
 XX
 XX Human ovarian cancer related cDNA clone SEQ ID NO:795.
 XX
 XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200192581-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 29-MAY-2001; 2001WO-US17756.
 XX
 XX 26-MAY-2000; 2000US-207484P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Algate PA, Harlocker SL, Jones R;
 XX
 XX WPI; 2002-122075/16.
 XX
 XX Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide -
 XX
 XX Claim 1; SEQ ID 795; 489pp; English.
 XX
 CC The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
 CC (S1) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumour cDNA library using well known
 CC techniques.
 XX
 SQ Sequence 218 BP; 64 A; 42 C; 55 G; 51 T; 6 other;
 Query Match 45.5%; Score 25; DB 24; Length 218;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 30 TTCGAGATCAGCCCTGGCCACATGA 54
 Db 53 TTCGAGATCAGCCCTGGCCACATGA 77
 RESULT 8
 ABA16332/c
 ID ABA16332 standard; DNA; 250 BP.
 XX
 XX ABA16332;
 AC
 XX 23-JAN-2002 (first entry)
 DT
 XX Human nervous system related polynucleotide SEQ ID NO 8663.
 DE

XX
 KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
 KW antihemagic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200159063-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01334.
 XX
 XX 31-JAN-2000; 2000US-0179065.
 XX
 XX 04-FEB-2000; 2000US-0180628.
 XX
 XX 24-FEB-2000; 2000US-0184664.
 XX
 XX 02-MAR-2000; 2000US-0186350.
 XX
 XX 16-MAR-2000; 2000US-0189874.
 XX
 XX 17-MAR-2000; 2000US-0190076.
 XX
 XX 18-APR-2000; 2000US-0198123.
 XX
 XX 19-MAY-2000; 2000US-0205515.
 XX
 XX 07-JUN-2000; 2000US-0209467.
 XX
 XX 28-JUN-2000; 2000US-0214886.
 XX
 XX 30-JUN-2000; 2000US-0215135.
 XX
 XX 07-JUL-2000; 2000US-0216647.
 XX
 XX 07-JUL-2000; 2000US-0216880.
 XX
 XX 11-JUL-2000; 2000US-0217487.
 XX
 XX 11-JUL-2000; 2000US-0217496.
 XX
 XX 14-JUL-2000; 2000US-0218290.
 XX
 XX 26-JUL-2000; 2000US-0220963.
 XX
 XX 26-JUL-2000; 2000US-0220964.
 XX
 XX 14-AUG-2000; 2000US-0224518.
 XX
 XX 14-AUG-2000; 2000US-0224519.
 XX
 XX 14-AUG-2000; 2000US-0225213.
 XX
 XX 14-AUG-2000; 2000US-0225214.
 XX
 XX 14-AUG-2000; 2000US-0225266.
 XX
 XX 14-AUG-2000; 2000US-0225267.
 XX
 XX 14-AUG-2000; 2000US-0225268.
 XX
 XX 14-AUG-2000; 2000US-0225270.
 XX
 XX 14-AUG-2000; 2000US-0225447.
 XX
 XX 14-AUG-2000; 2000US-0225757.
 XX
 XX 14-AUG-2000; 2000US-0225758.
 XX
 XX 14-AUG-2000; 2000US-0225759.
 XX
 XX 18-AUG-2000; 2000US-0226279.
 XX
 XX 22-AUG-2000; 2000US-0226681.
 XX
 XX 22-AUG-2000; 2000US-0226868.
 XX
 XX 22-AUG-2000; 2000US-0227182.
 XX
 XX 23-AUG-2000; 2000US-0227009.
 XX
 XX 30-AUG-2000; 2000US-0228924.
 XX
 XX 01-SEP-2000; 2000US-0229287.
 XX
 XX 01-SEP-2000; 2000US-0229343.
 XX
 XX 01-SEP-2000; 2000US-0229344.
 XX
 XX 01-SEP-2000; 2000US-0229345.
 XX
 XX 05-SEP-2000; 2000US-0229509.
 XX
 XX 05-SEP-2000; 2000US-0229513.
 XX
 XX 06-SEP-2000; 2000US-0230437.
 XX
 XX 06-SEP-2000; 2000US-0230438.
 XX
 XX 08-SEP-2000; 2000US-0231242.
 XX
 XX 08-SEP-2000; 2000US-0231243.
 XX
 XX 08-SEP-2000; 2000US-0231244.
 XX
 XX 08-SEP-2000; 2000US-0231413.
 XX
 XX 08-SEP-2000; 2000US-0231414.
 XX
 XX 08-SEP-2000; 2000US-0232080.
 XX
 XX 12-SEP-2000; 2000US-0232081.
 XX
 XX 12-SEP-2000; 2000US-0231968.
 XX
 XX 14-SEP-2000; 2000US-0232397.
 XX
 XX 14-SEP-2000; 2000US-0232398.
 XX
 XX 14-SEP-2000; 2000US-0232399.
 XX
 XX 14-SEP-2000; 2000US-0232400.

PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.

PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 03-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Baraah SC, Ruben SM;
PI
XX
XX WPI; 2001-541565/60.
DR
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases
PT
XX
XX Disclosure; SEQ ID NO 8663; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease; multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 250 BP; 48 A; 71 C; 52 G; 79 T; 0 other;

Query Match 45.5%; Score 25; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TTCGAGATCAGCTGGCCACATGA 54
|||||
Db 229 TTCGAGATCAGCTGGCCACATGA 205
|||||

RESULT 9
AAC05198
ID AAC05198 standard; cDNA; 320 BP.
XX
XX AAC05198;
XX
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 9273.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
XX EP1033401-A2.
XX
XX
PD 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX

PA (GSET) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 9273; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors.
XX
XX Sequence 320 BP; 86 A; 70 C; 71 G; 92 T; 1 other;
SQ
Query Match 45.5%; Score 25; DB 21; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 30 TTCGAGATCAGCCTGGCCACATGA 54
Db 212 TTCGAGATCAGCCTGGCCACATGA 236
RESULT 10
AAS91264/c
ID AAS91264 standard; cDNA; 1566 BP.
XX
XX AAS91264;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #27068.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSEQ-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG27077.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensic, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
PT

Claim 1; SEQ ID No 27068; 103pp; English.
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1566 BP; 377 A; 390 C; 452 G; 347 T; 0 other;
Query Match 45.5%; Score 25; DB 23; Length 1566;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 30 TTCGAGATCAGCCTGGCCACATGA 54
Db 36 TTCGAGATCAGCCTGGCCACATGA 12
RESULT 11
AAH17905
ID AAH17905 standard; cDNA; 3295 BP.
XX
XX AAH17905;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA sequence SEQ ID NO:17649.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-0116126.
XX
XX 29-JUL-1999; 99JP-0248036.
XX
XX 27-AUG-1999; 99JP-0300253.
XX
XX 11-JAN-2000; 2000JP-0118776.
XX
XX 02-MAY-2000; 2000JP-0183767.
XX
XX 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-316749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
PT

XX Claim 8; SEQ ID 17649; 2537pp + CD ROM; English.
 XX The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 3295 BP; 1013 A; 683 C; 768 G; 831 T; 0 other;

Query Match 45.58; Score 25; DB 22; Length 3295;
 Best Local Similarity 100.0%; Pred. NO. 0.0012;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATGA 54
 Db 1656 TTCGAGATCAGCTGGCCACATGA 1680

RESULT 12
 ABL55755
 ID ABL55755 standard; DNA; 10708 BP.
 XX
 AC ABL55755;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Human transporter protein related to permease subfamily gene.
 XX
 KW Human; permease; transporter; gene therapy; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(366,T)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism"
 FT replace(812,G)
 FT /*tag= b
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(825,G)
 FT /*tag= c
 FT /standard_name= "Single nucleotide polymorphism"
 FT CDS 1225..8132
 FT /*tag= f
 FT /product= "Transport protein"
 FT /note= "Contains 11 introns"
 FT 1225..1386
 FT /*tag= g
 FT /number= 1
 FT 1387..1530
 FT /*tag= h
 FT /number= 1
 FT 1531..1688
 FT /*tag= g

FT intron /number= 2
 FT 1689..1802
 FT /*tag= h
 FT /number= 2
 FT 1803..1900
 FT /*tag= g
 FT /number= 3
 FT 1901..2106
 FT /*tag= h
 FT /number= 3
 FT replace(1975,G)
 FT /tag= d
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2101,C)
 FT /*tag= e
 FT /standard_name= "Single nucleotide polymorphism"
 FT exon 2107..2180
 FT /*tag= g
 FT /number= 4
 FT 2181..2375
 FT /*tag= h
 FT /number= 4
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 FT 2891..3014
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 FT /*tag= h
 FT /number= 6
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 XX US2002028915-A1.
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 XX 27-DEC-2000; 2000US-0748107.

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XX 07-SEP-2000; 2000US-230721P.
PR (WEIM/) WEI M.
XX (YEJ/) YE J.
PA (MOOR/) MOORE H M.
PA (MERK/) MERKULOV G V.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
XX
XX Wei M, Ye J, Moore HM, Merkulo GV, Di Francesco V, Beasley EM;
PI MPI: 2002-315053/35.
XX P-PSDB; ABB77086.
DR
DR
XX Novel human transporter protein that is related to permease subfamily,
PT useful as models for development of human therapeutic targets and
PT serves as targets for developing human therapeutic agents -
XX
XX Claim 2; Fig 3; 36pp; English.
XX
XX The sequence encodes the novel human transporter protein related to the
CC permease subfamily of the invention. The sequence is found on chromosome
CC 2. The protein of the invention is useful for identifying a modulator of
CC a human permease. A pharmaceutical composition comprising an agent that
CC binds to the transporter protein is useful for treating a disease or
CC condition mediated by human transporter protein. A nucleic acid molecule
CC encoding the transporter protein of the invention provides vectors for
CC gene therapy in patients with aberrant transporter gene expression.
XX
XX Sequence 10708 BP; 2486 A; 2541 C; 2892 G; 2739 T; 50 other;
SQ
Query Match 45.5%; Score 25; DB 24; Length 10708;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 TTCGAGATCAGCTGGCCACATGA 54
DB 6117 TTCGAGATCAGCTGGCCACATGA 6141
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XX
XX ABA20815;
AC
AC
DT 23-JAN-2002 (first entry)
XX
XX Human nervous system related polynucleotide SEQ ID NO 13146.
XX
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX
XX WO200159063-A2.
FN
XX
XX 16-AUG-2001.
PD
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XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0175065.
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PR 18-APR-2000; 2000US-0198123.
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PR 13-OCT-2000; 2000US-0239937.

```

CC isolated from a range of human tissues disclosed in the specification.
CC the nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12842 BP; 2686 A; 3223 C; 3551 G; 3382 T; 0 other;
Query Match 45.5%; Score 25; DB 22; Length 12842;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 7182 GTCAGGAATTCGAGATCAGCCTGCG 7158
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XX
AC AAK71816;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26628.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01354.
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PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases -
XX
XX Disclosure; SEQ ID NO 13146; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
XX (AB114678-AB18001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are

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PR 08-DEC-2000; 2000US-0251989.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 26628; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 14417 BP; 3611 A; 3356 C; 3462 G; 3988 T; 0 other;
SQ Query Match 45.5%; Score 25; DB 22; Length 14417;
Best Local Similarity 100.0%; Pred. No. 0.0011;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATGA 54
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Db 10166 TTCGAGATCAGCTGGCCACATGA 10142

RESULT 15

AAK73113
ID AAK73113 standard; DNA; 14417 BP.

AC AAK73113;

XX DT 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27925.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cyostatic; gene therapy; vaccine; metastasis; db.

XX Homo sapiens.

XX WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

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PR 13-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

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PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249218.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 27925; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 14417 BP; 3988 A; 3462 C; 3356 G; 3611 T; 0 other;

Query Match 45.5%; Score 25; DB 22; Length 14417;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 TTCGAGATCAGCTGGCCACATGA 54
Db 4252 TTCGAGATCAGCTGGCCACATGA 4276
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Search completed: June 16, 2003, 20:02:46
Job time : 34.7096 secs

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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 2.15297 Seconds
(without alignments)
7834.381 Million cell updates/sec

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Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database : Issued Patents NA.*

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6: /cgn2_6/ptodata/1/ina/backfilesi.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	24	43.6	2387	4	US-09-375-318-38
C 2	23	41.8	18443	4	US-09-078-294-6
C 3	23	41.8	80246	4	US-09-078-294-4
C 4	23	41.8	80595	4	US-09-078-294-3
C 5	23	41.8	99500	4	US-09-798-096-10
C 6	23	41.8	112132	4	US-09-741-150-3
C 7	22	40.0	18596	4	US-09-318-448-11
C 8	22	40.0	81001	4	US-09-750-580-1
C 9	21	38.2	3350	3	US-09-110-116-2
C 10	21	38.2	8396	4	US-09-328-174A-1
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C 14	21	38.2	84495	4	US-09-797-506-3
C 15	21	38.2	99500	4	US-09-798-096-10
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C 17	20	36.4	17327	1	US-07-906-871-15
C 18	20	36.4	162450	4	US-09-345-882-1
C 19	20	36.4	246240	2	US-08-724-394A-20
C 20	20	36.4	246240	2	US-08-724-394A-21
C 21	19	34.5	246240	2	US-08-724-394A-22
C 22	19	34.5	240	1	US-08-222-177A-9
C 23	19	34.5	1420	2	US-08-909-965C-3
C 24	19	34.5	3336	4	US-09-026-033-1
C 25	19	34.5	3336	4	US-09-026-033-2
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C 69	17	30.9	4517	4	US-08-520-3730-5
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C 432	16	29.1	13865	3	US-09-009-217-11	Sequence 11, Appli	C 505	16	29.1	84495	4	US-09-797-906-3	Sequence 3, Appli
C 433	16	29.1	13865	3	US-09-009-656-11	Sequence 11, Appli	C 506	16	29.1	98844	4	US-09-791-211-10	Sequence 10, Appli
C 434	16	29.1	13953	4	US-09-738-884-3	Sequence 3, Appli	C 507	16	29.1	111282	4	US-09-754-250-3	Sequence 3, Appli
C 435	16	29.1	13953	4	US-09-738-884-3	Sequence 3, Appli	C 508	16	29.1	111282	4	US-09-754-250-3	Sequence 3, Appli
C 436	16	29.1	14581	4	US-08-520-373D-4	Sequence 4, Appli	C 509	16	29.1	112132	4	US-09-741-150-3	Sequence 3, Appli
C 437	16	29.1	14635	4	US-09-173-914-5	Sequence 5, Appli	C 510	16	29.1	152331	3	US-09-128-155-16	Sequence 16, Appli
C 438	16	29.1	14747	4	US-09-608-285A-42	Sequence 42, Appli	C 511	16	29.1	162450	4	US-09-345-882-1	Sequence 1, Appli
C 439	16	29.1	14753	4	US-09-821-736-3	Sequence 3, Appli	C 512	16	29.1	168575	4	US-09-426-290-1	Sequence 1, Appli
C 440	16	29.1	15602	4	US-09-844-634-17	Sequence 17, Appli	C 513	16	29.1	168575	4	US-09-426-290-1	Sequence 1, Appli
C 441	16	29.1	15602	4	US-09-844-634-17	Sequence 17, Appli	C 514	16	29.1	169998	4	US-09-676-610B-24	Sequence 24, Appli
C 442	16	29.1	15977	4	US-09-608-285A-59	Sequence 59, Appli	C 515	16	29.1	176373	3	US-09-128-155-17	Sequence 17, Appli
C 443	16	29.1	16389	4	US-09-741-154-3	Sequence 3, Appli	C 516	15	27.3	15	4	US-09-081-646-11	Sequence 11, Appli
C 444	16	29.1	16389	4	US-09-741-154-3	Sequence 3, Appli	C 517	15	27.3	15	4	US-09-081-646-11	Sequence 11, Appli
C 445	16	29.1	16595	4	US-09-146-053-7	Sequence 7, Appli	C 518	15	27.3	22	1	US-09-081-646-11	Sequence 483, App
C 446	16	29.1	17425	4	US-09-511-625B-5	Sequence 5, Appli	C 519	15	27.3	22	1	US-08-068-945A-58	Sequence 58, Appli
C 447	16	29.1	17606	4	US-08-943-731-4	Sequence 4, Appli	C 520	15	27.3	22	1	US-08-442-806-58	Sequence 58, Appli
C 448	16	29.1	17949	4	US-09-087-465-3	Sequence 3, Appli	C 521	15	27.3	30	2	US-08-859-998-318	Sequence 318, App
C 449	16	29.1	17949	4	US-09-087-465-3	Sequence 3, Appli	C 522	15	27.3	30	2	US-09-225-928-318	Sequence 318, App
C 450	16	29.1	18073	4	US-09-078-294-12	Sequence 12, Appli	C 523	15	27.3	75	4	US-09-357-740-14	Sequence 14, Appli
C 451	16	29.1	18596	4	US-09-318-448-11	Sequence 11, Appli	C 524	15	27.3	75	4	US-09-357-740-14	Sequence 14, Appli
C 452	16	29.1	19336	1	US-08-740-035-6	Sequence 6, Appli	C 525	15	27.3	281	4	US-09-103-875-15	Sequence 15, Appli
C 453	16	29.1	20303	1	US-08-370-975B-6	Sequence 6, Appli	C 526	15	27.3	283	4	US-08-118-200-11	Sequence 11, Appli
C 454	16	29.1	20674	4	US-09-641-638-651	Sequence 651, App	C 527	15	27.3	283	4	US-08-458-745-11	Sequence 11, Appli
C 455	16	29.1	26664	4	US-09-564-805-28	Sequence 28, Appli	C 528	15	27.3	327	1	US-08-741-406-6	Sequence 6, Appli
C 456	16	29.1	26764	1	US-08-370-975B-1	Sequence 1, Appli	C 529	15	27.3	327	2	US-09-024-472-6	Sequence 6, Appli
C 457	16	29.1	28720	4	US-09-341-587-7	Sequence 7, Appli	C 530	15	27.3	347	2	US-08-367-101-44	Sequence 44, Appli
C 458	16	29.1	28994	3	US-08-884-324-14	Sequence 14, Appli	C 531	15	27.3	347	2	US-08-592-541-44	Sequence 44, Appli
C 459	16	29.1	29629	4	US-09-729-995-3	Sequence 3, Appli	C 532	15	27.3	347	4	US-09-124-698-44	Sequence 44, Appli
C 460	16	29.1	29629	4	US-09-729-995-3	Sequence 3, Appli	C 533	15	27.3	347	4	US-09-127-480-44	Sequence 44, Appli
C 461	16	29.1	31571	1	US-08-323-443B-1	Sequence 1, Appli	C 534	15	27.3	347	4	US-08-496-841C-44	Sequence 44, Appli
C 462	16	29.1	32042	4	US-09-245-281-44	Sequence 44, Appli	C 535	15	27.3	388	2	US-09-124-523-44	Sequence 44, Appli
C 463	16	29.1	32042	4	US-09-245-281-44	Sequence 44, Appli	C 536	15	27.3	388	2	US-08-967-101-68	Sequence 68, Appli
C 464	16	29.1	35060	3	US-08-814-095-7	Sequence 7, Appli	C 537	15	27.3	388	2	US-08-592-541-68	Sequence 68, Appli
C 465	16	29.1	35100	1	US-08-306-691B-19	Sequence 19, Appli	C 538	15	27.3	388	4	US-09-124-698-68	Sequence 68, Appli
C 466	16	29.1	35100	1	US-08-306-691B-19	Sequence 19, Appli	C 538	15	27.3	388	4	US-09-124-698-68	Sequence 68, Appli

C 539	15	27.3	388	4	US-08-496-841C-68	Sequence 68, Appl	612	15	27.3	3715	4	US-09-085-199B-44	Sequence 44, Appl
C 540	15	27.3	388	4	US-09-124-523-68	Sequence 68, Appl	613	15	27.3	3885	1	US-08-688-105-1	Sequence 1, Appl
C 541	15	27.3	451	4	US-09-404-879A-101	Sequence 101, Appl	C 614	15	27.3	3993	4	US-09-167-109-5	Sequence 5, Appl
C 542	15	27.3	548	4	US-08-991-789A-15	Sequence 15, Appl	C 615	15	27.3	4066	4	US-09-367-750-1	Sequence 1, Appl
C 543	15	27.3	548	4	US-09-062-451-15	Sequence 15, Appl	C 616	15	27.3	4136	4	US-09-103-875-2	Sequence 2, Appl
C 544	15	27.3	548	4	US-09-598-226-15	Sequence 15, Appl	C 617	15	27.3	4326	2	US-08-852-807-12	Sequence 12, Appl
C 545	15	27.3	554	4	US-09-227-757-111	Sequence 111, Appl	C 618	15	27.3	4335	3	US-09-058-489-19	Sequence 19, Appl
C 546	15	27.3	567	1	US-08-480-784-30	Sequence 30, Appl	C 619	15	27.3	4630	4	US-09-442-143A-1	Sequence 1, Appl
C 547	15	27.3	567	1	US-08-483-553-30	Sequence 30, Appl	C 620	15	27.3	5375	3	US-08-757-223-7	Sequence 7, Appl
C 548	15	27.3	567	1	US-08-487-002-30	Sequence 30, Appl	C 621	15	27.3	5375	3	US-08-757-223-7	Sequence 7, Appl
C 549	15	27.3	567	1	US-08-483-554B-30	Sequence 30, Appl	C 622	15	27.3	5581	4	US-08-973-544-1	Sequence 1, Appl
C 550	15	27.3	567	1	US-08-488-011B-30	Sequence 30, Appl	C 623	15	27.3	5775	1	US-08-306-691B-15	Sequence 15, Appl
C 551	15	27.3	567	4	US-08-850-727-30	Sequence 30, Appl	C 624	15	27.3	5775	5	PCT-US93-06251-29	Sequence 29, Appl
C 552	15	27.3	567	5	PCT-US95-10202-30	Sequence 30, Appl	C 625	15	27.3	6232	4	US-08-456-200B-11	Sequence 11, Appl
C 553	15	27.3	567	5	PCT-US95-10203-30	Sequence 30, Appl	C 626	15	27.3	6330	4	US-09-880-427-2	Sequence 2, Appl
C 554	15	27.3	567	5	PCT-US95-10220-30	Sequence 30, Appl	C 627	15	27.3	6330	4	US-09-306-538B-2	Sequence 2, Appl
C 555	15	27.3	590	4	US-09-328-111-411	Sequence 411, Appl	C 628	15	27.3	6669	3	US-09-212-971-5	Sequence 5, Appl
C 556	15	27.3	603	4	US-08-949-155-3	Sequence 3, Appl	C 629	15	27.3	6669	3	US-08-800-929A-5	Sequence 5, Appl
C 557	15	27.3	603	4	US-09-819-964-3	Sequence 3, Appl	C 630	15	27.3	6669	4	US-09-617-053A-5	Sequence 5, Appl
C 558	15	27.3	621	4	US-09-328-111-7	Sequence 7, Appl	C 631	15	27.3	6709	4	US-09-285-601-3	Sequence 3, Appl
C 559	15	27.3	646	4	US-09-385-982-314	Sequence 314, Appl	C 632	15	27.3	6792	4	US-09-374-454-20	Sequence 20, Appl
C 560	15	27.3	661	2	US-08-529-878B-37	Sequence 37, Appl	C 633	15	27.3	6792	4	US-08-257-963B-10	Sequence 10, Appl
C 561	15	27.3	702	4	US-08-949-155-8	Sequence 8, Appl	C 634	15	27.3	7210	4	US-08-367-841A-10	Sequence 10, Appl
C 562	15	27.3	702	4	US-09-819-964-8	Sequence 8, Appl	C 635	15	27.3	7210	4	PCT-US95-07201-10	Sequence 10, Appl
C 563	15	27.3	755	4	US-09-288-143-29	Sequence 29, Appl	C 636	15	27.3	7605	4	US-09-417-455-8	Sequence 8, Appl
C 564	15	27.3	782	4	US-09-288-143-19	Sequence 19, Appl	C 637	15	27.3	7605	4	US-09-348-942-8	Sequence 8, Appl
C 565	15	27.3	900	2	US-08-518-862C-5	Sequence 5, Appl	C 638	15	27.3	7605	4	US-09-457-626-8	Sequence 8, Appl
C 566	15	27.3	901	1	US-08-832-883-65	Sequence 65, Appl	C 639	15	27.3	8133	4	US-09-659-791A-10	Sequence 10, Appl
C 567	15	27.3	901	2	US-08-832-877-65	Sequence 65, Appl	C 640	15	27.3	9278	1	US-08-243-542-9	Sequence 9, Appl
C 568	15	27.3	1000	4	US-09-018-584A-32	Sequence 32, Appl	C 641	15	27.3	9278	1	US-08-477-407-9	Sequence 9, Appl
C 569	15	27.3	1000	4	US-09-018-584A-34	Sequence 34, Appl	C 642	15	27.3	9278	1	US-08-484-355-9	Sequence 9, Appl
C 570	15	27.3	1000	4	US-09-641-638-460	Sequence 460, Appl	C 643	15	27.3	9301	4	US-09-449-218D-18	Sequence 18, Appl
C 571	15	27.3	1001	4	US-09-641-638-70	Sequence 70, Appl	C 644	15	27.3	9365	4	US-09-608-285A-8	Sequence 8, Appl
C 572	15	27.3	1001	4	US-09-641-638-293	Sequence 293, Appl	C 645	15	27.3	9365	4	US-09-350-836B-8	Sequence 8, Appl
C 573	15	27.3	1001	4	US-09-641-638-459	Sequence 459, Appl	C 646	15	27.3	9365	4	US-09-370-265-8	Sequence 8, Appl
C 574	15	27.3	1043	4	US-09-165-868-4	Sequence 4, Appl	C 647	15	27.3	9639	4	US-09-147-208-26	Sequence 26, Appl
C 575	15	27.3	1052	4	US-09-442-143A-9	Sequence 9, Appl	C 648	15	27.3	9690	4	US-09-182-145-55	Sequence 55, Appl
C 576	15	27.3	1145	3	US-08-755-587-36	Sequence 36, Appl	C 649	15	27.3	9704	4	US-09-814-951A-3	Sequence 3, Appl
C 577	15	27.3	1155	3	US-08-755-587-35	Sequence 35, Appl	C 650	15	27.3	10379	4	US-09-182-145-54	Sequence 54, Appl
C 578	15	27.3	1260	4	US-08-943-731-169	Sequence 169, Appl	C 651	15	27.3	11284	3	US-08-978-741-5	Sequence 5, Appl
C 579	15	27.3	1542	4	US-09-008-271A-13	Sequence 13, Appl	C 652	15	27.3	12565	4	US-09-345-217-3	Sequence 3, Appl
C 580	15	27.3	1804	1	US-08-306-691B-40	Sequence 40, Appl	C 653	15	27.3	12847	1	US-08-550-715-1	Sequence 1, Appl
C 581	15	27.3	1804	4	US-09-167-322-14	Sequence 14, Appl	C 654	15	27.3	13187	4	US-09-422-936-61	Sequence 61, Appl
C 582	15	27.3	1804	5	PCT-US93-06251-82	Sequence 82, Appl	C 655	15	27.3	13187	2	US-08-852-807-1	Sequence 1, Appl
C 583	15	27.3	1875	2	US-08-683-743-3	Sequence 3, Appl	C 656	15	27.3	13865	3	US-09-009-217-11	Sequence 11, Appl
C 584	15	27.3	1901	4	US-09-338-907-181	Sequence 181, Appl	C 657	15	27.3	13865	3	US-09-009-656-11	Sequence 11, Appl
C 585	15	27.3	1901	4	US-09-218-207-181	Sequence 181, Appl	C 658	15	27.3	13875	2	US-08-734-344-1	Sequence 1, Appl
C 586	15	27.3	1926	4	US-09-117-250-4	Sequence 4, Appl	C 659	15	27.3	14581	4	US-08-520-373D-4	Sequence 4, Appl
C 587	15	27.3	2048	1	US-07-602-608-11	Sequence 11, Appl	C 660	15	27.3	14796	4	US-08-975-080-35	Sequence 35, Appl
C 588	15	27.3	2048	1	US-08-261-578-11	Sequence 11, Appl	C 661	15	27.3	14796	4	US-09-630-706-10	Sequence 10, Appl
C 589	15	27.3	2061	2	US-08-960-022-11	Sequence 11, Appl	C 662	15	27.3	14796	4	US-09-496-694B-3	Sequence 3, Appl
C 590	15	27.3	2115	1	US-08-395-800A-7	Sequence 7, Appl	C 663	15	27.3	15297	4	US-09-817-180-3	Sequence 3, Appl
C 591	15	27.3	2141	1	US-08-463-931-1	Sequence 1, Appl	C 664	15	27.3	16063	4	US-09-801-052-3	Sequence 3, Appl
C 592	15	27.3	2141	4	US-09-224-048A-3	Sequence 3, Appl	C 665	15	27.3	17327	1	US-07-906-871-15	Sequence 15, Appl
C 593	15	27.3	2298	3	US-08-772-440-1	Sequence 1, Appl	C 666	15	27.3	19736	4	US-09-740-035-3	Sequence 3, Appl
C 594	15	27.3	2298	4	US-09-153-599A-1	Sequence 1, Appl	C 667	15	27.3	20303	1	US-08-370-975B-6	Sequence 6, Appl
C 595	15	27.3	2329	4	US-08-927-219-80	Sequence 80, Appl	C 668	15	27.3	21234	4	US-09-810-671-3	Sequence 3, Appl
C 596	15	27.3	2334	4	US-09-493-565-1	Sequence 1, Appl	C 669	15	27.3	22481	4	US-08-367-841A-43	Sequence 43, Appl
C 597	15	27.3	2409	1	US-07-911-531-18	Sequence 18, Appl	C 670	15	27.3	22481	5	PCT-US95-07201-43	Sequence 43, Appl
C 598	15	27.3	2409	1	US-07-693-636A-18	Sequence 18, Appl	C 671	15	27.3	22484	4	US-09-875-223-2	Sequence 2, Appl
C 599	15	27.3	2415	3	US-09-019-689-1	Sequence 1, Appl	C 672	15	27.3	24979	2	US-08-147-777-3	Sequence 3, Appl
C 600	15	27.3	2477	1	US-08-429-742-1	Sequence 1, Appl	C 673	15	27.3	24979	3	US-08-452-872-3	Sequence 3, Appl
C 601	15	27.3	2680	4	US-08-949-155-50	Sequence 50, Appl	C 674	15	27.3	24979	5	PCT-US93-03985-3	Sequence 3, Appl
C 602	15	27.3	2680	4	US-08-819-964-50	Sequence 50, Appl	C 675	15	27.3	26764	1	US-08-370-975B-1	Sequence 1, Appl
C 603	15	27.3	2721	3	US-08-921-195-1	Sequence 1, Appl	C 676	15	27.3	40352	3	US-08-846-111D-15	Sequence 15, Appl
C 604	15	27.3	2741	1	US-08-832-883-59	Sequence 59, Appl	C 677	15	27.3	40352	4	US-09-443-077-15	Sequence 15, Appl
C 605	15	27.3	2741	2	US-08-832-877-59	Sequence 59, Appl	C 678	15	27.3	42571	4	US-09-810-347-3	Sequence 3, Appl
C 606	15	27.3	2822	4	US-08-819-872A-1	Sequence 1, Appl	C 679	15	27.3	50000	4	US-09-146-053-4	Sequence 4, Appl
C 607	15	27.3	2822	4	US-08-819-872A-10	Sequence 10, Appl	C 680	15	27.3	50000	4	US-09-146-053-4	Sequence 4, Appl
C 608	15	27.3	2822	4	US-08-819-872A-11	Sequence 11, Appl	C 681	15	27.3	55827	4	US-09-813-133A-3	Sequence 3, Appl
C 609	15	27.3	3186	1	US-08-761-258-8	Sequence 8, Appl	C 682	15	27.3	56516	2	US-08-996-306-1	Sequence 1, Appl
C 610	15	27.3	3186	2	US-08-977-306-8	Sequence 8, Appl	C 683	15	27.3	56516	4	US-09-338-907-1	Sequence 1, Appl
C 611	15	27.3	3535	2	US-08-618-408B-1	Sequence 1, Appl	C 684	15	27.3	56516	4	US-09-218-207-1	Sequence 1, Appl

685	15	27.3	56520	4	US-09-338-907-179	Sequence 179, App	758	14	25.5	3611	3	US-08-447-314-1	Sequence 1, Appl
686	15	27.3	56520	4	US-09-218-207-179	Sequence 179, App	759	14	25.5	3611	3	US-08-445-461-1	Sequence 1, Appl
c 687	15	27.3	16998	4	US-09-676-610B-24	Sequence 2, Appl	c 760	14	25.5	4534	2	US-08-935-450-1	Sequence 1, Appl
c 688	15	27.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl	c 761	14	25.5	4534	4	US-09-166-350-25	Sequence 25, Appl
c 689	15	27.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl	c 762	14	25.5	4534	2	US-08-881-450A-22	Sequence 22, Appl
c 690	15	27.3	35	4	US-09-605-785-829	Sequence 829, App	c 763	14	25.5	5543	2	US-08-687-080-101	Sequence 101, App
c 691	14	25.5	249	2	US-08-687-080-100	Sequence 100, App	c 764	14	25.5	6078	4	US-09-173-914-1	Sequence 1, Appl
c 692	14	25.5	411	4	US-09-385-982-5	Sequence 5, Appl	c 765	14	25.5	6246	4	US-08-943-731-640	Sequence 640, App
c 693	14	25.5	451	4	US-09-404-879A-43	Sequence 43, Appl	c 766	14	25.5	6709	4	US-09-285-601-3	Sequence 3, Appl
c 694	14	25.5	454	4	US-09-991-789A-49	Sequence 49, Appl	c 767	14	25.5	6719	4	US-09-740-235-36	Sequence 36, Appl
c 695	14	25.5	454	4	US-09-062-451-49	Sequence 49, Appl	c 768	14	25.5	7676	1	US-08-451-777A-7	Sequence 7, Appl
c 696	14	25.5	454	4	US-09-598-326-49	Sequence 49, Appl	c 769	14	25.5	7676	2	US-08-451-778A-7	Sequence 7, Appl
c 697	14	25.5	481	5	PCT-US95-08295-15	Sequence 15, Appl	c 770	14	25.5	7676	2	US-08-998-208-7	Sequence 7, Appl
c 698	14	25.5	568	4	US-09-221-017B-491	Sequence 491, App	c 771	14	25.5	7676	5	PCT-US95-06743-7	Sequence 7, Appl
c 699	14	25.5	598	4	US-09-641-638-60	Sequence 60, App	c 772	14	25.5	7705	2	US-08-687-080-115	Sequence 115, App
c 700	14	25.5	598	4	US-09-641-638-574	Sequence 574, App	c 773	14	25.5	8021	4	US-09-740-235-2	Sequence 2, Appl
c 701	14	25.5	600	3	US-09-078-317-1	Sequence 1, Appl	c 774	14	25.5	9704	4	US-09-814-951A-3	Sequence 3, Appl
c 702	14	25.5	600	4	US-09-454-818-1	Sequence 1, Appl	c 775	14	25.5	10614	1	US-08-135-511-35	Sequence 35, Appl
c 703	14	25.5	601	4	US-08-814-951A-5	Sequence 5, Appl	c 776	14	25.5	10614	1	US-08-187-453-35	Sequence 35, Appl
c 704	14	25.5	656	3	US-08-921-195-2	Sequence 2, Appl	c 777	14	25.5	10684	4	US-09-221-017B-401	Sequence 401, App
c 705	14	25.5	683	4	US-09-740-235-19	Sequence 19, App	c 778	14	25.5	11288	4	US-08-481-968A-4	Sequence 4, Appl
c 706	14	25.5	687	3	US-09-048-052-5	Sequence 5, Appl	c 779	14	25.5	11288	4	US-08-154-712B-4	Sequence 4, Appl
c 707	14	25.5	687	4	US-09-160-246-5	Sequence 5, Appl	c 780	14	25.5	11288	4	US-08-402-282-3	Sequence 3, Appl
c 708	14	25.5	738	4	US-09-662-250A-23	Sequence 23, App	c 781	14	25.5	12141	4	US-09-488-671-10	Sequence 10, Appl
c 709	14	25.5	764	4	US-09-288-143-57	Sequence 57, App	c 782	14	25.5	15664	1	US-08-402-282-3	Sequence 3, Appl
c 710	14	25.5	789	2	US-08-394-152A-42	Sequence 42, App	c 783	14	25.5	15664	1	US-08-508-004-3	Sequence 3, Appl
c 711	14	25.5	799	4	US-09-166-350-11	Sequence 11, App	c 784	14	25.5	15664	1	US-08-402-066-3	Sequence 3, Appl
c 712	14	25.5	971	1	US-08-451-947-11	Sequence 11, App	c 785	14	25.5	15664	1	US-08-402-068-3	Sequence 3, Appl
c 713	14	25.5	971	5	US-08-928-694-11	Sequence 11, App	c 786	14	25.5	17041	1	US-08-076-011-1	Sequence 1, Appl
c 714	14	25.5	971	5	PCT-US91-06950-11	Sequence 11, App	c 787	14	25.5	29604	1	US-08-781-891-207	Sequence 207, App
c 715	14	25.5	985	4	US-09-160-246-9	Sequence 9, Appl	c 788	14	25.5	40352	3	US-08-846-111B-15	Sequence 15, Appl
c 716	14	25.5	985	4	US-09-160-246-13	Sequence 13, App	c 789	14	25.5	40352	4	US-09-443-077-15	Sequence 15, Appl
c 717	14	25.5	1000	2	US-08-747-121-20	Sequence 20, App	c 790	14	25.5	49136	4	US-09-422-869-1	Sequence 1, Appl
c 718	14	25.5	1001	4	US-09-641-638-291	Sequence 291, App	c 791	14	25.5	50000	4	US-09-146-053-3	Sequence 3, Appl
c 719	14	25.5	1001	4	US-09-641-638-304	Sequence 304, App	c 792	14	25.5	72928	3	US-09-009-913-1	Sequence 1, Appl
c 720	14	25.5	1001	4	US-09-641-638-458	Sequence 458, App	c 793	13	23.6	21	3	US-08-701-582D-22	Sequence 22, Appl
c 721	14	25.5	1045	1	US-08-599-252-92	Sequence 92, App	c 794	13	23.6	26	3	US-08-441-935-3	Sequence 3, Appl
c 722	14	25.5	1045	5	PCT-US96-06352-92	Sequence 92, App	c 795	13	23.6	26	4	US-08-441-943-3	Sequence 3, Appl
c 723	14	25.5	1045	5	PCT-US96-06583-92	Sequence 92, App	c 796	13	23.6	30	2	US-08-880-557-6	Sequence 6, Appl
c 724	14	25.5	1079	1	US-08-832-883-62	Sequence 62, App	c 797	13	23.6	30	3	US-08-441-935-4	Sequence 4, Appl
c 725	14	25.5	1079	2	US-08-832-877-62	Sequence 62, App	c 798	13	23.6	30	3	US-09-189-583-6	Sequence 6, Appl
c 726	14	25.5	1079	1	US-08-451-947-9	Sequence 9, App	c 799	13	23.6	30	4	US-08-441-943-4	Sequence 4, Appl
c 727	14	25.5	1190	2	US-08-424-826A-9	Sequence 9, App	c 800	13	23.6	36	3	US-08-441-935-5	Sequence 5, Appl
c 728	14	25.5	1190	3	US-08-928-694-9	Sequence 9, App	c 801	13	23.6	36	4	US-08-441-943-5	Sequence 5, Appl
c 729	14	25.5	1190	5	PCT-US91-06950-9	Sequence 9, App	c 802	13	23.6	37	2	US-08-902-516-49	Sequence 49, Appl
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c 731	14	25.5	1404	1	US-07-796-106-22	Sequence 22, App	c 804	13	23.6	53	5	PCT-US95-10219-21	Sequence 21, App
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c 734	14	25.5	1620	2	US-08-977-847-2	Sequence 2, App	c 807	13	23.6	64	3	US-08-836-561-8	Sequence 8, Appl
c 735	14	25.5	1620	2	US-09-195-021-2	Sequence 2, App	c 808	13	23.6	71	6	5439679-10	Patent No. 5439679
c 736	14	25.5	1773	4	US-08-943-731-215	Sequence 215, App	c 809	13	23.6	74	1	US-08-282-030-22	Sequence 22, Appl
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c 740	14	25.5	2002	2	US-08-747-121-1	Sequence 1, App	c 813	13	23.6	78	4	US-09-543-921-22	Sequence 22, Appl
c 741	14	25.5	2173	6	5168051-10	Sequence 10, App	c 814	13	23.6	122	1	US-08-282-030-54	Sequence 54, Appl
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c 748	14	25.5	2743	1	US-08-317-707-1	Sequence 1, App	c 821	13	23.6	145	4	US-09-351-348-6	Sequence 6, Appl
c 749	14	25.5	2813	4	US-09-689-255C-3	Sequence 3, App	c 822	13	23.6	146	4	US-09-450-072-5	Sequence 5, Appl
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c 754	14	25.5	3303	1	US-08-081-610-3	Sequence 3, App	c 827	13	23.6	282	2	US-08-440-725A-4	Sequence 4, Appl
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c 756	14	25.5	3611	1	US-08-445-640-1	Sequence 1, App	c 829	13	23.6	289	2	US-08-481-658B-63	Sequence 63, Appl
c 757	14	25.5	3611	3	US-08-170-558-1	Sequence 1, App	c 830	13	23.6	289	2	US-08-477-504A-63	Sequence 63, Appl

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C 833	13	23.6	289	3	US-08-787-739-63	Sequence 63, Appl	906	13	23.6	998	4	US-09-237-357-62	Sequence 62, Appl
C 834	13	23.6	289	3	US-08-487-077A-63	Sequence 63, Appl	C 907	13	23.6	1000	4	US-09-018-584A-33	Sequence 33, Appl
C 835	13	23.6	289	3	US-08-485-863A-63	Sequence 63, Appl	C 908	13	23.6	1001	4	US-09-641-638-131	Sequence 131, App
C 836	13	23.6	289	4	US-08-485-049D-63	Sequence 63, Appl	C 909	13	23.6	1001	4	US-09-641-638-131	Sequence 131, App
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C 847	13	23.6	334	5	PCT-US95-15991-7	Sequence 7, Appl	C 920	13	23.6	1227	1	US-08-910-991-3	Sequence 3, Appl
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C 849	13	23.6	338	4	US-09-543-921-27	Sequence 27, Appl	C 922	13	23.6	1267	4	US-08-390-000A-1	Sequence 1, Appl
C 850	13	23.6	341	4	US-09-404-879A-136	Sequence 136, App	C 923	13	23.6	1279	3	US-09-422-869-15	Sequence 15, Appl
C 851	13	23.6	440	2	US-08-967-101-105	Sequence 105, App	C 924	13	23.6	1298	3	US-08-985-950-5	Sequence 5, Appl
C 852	13	23.6	440	2	US-08-592-541-105	Sequence 105, App	C 925	13	23.6	1298	3	US-08-948-705-3	Sequence 3, Appl
C 853	13	23.6	440	3	US-09-124-698-105	Sequence 105, App	C 926	13	23.6	1301	4	US-08-804-166-7	Sequence 7, Appl
C 854	13	23.6	440	4	US-09-127-480-105	Sequence 105, App	C 927	13	23.6	1301	4	US-08-804-166-7	Sequence 7, Appl
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C 856	13	23.6	440	4	US-09-124-523-105	Sequence 105, App	C 929	13	23.6	1313	4	US-09-035-648-22	Sequence 22, Appl
C 857	13	23.6	461	4	US-09-404-879A-1	Sequence 1, Appl	C 930	13	23.6	1320	4	US-09-001-951-22	Sequence 22, Appl
C 858	13	23.6	461	4	US-09-404-879A-3	Sequence 3, Appl	C 931	13	23.6	1320	4	US-08-818-829-22	Sequence 22, Appl
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C 860	13	23.6	488	4	US-09-385-982-471	Sequence 47, Appl	C 933	13	23.6	1331	4	US-09-370-838-27	Sequence 27, Appl
C 861	13	23.6	503	4	US-08-936-165A-155	Sequence 155, App	C 934	13	23.6	1334	4	US-09-370-838-28	Sequence 28, Appl
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C 864	13	23.6	526	4	US-09-175-928-35	Sequence 35, Appl	C 937	13	23.6	1334	2	US-08-486-756A-44	Sequence 44, Appl
C 865	13	23.6	540	4	US-09-221-017B-1084	Sequence 1084, App	C 938	13	23.6	1334	2	US-08-485-862B-44	Sequence 44, Appl
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C 869	13	23.6	552	4	US-09-370-838-266	Sequence 35, Appl	C 942	13	23.6	1334	4	US-08-485-049D-44	Sequence 44, Appl
C 870	13	23.6	568	3	US-08-985-950-9	Sequence 9, Appl	C 943	13	23.6	1334	4	US-09-178-115-44	Sequence 44, Appl
C 871	13	23.6	573	4	US-09-328-111-89	Sequence 89, Appl	C 944	13	23.6	1336	4	US-09-177-776-44	Sequence 44, Appl
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C 877	13	23.6	603	5	PCT-US94-12873-5	Sequence 5, Appl	C 950	13	23.6	1461	1	US-08-403-634-1	Sequence 1, Appl
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C 881	13	23.6	633	4	US-09-277-720-1	Sequence 1, Appl	C 954	13	23.6	1600	2	US-08-487-113D-117	Sequence 117, App
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							C 977	13	23.6	1829	2	US-08-687-080-57	Sequence 57, Appl

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ALIGNMENTS

RESULT 1
US-09-375-318-38/c
; Sequence 38, Application US/09375318
; Patent No. 6468791
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; Schellenberg, Gerard D.
; Wasco, Wilma
; Levy-Lahad, Ephrat
; Bird, Thomas D.
; Galas, David J.
; TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
; ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BEERY LLP
; STREET: 701 Fifth Ave, Suite 6300
; City: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,318
; FILING DATE: 16-Aug-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Verna, James M.
; REGISTRATION NUMBER: 33,287
; REFERENCE/DOCKET NUMBER: 920010.571C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-375-318-38
Query Match 43.6%; Score 24; DB 4; Length 2387;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 TTCGAGATCAGCCTGGCCCAACATG 53
DB 2207 TTCGAGATCAGCCTGGCCCAACATG 2184
RESULT 2
US-09-078-294-6/c
; Sequence 6, Application US/09078294
; Patent No. 6265211
; GENERAL INFORMATION:
; APPLICANT: Choo, Kong-Hong Andy
; APPLICANT: Du Sart, Desiree
; APPLICANT: Cancilla, Michael R.
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
; FILE REFERENCE: Davies Col
; CURRENT APPLICATION NUMBER: US/09/078,294
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 18443
; TYPE: DNA
; ORGANISM: BAC-F2 contig 2
US-09-078-294-6
Query Match 41.8%; Score 23; DB 4; Length 18443;
Best Local Similarity 100.0%; Pred. No. 0.00098;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 TTCGAGATCAGCCTGGCCCAACAT 52
DB 10385 TTCGAGATCAGCCTGGCCCAACAT 10363
RESULT 3
US-09-078-294-4
; Sequence 4, Application US/09078294
; Patent No. 6265211
; GENERAL INFORMATION:
; APPLICANT: Choo, Kong-Hong Andy
; APPLICANT: Du Sart, Desiree
; APPLICANT: Cancilla, Michael R.
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
; FILE REFERENCE: Davies Col
; CURRENT APPLICATION NUMBER: US/09/078,294
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 80246
; TYPE: DNA
; ORGANISM: Nucleotide sequence of NC-contig
US-09-078-294-4
Query Match 41.8%; Score 23; DB 4; Length 80246;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 CACTTGAGGTCAGGAATTCGAGA 36
DB 3415 CACTTGAGGTCAGGAATTCGAGA 3437
RESULT 4
US-09-078-294-3
; Sequence 3, Application US/09078294
; Patent No. 6265211


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; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3

Query Match 41.8%; Score 23; DB 4; Length 112132;
Best Local Similarity 100.0%; Pred.No. 0.0009;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTGAGGTCAGGAATTGCAGA 36
Db 54719 CACTTGAGGTCAGGAATTGCAGA 54741

RESULT 7
US-09-318-448-11/c
; Sequence 11, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18596
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-11

Query Match 40.0%; Score 22; DB 4; Length 18596;
Best Local Similarity 100.0%; Pred.No. 0.0033;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GAGATCAGCCTGGCCCAACATGA 54
Db 14751 GAGATCAGCCTGGCCCAACATGA 14730

RESULT 8
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL
; FILE REFERENCE: 89.US2.CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6

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SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 10945..12946
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc feature
LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
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LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
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Query Match 40.0%; Score 22; DB 4; Length 81001;

Best Local Similarity 100.0%; Pred. No. 0.0031; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 32 CGAGATCAGCCTGGCCCAACATG 53

Db 58206 CGAGATCAGCCTGGCCCAACATG 58185

RESULT 9

US-09-110-116-2/c

; Sequence 2, Application US/09110116

; Patent No. 6013479
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: HUMAN ENR1-LIKE G PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: PF-0550 US
; CURRENT APPLICATION NUMBER: US/09/110,116
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3350
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3293)...(3293)
; OTHER INFORMATION: a or g or c or t/u, unknown, or other
; OTHER INFORMATION: 429905, EOSINOT03
US-09-110-116-2

Query Match 38.2%; Score 21; DB 3; Length 3350;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GAGATCAGCTGGCCCAACATG 53
|||||
DB 3066 GAGATCAGCTGGCCCAACATG 3046

RESULT 10

US-09-328-174A-1
; Sequence 1, Application US/09328174A
; Patent No. 6448003
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Kurth, Janice
; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
; TITLE OF INVENTION: (STP2)
; FILE REFERENCE: 4389-6 (formerly SEQ-16P)
; CURRENT APPLICATION NUMBER: US/09/328,174A
; CURRENT FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 09/328,174
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8396
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-328-174A-1

Query Match 38.2%; Score 21; DB 4; Length 8396;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GAGATCAGCTGGCCCAACATG 53
|||||
DB 4657 GAGATCAGCTGGCCCAACATG 4677

RESULT 11

US-09-167-681-37
; Sequence 37, Application US/09167681A
; Patent No. 6265561
; GENERAL INFORMATION:
; APPLICANT: Weinsilboum, M.D., Richard M.
; APPLICANT: Raftogiannis, Rebecca B.
; APPLICANT: Wood, Thomas C.
; APPLICANT: Otterness, Diane M.
; TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS

; FILE REFERENCE: 07039/118001
; CURRENT APPLICATION NUMBER: US/09/167,681A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 8397
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3730)...(3879)
; NAME/KEY: CDS
; LOCATION: (3987)...(4112)
; NAME/KEY: CDS
; LOCATION: (4198)...(4293)
; NAME/KEY: CDS
; LOCATION: (6088)...(6213)
; NAME/KEY: CDS
; LOCATION: (6309)...(6404)
; NAME/KEY: CDS
; LOCATION: (7214)...(7393)
; NAME/KEY: CDS
; LOCATION: (7516)...(7629)
US-09-167-681-37

Query Match 38.2%; Score 21; DB 4; Length 8409;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GAGATCAGCTGGCCCAACATG 53
|||||
DB 4658 GAGATCAGCTGGCCCAACATG 4678

RESULT 12

US-09-851-896-3
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match 38.2%; Score 21; DB 4; Length 70000;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 AGATCAGCTGGCCCAACATGA 54
|||||
DB 33721 AGATCAGCTGGCCCAACATGA 33741

RESULT 13

US-09-750-580-1
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara

APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US2.CIP
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 10946..12946
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc feature
LOCATION: 15969..17969
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-41-250.probe
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe

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; NAME/KEY: misc binding
; LOCATION: 42206..42230
; OTHER INFORMATION: 20-841-149.probe
; NAME/KEY: misc binding
; LOCATION: 45430..45454
; OTHER INFORMATION: 20-842-115.probe
; NAME/KEY: misc binding
; LOCATION: 77046..77070
; OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match      38.2%; Score 21; DB 4; Length 81001;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      33 GAGATCAGCCTGGCCCAACATG 53
      |||||
Db      7636 GAGATCAGCCTGGCCCAACATG 7656

RESULT 14
US-09-797-906-3/c
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match      38.2%; Score 21; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      33 GAGATCAGCCTGGCCCAACATG 53
      |||||
Db      7797 GAGATCAGCCTGGCCCAACATG 7777

RESULT 15
US-09-798-096-10
; Sequence 10, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

Query Match      38.2%; Score 21; DB 4; Length 99500;
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Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      33 GAGATCAGCCTGGCCCAACATG 53
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Db      82529 GAGATCAGCCTGGCCCAACATG 82549

Search completed: June 17, 2003, 06:28:01
Job time : 31.153 secs
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 5.81445 Seconds
(without alignments)

13697.491 Million cell updates/sec

Title: US-09-513-888c-1_COPY_4365_4419

Perfect score: 55

Sequence: 1 gaggcagcagcagcacttga.....atcagctggccaacatgag 55

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Searched: 1029858 seqs, 724030393 residues

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Minimum DB seq length: 0

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Database : Published Applications NA.*

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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
	1	27	49.1	490	9	US-09-918-995-22754
	2	25	45.5	218	10	US-09-867-701-795
	3	25	45.5	506	9	US-09-918-995-23432
	4	25	45.5	1078	10	US-09-748-107-3
	5	25	45.5	14417	9	US-09-860-670-251
	6	25	45.5	14426	9	US-09-860-670-249
	7	24	43.6	98	9	US-10-074-095-818
	8	24	43.6	98	10	US-09-764-860-818
	9	24	43.6	98	10	US-09-764-860-819
	10	24	43.6	379	9	US-09-764-891-5685
	11	24	43.6	392	9	US-09-918-995-3449
	12	24	43.6	433	10	US-09-867-701-7253
	13	24	43.6	433	10	US-09-867-701-7253
	14	24	43.6	498	9	US-09-918-995-26320
	15	24	43.6	1160	9	US-09-764-891-5684
	16	24	43.6	1278	10	US-09-822-849A-168
	17	24	43.6	1592	10	US-09-764-877-3805
	18	24	43.6	2756	10	US-09-764-853-898
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C 95	22	40.0	20210	9	US-10-125-540-598	Sequence 598, App	C 168	21	38.2	26928	9	US-10-020-141-7	Sequence 7, Appli
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C 138	21	38.2	2455	10	US-09-759-143-881	Sequence 881, App	C 211	20	36.4	491	9	US-09-764-891-7969	Sequence 7969, Ap
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C 272	19	34.5	102	10	US-09-764-887-540	Sequence 540, App	C 345	19	34.5	2120	9	US-10-131-824A-73	Sequence 73, Appl
C 273	19	34.5	216	10	US-09-764-877-3514	Sequence 3514, Ap	C 346	19	34.5	2120	9	US-10-131-830A-73	Sequence 73, Appl
C 274	19	34.5	320	10	US-09-867-701-9832	Sequence 9832, Ap	C 347	19	34.5	2120	9	US-10-137-872A-73	Sequence 73, Appl
C 275	19	34.5	353	10	US-09-867-701-3577	Sequence 3577, Ap	C 348	19	34.5	2120	9	US-10-147-517-73	Sequence 73, Appl
C 276	19	34.5	370	9	US-09-918-995-37699	Sequence 37699, A	C 349	19	34.5	2120	9	US-10-147-515-73	Sequence 73, Appl
C 277	19	34.5	390	9	US-09-764-891-2014	Sequence 2014, Ap	C 350	19	34.5	2120	9	US-10-140-860-73	Sequence 73, Appl
C 278	19	34.5	401	10	US-09-918-995-35883	Sequence 35883, A	C 351	19	34.5	2120	9	US-10-142-417-73	Sequence 73, Appl
C 279	19	34.5	401	10	US-09-967-701-10043	Sequence 10043, A	C 352	19	34.5	2120	9	US-10-147-500-73	Sequence 73, Appl
C 280	19	34.5	410	10	US-09-764-877-3416	Sequence 3416, Ap	C 353	19	34.5	2120	9	US-10-147-502-73	Sequence 73, Appl
C 281	19	34.5	411	9	US-09-986-480-104	Sequence 104, App	C 354	19	34.5	2120	9	US-10-147-515-73	Sequence 73, Appl
C 282	19	34.5	418	9	US-09-918-995-14847	Sequence 14847, A	C 355	19	34.5	2120	9	US-10-147-517-73	Sequence 73, Appl
C 283	19	34.5	418	10	US-09-867-701-3670	Sequence 3670, Ap	C 356	19	34.5	2120	9	US-10-147-519-73	Sequence 73, Appl
C 284	19	34.5	420	10	US-09-764-877-689	Sequence 689, App	C 357	19	34.5	2120	9	US-10-147-526-73	Sequence 73, Appl
C 285	19	34.5	437	10	US-09-967-701-4628	Sequence 4628, Ap	C 358	19	34.5	2120	9	US-10-152-395-73	Sequence 73, Appl
C 286	19	34.5	457	9	US-09-918-995-16149	Sequence 16149, A	C 359	19	34.5	2120	9	US-10-157-782-73	Sequence 73, Appl
C 287	19	34.5	534	9	US-09-918-995-30665	Sequence 30665, A	C 360	19	34.5	2120	9	US-10-121-040-73	Sequence 73, Appl
C 288	19	34.5	612	9	US-09-764-872-70	Sequence 70, Appl	C 361	19	34.5	2120	9	US-10-121-056-73	Sequence 73, Appl
C 289	19	34.5	1027	9	US-09-764-872-617	Sequence 617, App	C 362	19	34.5	2120	9	US-10-121-061-73	Sequence 73, Appl
C 290	19	34.5	1027	9	US-09-764-872-617	Sequence 617, App	C 363	19	34.5	2120	9	US-10-123-235-73	Sequence 73, Appl
C 291	19	34.5	1383	9	US-09-764-891-8325	Sequence 8325, Ap	C 364	19	34.5	2120	9	US-10-124-818-73	Sequence 73, Appl
C 292	19	34.5	2104	9	US-09-953-133-1	Sequence 1, Appli	C 365	19	34.5	2120	9	US-10-125-926A-73	Sequence 73, Appl
C 293	19	34.5	2120	9	US-10-028-072-73	Sequence 73, Appl	C 366	19	34.5	2120	9	US-10-125-930A-73	Sequence 73, Appl
C 294	19	34.5	2120	9	US-10-121-049-73	Sequence 73, Appl	C 367	19	34.5	2120	9	US-10-127-831A-73	Sequence 73, Appl
C 295	19	34.5	2120	9	US-10-123-904-73	Sequence 73, Appl	C 368	19	34.5	2120	9	US-10-127-837A-73	Sequence 73, Appl
C 296	19	34.5	2120	9	US-10-140-470-73	Sequence 73, Appl	C 369	19	34.5	2120	9	US-10-127-838B-73	Sequence 73, Appl
C 297	19	34.5	2120	9	US-10-140-470-73	Sequence 73, Appl	C 370	19	34.5	2120	9	US-10-127-842A-73	Sequence 73, Appl
C 298	19	34.5	2120	9	US-10-175-746-73	Sequence 73, Appl	C 371	19	34.5	2120	9	US-10-127-843A-73	Sequence 73, Appl
C 299	19	34.5	2120	9	US-10-176-918-73	Sequence 73, Appl	C 372	19	34.5	2120	9	US-10-127-843A-73	Sequence 73, Appl
C 300	19	34.5	2120	9	US-10-176-921-73	Sequence 73, Appl	C 373	19	34.5	2120	9	US-10-127-845A-73	Sequence 73, Appl
C 301	19	34.5	2120	9	US-10-137-865-73	Sequence 73, Appl	C 374	19	34.5	2120	9	US-10-127-846A-73	Sequence 73, Appl
C 302	19	34.5	2120	9	US-10-140-474-73	Sequence 73, Appl	C 375	19	34.5	2120	9	US-10-127-848A-73	Sequence 73, Appl
C 303	19	34.5	2120	9	US-10-142-431-73	Sequence 73, Appl	C 376	19	34.5	2120	9	US-10-127-849A-73	Sequence 73, Appl
C 304	19	34.5	2120	9	US-10-143-114-73	Sequence 73, Appl	C 377	19	34.5	2120	9	US-10-127-850A-73	Sequence 73, Appl
C 305	19	34.5	2120	9	US-10-140-002-73	Sequence 73, Appl	C 378	19	34.5	2120	9	US-10-127-851A-73	Sequence 73, Appl
C 306	19	34.5	2120	9	US-10-142-419-73	Sequence 73, Appl	C 379	19	34.5	2120	9	US-10-128-684A-73	Sequence 73, Appl
C 307	19	34.5	2120	9	US-10-123-362-73	Sequence 73, Appl	C 380	19	34.5	2120	9	US-10-128-686A-73	Sequence 73, Appl
C 308	19	34.5	2120	9	US-10-142-423-73	Sequence 73, Appl	C 381	19	34.5	2120	9	US-10-128-690A-73	Sequence 73, Appl
C 309	19	34.5	2120	9	US-10-121-050-73	Sequence 73, Appl	C 382	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 310	19	34.5	2120	9	US-10-141-755-73	Sequence 73, Appl	C 383	19	34.5	2120	9	US-10-131-819A-73	Sequence 73, Appl
C 311	19	34.5	2120	9	US-10-143-012-73	Sequence 73, Appl	C 384	19	34.5	2120	9	US-10-131-829A-73	Sequence 73, Appl

C 385	19	34.5	2120	9	US-10-131-836A-73	Sequence 73, Appl	C 458	19	34.5	13485	10	US-09-764-870-548	Sequence 548, App
C 386	19	34.5	2120	9	US-10-137-868-73	Sequence 73, Appl	C 459	19	34.5	15295	10	US-09-764-877-3404	Sequence 3404, Ap
C 387	19	34.5	2120	9	US-10-146-729-73	Sequence 73, Appl	C 460	19	34.5	17240	10	US-09-764-877-3336	Sequence 3336, Ap
C 388	19	34.5	2120	9	US-10-146-791-73	Sequence 73, Appl	C 461	19	34.5	17245	10	US-09-764-877-3390	Sequence 3390, Ap
C 389	19	34.5	2120	9	US-10-147-484-73	Sequence 73, Appl	C 462	19	34.5	18318	10	US-09-764-877-3306	Sequence 3306, Ap
C 390	19	34.5	2120	9	US-10-147-482-73	Sequence 73, Appl	C 463	19	34.5	19315	9	US-10-091-438-245	Sequence 245, App
C 391	19	34.5	2120	9	US-10-147-492-73	Sequence 73, Appl	C 464	19	34.5	19315	9	US-09-764-872-816	Sequence 816, App
C 392	19	34.5	2120	9	US-10-147-508-73	Sequence 73, Appl	C 465	19	34.5	21358	9	US-09-764-872-816	Sequence 816, App
C 393	19	34.5	2120	9	US-10-147-512-73	Sequence 73, Appl	C 466	19	34.5	21358	9	US-09-764-891-9107	Sequence 9107, Ap
C 394	19	34.5	2120	9	US-10-158-782-73	Sequence 73, Appl	C 467	19	34.5	21470	9	US-10-092-154-1157	Sequence 1157, Ap
C 395	19	34.5	2120	9	US-10-175-735-73	Sequence 73, Appl	C 468	19	34.5	21470	10	US-09-764-847-1157	Sequence 1157, Ap
C 396	19	34.5	2120	9	US-10-123-905-73	Sequence 73, Appl	C 469	19	34.5	21676	9	US-09-764-872-815	Sequence 815, App
C 397	19	34.5	2120	9	US-10-123-907-73	Sequence 73, Appl	C 470	19	34.5	21676	9	US-09-764-891-9106	Sequence 9106, Ap
C 398	19	34.5	2120	9	US-10-124-815-73	Sequence 73, Appl	C 471	19	34.5	21913	9	US-09-764-891-6065	Sequence 6065, Ap
C 399	19	34.5	2120	9	US-10-125-921A-73	Sequence 73, Appl	C 472	19	34.5	21913	9	US-09-764-891-6066	Sequence 6066, Ap
C 400	19	34.5	2120	9	US-10-125-928A-73	Sequence 73, Appl	C 473	19	34.5	21913	9	US-09-764-891-6067	Sequence 6067, Ap
C 401	19	34.5	2120	9	US-10-127-821A-73	Sequence 73, Appl	C 474	19	34.5	23106	9	US-09-863-049A-1	Sequence 1, Appl1
C 402	19	34.5	2120	9	US-10-127-822A-73	Sequence 73, Appl	C 475	19	34.5	23106	9	US-10-074-095-990	Sequence 990, App
C 403	19	34.5	2120	9	US-10-127-824A-73	Sequence 73, Appl	C 476	19	34.5	23580	10	US-09-764-860-990	Sequence 264, App
C 404	19	34.5	2120	9	US-10-127-826A-73	Sequence 73, Appl	C 477	19	34.5	23603	9	US-09-860-670-258	Sequence 258, App
C 405	19	34.5	2120	9	US-10-127-827A-73	Sequence 73, Appl	C 478	19	34.5	23603	9	US-09-860-670-263	Sequence 263, App
C 406	19	34.5	2120	9	US-10-127-830A-73	Sequence 73, Appl	C 479	19	34.5	24218	9	US-10-073-961-602	Sequence 602, App
C 407	19	34.5	2120	9	US-10-127-832A-73	Sequence 73, Appl	C 480	19	34.5	24768	10	US-09-764-887-602	Sequence 602, App
C 408	19	34.5	2120	9	US-10-127-833A-73	Sequence 73, Appl	C 481	19	34.5	27062	9	US-09-764-891-8034	Sequence 8034, Ap
C 409	19	34.5	2120	9	US-10-127-834A-73	Sequence 73, Appl	C 482	19	34.5	32134	9	US-09-764-891-6303	Sequence 6303, Ap
C 410	19	34.5	2120	9	US-10-127-836A-73	Sequence 73, Appl	C 483	19	34.5	32148	9	US-09-764-891-6906	Sequence 6906, Ap
C 411	19	34.5	2120	9	US-10-127-841A-73	Sequence 73, Appl	C 484	19	34.5	32184	9	US-09-764-891-8538	Sequence 8538, Ap
C 412	19	34.5	2120	9	US-10-127-844A-73	Sequence 73, Appl	C 485	19	34.5	32191	9	US-09-764-891-6304	Sequence 6304, Ap
C 413	19	34.5	2120	9	US-10-128-687A-73	Sequence 73, Appl	C 486	19	34.5	32204	9	US-09-764-891-6454	Sequence 6454, Ap
C 414	19	34.5	2120	9	US-10-128-688A-73	Sequence 73, Appl	C 487	19	34.5	32204	9	US-09-764-891-8537	Sequence 8537, Ap
C 415	19	34.5	2120	9	US-10-128-689A-73	Sequence 73, Appl	C 488	19	34.5	32367	9	US-10-158-160A-14	Sequence 14, Appl
C 416	19	34.5	2120	9	US-10-128-694A-73	Sequence 73, Appl	C 489	19	34.5	36741	10	US-09-782-378A-12	Sequence 12, Appl
C 417	19	34.5	2120	9	US-10-131-825A-73	Sequence 73, Appl	C 490	19	34.5	53332	9	US-10-424-562-3	Sequence 3, Appl1
C 418	19	34.5	2120	9	US-10-230-417-73	Sequence 73, Appl	C 491	19	34.5	53332	10	US-09-801-861-3	Sequence 3, Appl1
C 419	19	34.5	2120	9	US-10-121-051-73	Sequence 73, Appl	C 492	19	34.5	60153	9	US-10-222-334-7	Sequence 7, Appl1
C 420	19	34.5	2120	9	US-10-131-815A-73	Sequence 73, Appl	C 493	19	34.5	62804	12	US-10-096-960-3	Sequence 3, Appl1
C 421	19	34.5	2120	9	US-10-131-817A-73	Sequence 73, Appl	C 494	19	34.5	62944	10	US-09-954-456-2257	Sequence 2257, Ap
C 422	19	34.5	2120	9	US-10-131-821A-73	Sequence 73, Appl	C 495	19	34.5	73308	10	US-09-954-456-2276	Sequence 2276, Ap
C 423	19	34.5	2120	9	US-10-131-822A-73	Sequence 73, Appl	C 496	19	34.5	98829	9	US-10-017-724-3	Sequence 3, Appl1
C 424	19	34.5	2120	9	US-10-131-828A-73	Sequence 73, Appl	C 497	19	34.5	147309	10	US-09-742-312-3	Sequence 3, Appl1
C 425	19	34.5	2120	9	US-10-131-835A-73	Sequence 73, Appl	C 498	19	34.5	254366	10	US-09-967-768A-314	Sequence 314, App
C 426	19	34.5	2120	9	US-10-137-864A-73	Sequence 73, Appl	C 499	19	34.5	326014	10	US-09-932-871-3	Sequence 3, Appl1
C 427	19	34.5	2120	9	US-10-137-869A-73	Sequence 73, Appl	C 500	19	34.5	326014	10	US-09-731-231A-3	Sequence 3, Appl1
C 428	19	34.5	2120	9	US-10-147-523-73	Sequence 73, Appl	C 501	19	34.5	465237	10	US-09-933-267A-1	Sequence 1, Appl1
C 429	19	34.5	2120	9	US-10-158-785-73	Sequence 73, Appl	C 502	19	34.5	1503841	9	US-09-946-807-1	Sequence 1, Appl1
C 430	19	34.5	2120	9	US-10-123-912-73	Sequence 73, Appl	C 503	19	34.5	1503841	10	US-09-795-668-1	Sequence 1, Appl1
C 431	19	34.5	2120	9	US-10-123-912-73	Sequence 73, Appl	C 504	19	34.5	1503841	10	US-09-795-668-1	Sequence 1, Appl1
C 432	19	34.5	2120	9	US-10-192-007-73	Sequence 73, Appl	C 505	18	32.7	129	9	US-09-764-872-731	Sequence 557, App
C 433	19	34.5	2120	9	US-10-194-359-73	Sequence 73, Appl	C 506	18	32.7	129	9	US-10-073-961-557	Sequence 557, App
C 434	19	34.5	2594	10	US-09-822-849A-338	Sequence 338, App	C 507	18	32.7	129	10	US-09-764-887-557	Sequence 557, App
C 435	19	34.5	2907	10	US-09-954-456-318	Sequence 318, App	C 508	18	32.7	254	10	US-09-867-701-1718	Sequence 1718, Ap
C 436	19	34.5	2907	10	US-09-954-456-823	Sequence 823, App	C 509	18	32.7	254	10	US-09-867-701-9327	Sequence 9327, Ap
C 437	19	34.5	2907	10	US-09-954-456-1226	Sequence 1226, Ap	C 510	18	32.7	334	10	US-09-867-701-6897	Sequence 6897, Ap
C 438	19	34.5	2907	10	US-09-880-107-2318	Sequence 2318, Ap	C 511	18	32.7	334	10	US-09-867-701-416	Sequence 416, App
C 439	19	34.5	3116	9	US-09-764-872-585	Sequence 585, App	C 512	18	32.7	375	9	US-09-803-719-1151	Sequence 1151, Ap
C 440	19	34.5	3336	9	US-10-118-783-1	Sequence 1, Appl	C 513	18	32.7	385	10	US-09-867-701-236	Sequence 236, App
C 441	19	34.5	3336	9	US-10-118-783-2	Sequence 2, Appl	C 514	18	32.7	410	10	US-09-867-701-444	Sequence 444, App
C 442	19	34.5	5080	9	US-10-092-154-1197	Sequence 1197, Ap	C 515	18	32.7	422	10	US-09-867-701-7383	Sequence 7383, Ap
C 443	19	34.5	5080	9	US-10-092-154-1198	Sequence 1198, Ap	C 516	18	32.7	430	9	US-09-918-995-16743	Sequence 16743, A
C 444	19	34.5	5080	10	US-09-764-847-1197	Sequence 1197, Ap	C 517	18	32.7	433	9	US-09-918-995-37132	Sequence 37132, A
C 445	19	34.5	5080	10	US-09-764-847-1198	Sequence 1198, Ap	C 518	18	32.7	434	9	US-09-918-995-28768	Sequence 28768, A
C 446	19	34.5	5797	9	US-09-764-891-6093	Sequence 6093, Ap	C 519	18	32.7	440	10	US-09-918-995-4317	Sequence 4317, Ap
C 447	19	34.5	5987	9	US-10-118-783-3	Sequence 3, Appl	C 520	18	32.7	443	10	US-09-867-701-1719	Sequence 1719, Ap
C 448	19	34.5	6990	9	US-10-118-783-23	Sequence 23, Appl	C 521	18	32.7	447	10	US-09-867-701-430	Sequence 430, App
C 449	19	34.5	7133	9	US-10-198-846-13766	Sequence 13766, A	C 522	18	32.7	455	9	US-09-918-995-9772	Sequence 9772, Ap
C 450	19	34.5	7389	9	US-09-764-868-1448	Sequence 1448, A	C 523	18	32.7	458	9	US-09-918-995-11365	Sequence 11365, A
C 451	19	34.5	10126	10	US-09-764-877-2194	Sequence 2194, Ap	C 524	18	32.7	467	9	US-09-918-995-26473	Sequence 26473, A
C 452	19	34.5	10377	9	US-09-764-891-6453	Sequence 6453, Ap	C 525	18	32.7	484	9	US-09-918-995-30630	Sequence 30630, A
C 453	19	34.5	12754	9	US-09-984-827-5	Sequence 5, Appl	C 526	18	32.7	486	9	US-10-158-846-2363	Sequence 2363, Ap
C 454	19	34.5	13271	10	US-09-764-877-3923	Sequence 3923, Ap	C 527	18	32.7	489	10	US-09-783-590-11928	Sequence 11928, A
C 455	19	34.5	13223	9	US-09-764-891-5777	Sequence 5777, Ap	C 528	18	32.7	502	9	US-09-918-995-20295	Sequence 20295, A
C 456	19	34.5	13223	9	US-10-074-045-67	Sequence 67, Appl	C 529	18	32.7	505	9	US-09-918-995-22293	Sequence 22293, A
C 457	19	34.5	13485	9	US-10-125-540-548	Sequence 548, App	C 530	18	32.7	506	9	US-09-918-995-3126	Sequence 3126, Ap

c 531	18	32.7	528	9	US-09-918-395-32424	Sequence 32424, A	604	18	32.7	57130	10	US-09-835-081-3	Sequence 3, Appli
c 532	18	32.7	565	9	US-10-198-846-11213	Sequence 11213, A	c 605	18	32.7	75270	9	US-09-790-852-1	Sequence 1, Appli
c 533	18	32.7	606	9	US-09-871-161-217	Sequence 217, App	c 606	18	32.7	83450	9	US-09-811-469-3	Sequence 3, Appli
c 534	18	32.7	622	9	US-09-871-161-312	Sequence 312, App	c 607	18	32.7	113604	9	US-10-227-195A-1	Sequence 1, Appli
c 535	18	32.7	646	9	US-10-198-846-8147	Sequence 8147, App	c 608	18	32.7	113604	9	US-10-227-195A-2	Sequence 2, Appli
c 536	18	32.7	781	9	US-10-062-831-36	Sequence 36, Appl	c 609	18	32.7	139257	9	US-09-820-671-11	Sequence 11, Appl
c 537	18	32.7	890	9	US-10-198-846-499	Sequence 499, App	c 610	18	32.7	174566	9	US-10-020-141-1	Sequence 1, Appl
c 538	18	32.7	950	10	US-09-954-456-1228	Sequence 1228, App	c 611	18	32.7	176373	9	US-10-095-407-17	Sequence 17, Appl
c 539	18	32.7	950	10	US-09-954-456-12107	Sequence 2107, App	c 612	18	32.7	198285	10	US-09-880-107-3814	Sequence 3814, App
c 540	18	32.7	1013	9	US-10-198-846-13012	Sequence 13012, A	c 613	18	32.7	203654	10	US-09-820-905-3	Sequence 3, Appli
c 541	18	32.7	1070	9	US-10-198-846-12458	Sequence 12458, A	c 614	18	32.7	368004	10	US-09-949-654-3	Sequence 3, Appli
c 542	18	32.7	1086	9	US-10-091-504-2140	Sequence 2140, App	c 615	18	32.7	684973	10	US-09-263-959-1	Sequence 1, Appli
c 543	18	32.7	1086	10	US-09-764-869-21140	Sequence 21140, App	c 616	17	30.9	96	9	US-10-060-036-3542	Sequence 3542, App
c 544	18	32.7	1122	9	US-09-764-872-923	Sequence 923, App	c 617	17	30.9	98	9	US-09-764-891-8151	Sequence 8151, App
c 545	18	32.7	1432	9	US-10-125-540-164	Sequence 164, App	c 618	17	30.9	129	9	US-09-764-891-7661	Sequence 7661, App
c 546	18	32.7	1432	10	US-09-764-870-164	Sequence 164, App	c 619	17	30.9	262	9	US-10-040-739-857	Sequence 857, App
c 547	18	32.7	1808	9	US-09-989-920-46	Sequence 46, Appl	c 620	17	30.9	279	9	US-10-198-846-13352	Sequence 13352, A
c 548	18	32.7	2024	9	US-10-218-574-1	Sequence 1, Appli	c 621	17	30.9	332	10	US-09-867-701-8396	Sequence 8396, App
c 549	18	32.7	2024	10	US-09-867-569-1	Sequence 1, Appli	c 622	17	30.9	333	10	US-09-867-701-4810	Sequence 4810, App
c 550	18	32.7	2171	9	US-10-074-475-31	Sequence 31, Appl	c 623	17	30.9	338	10	US-09-867-701-5553	Sequence 5553, App
c 551	18	32.7	2446	9	US-09-764-868-1270	Sequence 1270, App	c 624	17	30.9	344	9	US-09-803-719-1905	Sequence 1905, App
c 552	18	32.7	2446	9	US-09-764-868-1407	Sequence 1407, App	c 625	17	30.9	365	10	US-09-867-701-8179	Sequence 8179, App
c 553	18	32.7	2525	9	US-09-984-271-20	Sequence 20, Appl	c 626	17	30.9	370	10	US-09-867-701-6365	Sequence 6365, App
c 554	18	32.7	3243	9	US-10-092-154-1176	Sequence 1176, App	c 627	17	30.9	377	9	US-09-918-995-30035	Sequence 30035, A
c 555	18	32.7	3243	10	US-09-764-847-1176	Sequence 1176, App	c 628	17	30.9	386	9	US-09-954-531-1316	Sequence 1316, A
c 556	18	32.7	3328	9	US-09-764-891-7823	Sequence 7823, App	c 629	17	30.9	392	9	US-09-918-995-5085	Sequence 5085, App
c 557	18	32.7	4160	9	US-09-764-868-1269	Sequence 1269, App	c 630	17	30.9	395	9	US-09-918-995-35472	Sequence 35472, A
c 558	18	32.7	4160	9	US-09-764-868-1406	Sequence 1406, App	c 631	17	30.9	397	10	US-09-867-701-8024	Sequence 8024, App
c 559	18	32.7	4185	9	US-09-764-868-1271	Sequence 1271, App	c 632	17	30.9	399	10	US-09-867-701-9758	Sequence 9758, App
c 560	18	32.7	4185	9	US-09-764-868-1408	Sequence 1408, App	c 633	17	30.9	402	9	US-09-918-995-17309	Sequence 17309, A
c 561	18	32.7	5238	10	US-09-764-871-2036	Sequence 2036, App	c 634	17	30.9	403	10	US-09-867-701-8405	Sequence 8405, App
c 562	18	32.7	5629	10	US-10-092-154-1162	Sequence 1162, App	c 635	17	30.9	407	10	US-09-867-701-10646	Sequence 10646, A
c 563	18	32.7	5629	9	US-09-764-847-1162	Sequence 1162, App	c 636	17	30.9	414	9	US-09-867-701-642	Sequence 642, App
c 564	18	32.7	5876	9	US-09-764-891-8264	Sequence 8264, App	c 637	17	30.9	416	9	US-09-918-995-37267	Sequence 37267, A
c 565	18	32.7	6265	9	US-10-092-154-1161	Sequence 1161, App	c 638	17	30.9	431	9	US-09-918-995-17799	Sequence 17799, A
c 566	18	32.7	6265	10	US-09-764-847-1161	Sequence 1161, App	c 639	17	30.9	436	9	US-09-918-995-35954	Sequence 35954, A
c 567	18	32.7	6892	9	US-10-091-504-1720	Sequence 1720, App	c 640	17	30.9	437	10	US-09-867-701-10212	Sequence 10212, A
c 568	18	32.7	6892	10	US-09-764-869-1720	Sequence 1720, App	c 641	17	30.9	444	10	US-09-867-701-6812	Sequence 6812, App
c 569	18	32.7	7733	9	US-09-860-670-159	Sequence 159, App	c 642	17	30.9	453	9	US-09-918-995-8886	Sequence 8886, App
c 570	18	32.7	8429	10	US-09-738-885-3	Sequence 3, Appli	c 643	17	30.9	458	9	US-09-918-995-10753	Sequence 10753, A
c 571	18	32.7	8807	9	US-10-091-504-1415	Sequence 1415, App	c 644	17	30.9	458	9	US-09-918-995-15908	Sequence 15908, A
c 572	18	32.7	8807	10	US-09-764-869-1415	Sequence 1415, App	c 645	17	30.9	461	9	US-09-918-995-16135	Sequence 16135, A
c 573	18	32.7	8879	9	US-10-092-154-1402	Sequence 1402, App	c 646	17	30.9	468	9	US-09-918-995-32510	Sequence 32510, A
c 574	18	32.7	8879	10	US-09-764-847-1402	Sequence 1402, App	c 647	17	30.9	470	9	US-09-918-995-33567	Sequence 33567, A
c 575	18	32.7	10236	9	US-10-091-438-242	Sequence 242, App	c 648	17	30.9	470	9	US-10-198-846-11811	Sequence 11811, A
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c 577	18	32.7	10236	10	US-09-764-853-878	Sequence 878, App	c 650	17	30.9	476	9	US-10-198-846-12072	Sequence 12072, A
c 578	18	32.7	10482	9	US-09-790-852-10	Sequence 10, Appl	c 651	17	30.9	477	10	US-09-867-701-6870	Sequence 6870, App
c 579	18	32.7	11185	9	US-10-074-095-1096	Sequence 1096, App	c 652	17	30.9	480	9	US-09-918-995-12113	Sequence 12113, A
c 580	18	32.7	11185	10	US-09-764-860-1096	Sequence 1096, App	c 653	17	30.9	493	9	US-09-918-995-31750	Sequence 31750, A
c 581	18	32.7	11221	10	US-09-764-864-1773	Sequence 1773, App	c 654	17	30.9	519	9	US-10-060-036-3578	Sequence 3578, App
c 582	18	32.7	11627	9	US-09-764-891-10051	Sequence 10051, A	c 655	17	30.9	537	10	US-09-867-701-5683	Sequence 5683, App
c 583	18	32.7	11960	9	US-09-764-891-8501	Sequence 8501, App	c 656	17	30.9	601	10	US-09-820-003A-38	Sequence 38, Appl
c 584	18	32.7	11991	9	US-09-764-891-9893	Sequence 9893, App	c 657	17	30.9	601	10	US-09-820-003A-30	Sequence 30, Appl
c 585	18	32.7	11991	10	US-09-764-877-2942	Sequence 2942, App	c 658	17	30.9	618	9	US-09-871-161-1	Sequence 1, Appli
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c 587	18	32.7	13873	9	US-09-764-868-1282	Sequence 1282, App	c 660	17	30.9	780	9	US-10-198-846-4320	Sequence 4320, App
c 588	18	32.7	15054	9	US-10-091-572-577	Sequence 577, App	c 661	17	30.9	863	9	US-10-198-846-3448	Sequence 3448, App
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c 590	18	32.7	16491	9	US-09-764-891-5505	Sequence 5505, App	c 663	17	30.9	908	9	US-10-198-846-5950	Sequence 5950, App
c 591	18	32.7	19429	9	US-09-764-891-8911	Sequence 8911, App	c 664	17	30.9	912	9	US-10-198-846-9015	Sequence 9015, App
c 592	18	32.7	20300	10	US-09-764-891-8909	Sequence 8909, App	c 665	17	30.9	952	9	US-09-974-879-116	Sequence 116, App
c 593	18	32.7	21721	10	US-09-764-853-861	Sequence 861, App	c 666	17	30.9	952	9	US-09-305-736-117	Sequence 117, App
c 594	18	32.7	22140	9	US-09-764-891-8912	Sequence 8912, App	c 667	17	30.9	981	9	US-09-822-846-282	Sequence 282, App
c 595	18	32.7	22141	9	US-09-764-891-8910	Sequence 8910, App	c 668	17	30.9	985	9	US-10-062-548-54	Sequence 54, Appl
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c 597	18	32.7	28588	9	US-10-073-961-399	Sequence 399, App	c 670	17	30.9	1086	10	US-09-880-192-40	Sequence 40, Appl
c 598	18	32.7	28588	10	US-09-764-887-399	Sequence 399, App	c 671	17	30.9	1160	8	US-08-927-939-78	Sequence 78, Appl
c 599	18	32.7	38374	10	US-09-880-107-3463	Sequence 3463, App	c 672	17	30.9	1160	9	US-09-954-531-146	Sequence 146, App
c 600	18	32.7	41907	10	US-09-967-013-5	Sequence 5, Appli	c 673	17	30.9	1220	9	US-09-983-802-54	Sequence 54, Appl
c 601	18	32.7	48841	9	US-09-844-653-32	Sequence 32, Appl	c 674	17	30.9	1334	10	US-09-789-561-30	Sequence 30, Appl
c 602	18	32.7	50000	9	US-10-152-724A-20	Sequence 20, Appl	c 675	17	30.9	1373	10	US-09-263-959-285	Sequence 285, App
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678	17	30.9	1603	10	US-09-834-975-1033	Sequence 1033, Ap	751	17	30.9	9566	10	US-09-764-864-1768	Sequence 1768, Ap
c 679	17	30.9	1745	9	US-09-764-891-10218	Sequence 10218, A	752	17	30.9	9566	10	US-09-764-877-3486	Sequence 3486, Ap
c 680	17	30.9	1811	9	US-09-822-830A-10	Sequence 10, Appl	753	17	30.9	9669	9	US-10-091-504-2072	Sequence 2072, Ap
c 681	17	30.9	1811	9	US-09-822-846-283	Sequence 283, App	754	17	30.9	9669	9	US-09-764-869-2072	Sequence 2072, Ap
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c 683	17	30.9	1884	10	US-09-764-864-80	Sequence 80, Appl	756	17	30.9	9883	9	US-10-016-157A-71	Sequence 71, Appl
c 684	17	30.9	1965	10	US-09-822-849A-118	Sequence 118, App	757	17	30.9	9969	9	US-09-764-891-6905	Sequence 6905, Ap
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c 689	17	30.9	2259	10	US-09-822-849A-491	Sequence 491, App	762	17	30.9	10678	9	US-09-764-891-7832	Sequence 7832, Ap
c 690	17	30.9	2347	10	US-09-962-832-113	Sequence 113, App	763	17	30.9	11172	9	US-10-079-854-231	Sequence 231, App
c 691	17	30.9	2364	9	US-10-073-961-513	Sequence 513, App	764	17	30.9	11172	10	US-09-764-878-231	Sequence 231, App
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c 693	17	30.9	2425	9	US-10-125-540-639	Sequence 639, App	766	17	30.9	12167	9	US-09-764-877-3240	Sequence 3240, Ap
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c 697	17	30.9	2631	9	US-10-007-280A-55	Sequence 55, Appl	770	17	30.9	14176	10	US-09-764-864-1644	Sequence 1644, Ap
c 698	17	30.9	2682	10	US-09-799-983-1	Sequence 1, Appli	c 771	17	30.9	14426	9	US-09-860-670-252	Sequence 252, App
c 699	17	30.9	2866	10	US-09-320-300A-1686	Sequence 1686, Ap	c 772	17	30.9	14448	9	US-09-860-670-250	Sequence 250, App
c 700	17	30.9	2866	12	US-10-033-528-1686	Sequence 1686, Ap	c 773	17	30.9	14451	9	US-09-860-670-253	Sequence 253, App
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c 702	17	30.9	3032	10	US-09-822-849A-348	Sequence 348, App	c 775	17	30.9	14781	10	US-09-764-877-2668	Sequence 2668, Ap
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c 704	17	30.9	3257	9	US-10-092-154-1410	Sequence 1410, Ap	c 777	17	30.9	14796	10	US-09-954-456-973	Sequence 973, App
c 705	17	30.9	3257	9	US-10-092-154-1411	Sequence 1411, Ap	c 778	17	30.9	14796	10	US-09-954-456-1636	Sequence 1636, Ap
c 706	17	30.9	3257	10	US-09-764-847-1410	Sequence 1410, Ap	c 779	17	30.9	14796	10	US-09-918-186A-3	Sequence 3, Appli
c 707	17	30.9	3257	10	US-09-764-847-1411	Sequence 1411, Ap	c 780	17	30.9	14796	10	US-09-880-107-3421	Sequence 3421, Ap
c 708	17	30.9	3619	9	US-09-764-872-639	Sequence 639, App	c 781	17	30.9	14874	9	US-09-764-891-7672	Sequence 7672, Ap
c 709	17	30.9	3991	9	US-10-074-045-60	Sequence 60, Appl	c 782	17	30.9	14962	9	US-10-079-854-244	Sequence 244, App
c 710	17	30.9	4025	10	US-09-764-877-2340	Sequence 2340, Ap	c 783	17	30.9	14962	10	US-09-764-878-244	Sequence 244, App
c 711	17	30.9	4025	10	US-09-764-877-2343	Sequence 2343, Ap	c 784	17	30.9	15061	9	US-10-092-154-991	Sequence 991, App
c 712	17	30.9	4025	10	US-09-764-877-2345	Sequence 2345, Ap	c 785	17	30.9	15061	9	US-09-764-891-6914	Sequence 991, App
c 713	17	30.9	4453	9	US-10-116-016-49	Sequence 49, Appl	c 786	17	30.9	15061	10	US-09-764-847-991	Sequence 3797, Ap
c 714	17	30.9	4453	10	US-09-764-848-49	Sequence 49, Appl	c 787	17	30.9	15266	10	US-09-764-877-3797	Sequence 3797, Ap
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c 721	17	30.9	4837	10	US-09-764-877-2839	Sequence 2839, Ap	c 794	17	30.9	17146	10	US-09-764-877-3850	Sequence 3850, Ap
c 722	17	30.9	4873	9	US-09-971-490-4	Sequence 4, Appli	c 795	17	30.9	17216	10	US-09-764-877-3566	Sequence 3566, Ap
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c 729	17	30.9	5786	9	US-10-079-854-240	Sequence 240, App	c 802	17	30.9	17965	9	US-09-764-891-8198	Sequence 8198, Ap
c 730	17	30.9	5786	10	US-09-764-878-240	Sequence 240, App	c 803	17	30.9	17993	9	US-09-768-781-5	Sequence 5, Appli
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c 740	17	30.9	6660	10	US-09-764-877-2529	Sequence 2529, Ap	c 813	17	30.9	20966	9	US-10-277-032-3	Sequence 3, Appli
c 741	17	30.9	6964	9	US-09-816-653A-5	GENERAL INFORMATI	c 814	17	30.9	20966	9	US-10-231-814-7	Sequence 7, Appli
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c 745	17	30.9	7809	9	US-09-764-891-6094	Sequence 6094, Ap	c 818	17	30.9	21606	9	US-10-091-504-1733	Sequence 1733, Ap
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c 747	17	30.9	8575	9	US-09-764-891-8707	Sequence 8707, Ap	c 820	17	30.9	21606	10	US-09-764-869-1733	Sequence 1733, Ap
c 748	17	30.9	8701	9	US-10-092-154-1976	Sequence 1976, Ap	c 821	17	30.9	21606	10	US-09-764-869-1733	Sequence 1733, Ap
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c 894	17	30.9	32216	9	US-09-764-891-9613	Sequence 9613, Ap	c 967	16	29.1	87	10	US-09-764-860-962	Sequence 962, App
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ALIGNMENTS

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RESULT 1
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22754
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(490)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22754

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; Sequence 795, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 218
; TYPE: DNA
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US-09-867-701-795

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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
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US-09-918-995-23432

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RESULT 4

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US-09-748-107-3
; Sequence 3, Application US/09748107
; Patent No. US20020028915A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

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; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00784
; CURRENT APPLICATION NUMBER: US/09/748,107
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10708
; TYPE: DNA
; ORGANISM: Human
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; OTHER INFORMATION: n = A,T,C or G
US-09-748-107-3

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RESULT 5

US-09-860-670-251/c
; Sequence 251, Application US/09860670
; Patent No. US20020165137A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA12791
; CURRENT APPLICATION NUMBER: US/09/860,670
; CURRENT FILING DATE: 2001-05-21
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 251
; LENGTH: 14417
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-860-670-251
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Best Local Similarity 100.0%; Pred. No. 0.0001;
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RESULT 6

US-09-860-670-249/c
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; Patent No. US20020165137A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA12791
; CURRENT APPLICATION NUMBER: US/09/860,670
; CURRENT FILING DATE: 2001-05-21
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 249
; LENGTH: 14426
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-860-670-249
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Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7

US-10-074-095-818/c
; Sequence 818, Application US/10074095
; Publication No. US2003007704A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC008C1
; CURRENT APPLICATION NUMBER: US/10/074,095
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
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;; PRIOR APPLICATION NUMBER: 60/227,182
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;; PRIOR APPLICATION NUMBER: 60/225,214
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/235,836
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: 60/230,438

;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/215,135
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: 60/225,266
;; PRIOR FILING DATE: 2000-08-14
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;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/231,242
;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
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;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
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;; PRIOR FILING DATE: 2000-11-08
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;; PRIOR FILING DATE: 2000-09-08

Query Match 43.6%; Score 24; DB 9; Length 98;
Best Local Similarity 100.0%; Pred.No. 0.00084;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 TTGAGATCAGCTGGCCACATG 53
Db 42 TTGAGATCAGCTGGCCACATG 19
|||||

RESULT 8

US-10-074-095-819/c
; Sequence 819, Application US/10074095
; Publication No. US2003007704A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C1
; CURRENT APPLICATION NUMBER: US/10/074,095
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
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; PRIOR FILING DATE: 2000-07-11
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; PRIOR FILING DATE: 2000-09-08

Query Match 43.6%; Score 24; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCAAACATG 53
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Db 42 TTCGAGATCAGCTGGCCAAACATG 19

RESULT 9

US-09-764-860-818/c
; Sequence 818, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 818
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-818

Query Match 43.6%; Score 24; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCAAACATG 53
|||
Db 42 TTCGAGATCAGCTGGCCAAACATG 19

RESULT 10

US-09-764-860-819/c
; Sequence 819, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 819
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-819

Query Match 43.6%; Score 24; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCAAACATG 53
|||
Db 42 TTCGAGATCAGCTGGCCAAACATG 19

RESULT 11

US-09-764-891-5685
; Sequence 5685, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5685
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-5685

Query Match 43.6%; Score 24; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53
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Db 18 TTCGAGATCAGCCTGGCCCAACATG 41

RESULT 12

US-09-918-995-3449
; Sequence 3449, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3449
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-3449

Query Match 43.6%; Score 24; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53
|
Db 41 TTCGAGATCAGCCTGGCCCAACATG 64

RESULT 13

US-09-867-701-7253
; Sequence 7253, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7253
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-7253

Query Match 43.6%; Score 24; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53
|
Db 321 TTCGAGATCAGCCTGGCCCAACATG 344

RESULT 14

US-09-867-701-10214/c
; Sequence 10214, Application US/09867701

Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10214
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-10214

Query Match 43.6%; Score 24; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53
|
Db 223 TTCGAGATCAGCCTGGCCCAACATG 200

RESULT 15

US-09-918-995-26320
; Sequence 26320, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26320
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(498)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26320

Query Match 43.6%; Score 24; DB 9; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53
|
Db 187 TTCGAGATCAGCCTGGCCCAACATG 210

Search completed: June 17, 2003, 09:58:44
Job time : 25.8144 secs

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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 62.5 Seconds
(without alignments)

14252.028 Million cell updates/sec

Title: US-09-513-888C-1_COPY_4365_4419

Perfect score: 55

Sequence: 1 gaggcaggcagacacttga.....atcagctggccaacatgag 55

- Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST.*

1: em_estba.*

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25: em_gss_othr.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	65.5	388	12	BG284780
2	36	65.5	412	10	AW503185
3	36	65.5	574	17	AQ582126
4	36	65.5	814	9	AU119400
5	36	65.5	824	9	AU119141
6	36	65.5	933	14	BQ643665

7	32	58.2	528	17	AQ460151
8	32	58.2	569	17	AQ298954
c	9	32	58.2	10	BE279465
c	10	31	56.4	12	BF927015
c	11	30	54.5	12	AW834360
c	12	29	52.7	10	BE395893
c	13	28	50.9	108	BQ331585
c	14	28	50.9	175	AQ467676
c	15	28	50.9	302	AQ412104
c	16	28	50.9	425	BF763443
c	17	28	50.9	440	AQ630534
c	18	28	50.9	458	AQ267662
c	19	28	50.9	459	BF764119
c	20	28	50.9	459	AQ474879
c	21	28	50.9	685	BE869257
c	22	28	50.9	935	BQ643902
c	23	26	47.3	436	AQ190517
c	24	26	47.3	443	BF816502
c	25	26	47.3	448	BI012879
c	26	26	47.3	549	AQ771806
c	27	26	47.3	608	AQ238278
c	28	26	47.3	633	AQ236772
c	29	26	47.3	642	AQ239803
c	30	26	47.3	652	AQ385572
c	31	26	47.3	965	BQ651708
c	32	25	45.5	151	AW805822
c	33	25	45.5	189	T50366
c	34	25	45.5	218	T59444
c	35	25	45.5	232	AI335526
c	36	25	45.5	239	AI821292
c	37	25	45.5	239	AI821295
c	38	25	45.5	258	T51057
c	39	25	45.5	267	AI821003
c	40	25	45.5	271	AA243579
c	41	25	45.5	301	B85490
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c	50	25	45.5	560	BF997507
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c	53	25	45.5	613	AQ419352
c	54	25	45.5	615	AV731405
c	55	25	45.5	622	BQ181069
c	56	25	45.5	647	AG036825
c	57	25	45.5	704	BE894065
c	58	25	45.5	712	AV731128
c	59	25	45.5	743	BG925349
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c	61	24	43.6	101	AA583697
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c	64	24	43.6	211	AA225588
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c	67	24	43.6	228	B48809
c	68	24	43.6	229	AI591240
c	69	24	43.6	231	AA225589
c	70	24	43.6	235	AW505605
c	71	24	43.6	236	W20344
c	72	24	43.6	241	B05057
c	73	24	43.6	245	C14783
c	74	24	43.6	248	AA338635
c	75	24	43.6	250	BF766138
c	76	24	43.6	253	AQ281285
c	77	24	43.6	259	BG980118
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C 81	24	43.6	270	17	BH860999	BH860999 UP 463-2L	154	24	43.6	419	17	AQ185304
C 82	24	43.6	273	9	AA985391	AA985391 AM51910.s	C 155	24	43.6	422	9	AA226309
C 83	24	43.6	279	17	AQ095901	AQ095901 HS 3033_A	156	24	43.6	422	17	AQ680662
C 84	24	43.6	281	9	AA630672	AA630672 ae65g02.s	157	24	43.6	423	12	BG012230
C 85	24	43.6	287	13	BI003144	BI003144 PM3-HN007	158	24	43.6	426	12	BG14780
C 86	24	43.6	292	14	C15146	C15146 C15146 Clon	159	24	43.6	426	17	AQ834205
C 87	24	43.6	295	14	C14966	C14966 C14966 Clon	C 160	24	43.6	428	14	C15184
C 88	24	43.6	297	13	BI048973	BI048973 PM2-UM005	C 161	24	43.6	430	14	C15504
C 89	24	43.6	299	9	AA947551	AA947551 od87c06.s	162	24	43.6	430	17	AQ108371
C 90	24	43.6	300	12	BF771587	BF771587 IL5-IT002	163	24	43.6	431	9	AA808970
C 91	24	43.6	309	10	BE246822	BE246822 TCBAPEL51	164	24	43.6	431	13	BM504315
C 92	24	43.6	309	13	BM504093	BM504093 IL20G08.x	C 165	24	43.6	432	9	AL135696
C 93	24	43.6	312	9	A1798493	A1798493 tr36b03.x	C 166	24	43.6	432	9	AA467963
C 94	24	43.6	313	9	A1249447	A1249447 qx02f12.x	C 167	24	43.6	433	9	AI590592
C 95	24	43.6	314	12	BF875954	BF875954 CM0-ET016	C 168	24	43.6	434	10	AW081303
C 96	24	43.6	315	9	A1471918	A1471918 t152h02.x	C 169	24	43.6	435	14	T60046
C 97	24	43.6	329	9	AA722327	AA722327 ag88b03.r	170	24	43.6	436	10	AW503442
C 98	24	43.6	330	9	AL710569	AL710569 DKF2P686M	171	24	43.6	438	14	T85300
C 99	24	43.6	330	10	AW779451	AW779451 hu95a07.x	C 172	24	43.6	439	9	AA226133
C 100	24	43.6	336	12	EG231091	EG231091 nah77g12.	C 173	24	43.6	439	13	EG960549
C 101	24	43.6	339	9	AA569222	AA569222 nm30h06.s	C 174	24	43.6	441	9	AI953861
C 102	24	43.6	340	12	BF873355	BF873355 IL5-ET011	C 175	24	43.6	443	17	B88683
C 103	24	43.6	341	10	AW518758	AW518758 ha39f09.x	176	24	43.6	445	17	AQ145851
C 104	24	43.6	343	9	AI932871	AI932871 wo39a03.x	177	24	43.6	448	14	H56208
C 105	24	43.6	346	9	AI313280	AI313280 ta92a02.x	C 178	24	43.6	449	10	BE146587
C 106	24	43.6	346	9	AA281325	AA281325 z893h02.s	C 179	24	43.6	449	17	AQ174482
C 107	24	43.6	348	9	AA737564	AA737564 ca50g03.s	C 180	24	43.6	453	9	AI057041
C 108	24	43.6	350	9	AA766585	AA766585 ca32g09.s	181	24	43.6	454	17	AQ704155
C 109	24	43.6	355	17	AZ515827	AZ515827 RPT1-11-1	C 182	24	43.6	457	9	AA115865
C 110	24	43.6	357	9	AA516038	AA516038 ng65b12.s	183	24	43.6	457	9	AI828742
C 111	24	43.6	357	12	BG180976	BG180976 602327459	C 184	24	43.6	460	17	AQ138759
C 112	24	43.6	358	17	AQ085118	AQ085118 HS 2268_A	C 185	24	43.6	462	17	AQ663932
C 113	24	43.6	363	10	AV729669	AV729669 AV729669	C 186	24	43.6	464	9	AA486867
C 114	24	43.6	368	9	A1623846	A1623846 ts39a06.x	187	24	43.6	465	12	BF795203
C 115	24	43.6	368	10	AW834010	AW834010 QV0-TT001	C 188	24	43.6	466	17	AQ477039
C 116	24	43.6	370	9	AA810565	AA810565 ca84g07.s	C 189	24	43.6	466	9	AI280266
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C 118	24	43.6	377	13	BI335326	BI335326 602998255	C 191	24	43.6	471	10	AW903790
C 119	24	43.6	379	9	A1472726	A1472726 ta13b03.x	C 192	24	43.6	472	9	AA860881
C 120	24	43.6	379	9	AA351153	AA351153 EST58819	C 193	24	43.6	472	10	AW974110
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C 125	24	43.6	388	17	AQ095261	AQ095261 HS 3027_A	C 198	24	43.6	476	9	AA468416
C 126	24	43.6	389	10	BE145383	BE145383 IL5-HT019	C 199	24	43.6	478	17	AQ580410
C 127	24	43.6	391	14	RI1545	RI1545 yf47b04.r1	200	24	43.6	479	17	AQ121918
C 128	24	43.6	392	10	AW856380	AW856380 RC6-CT028	C 201	24	43.6	479	17	AQ425628
C 129	24	43.6	392	17	B48911	B48911 RPT11-3P22	C 202	24	43.6	480	9	AA776909
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C 131	24	43.6	395	9	AA658934	AA658934 nt85g01.s	C 204	24	43.6	481	17	AQ343577
C 132	24	43.6	395	9	B31665	B31665 HS-1011-A2-	C 205	24	43.6	485	9	AA214042
C 133	24	43.6	397	9	AA603885	AA603885 np11e03.s	C 206	24	43.6	486	9	AA668229
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C 135	24	43.6	404	14	C14627	C14627 C14627 Clon	C 208	24	43.6	496	9	AL046526
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C 137	24	43.6	405	10	BE065718	BE065718 RC2-BT031	C 210	24	43.6	498	17	AQ358615
C 138	24	43.6	405	14	T84567	T84567 yd50a06.r1	C 211	24	43.6	499	9	AA626505
C 139	24	43.6	406	9	A1923052	A1923052 wn24f12.x	C 212	24	43.6	502	14	N30016
C 140	24	43.6	407	9	AI686470	AI686470 tu34b06.x	C 213	24	43.6	504	10	AW608552
C 141	24	43.6	407	17	AQ789976	AQ789976 HS 3177_B	C 214	24	43.6	504	17	AZ303212
C 142	24	43.6	409	10	AV762828	AV762828 AV762828	C 215	24	43.6	505	12	BF737479
C 143	24	43.6	409	17	AQ119443	AQ119443 HS 2171_B	C 216	24	43.6	508	10	AW819483
C 144	24	43.6	410	9	A1469564	A1469564 tm19b11.x	C 217	24	43.6	509	17	AQ013431
C 145	24	43.6	411	17	AQ010110	AQ010110 HS 2263_A	C 218	24	43.6	514	10	AW172858
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C 147	24	43.6	413	12	BG007564	BG007564 RC3-GN026	C 220	24	43.6	515	14	BQ365056
C 148	24	43.6	414	17	AQ588411	AQ588411 CTBTI-E1-	C 221	24	43.6	516	10	AW130591
C 149	24	43.6	415	9	A1368862	A1368862 qv97g12.x	C 222	24	43.6	521	17	AA161198
C 150	24	43.6	415	14	BQ954256	BQ954256 AGENCOURT	C 223	24	43.6	521	9	AQ350115
C 151	24	43.6	417	9	A1524515	A1524515 to37f08.x	C 224	24	43.6	522	17	AQ532619
C 152	24	43.6	419	9			C 225	24	43.6	523	12	BG573623

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AA115865	zn81e09.s
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AQ138759	HS 3071_B
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C 229	24	43.6	542	14	BM999729	UI-H-DIO-	C 302	24	43.6	867	17	AQ894479
C 230	24	43.6	543	12	BG250044	BG250044	C 303	24	43.6	868	17	BQ967689
C 231	24	43.6	545	9	AUI146155	AUI146155	C 304	24	43.6	869	17	AQ738714
C 232	24	43.6	547	17	AQ930957	AQ930957	C 305	24	43.6	894	17	AQ738714
C 233	24	43.6	547	17	AQ930957	AQ930957	C 306	24	43.6	909	12	BG746234
C 234	24	43.6	547	17	AQ930957	AQ930957	C 307	24	43.6	932	12	BG746234
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C 236	24	43.6	552	17	AQ930957	AQ930957	C 309	24	43.6	959	9	AL043979
C 237	24	43.6	556	17	AQ930957	AQ930957	C 310	24	43.6	1006	12	BG746234
C 238	24	43.6	557	17	AQ930957	AQ930957	C 311	24	43.6	1050	12	BG746234
C 239	24	43.6	559	14	BG746234	BG746234	C 312	24	43.6	1074	14	BG746234
C 240	24	43.6	562	17	AQ930957	AQ930957	C 313	24	43.6	1108	14	BG746234
C 241	24	43.6	563	14	BM706294	BM706294	C 314	24	43.6	1267	11	BC014134
C 242	24	43.6	564	13	BM559468	BM559468	C 315	24	43.6	1738	11	BC014134
C 243	24	43.6	565	13	BM559468	BM559468	C 316	24	43.6	1738	11	BC014134
C 244	24	43.6	565	13	BM559468	BM559468	C 317	24	43.6	142	10	BE180038
C 245	24	43.6	565	13	BM559468	BM559468	C 318	24	43.6	150	17	BE180038
C 246	24	43.6	569	9	AUI148206	AUI148206	C 319	24	43.6	194	10	BE174114
C 247	24	43.6	576	10	AW249541	AW249541	C 320	24	43.6	196	13	BE174114
C 248	24	43.6	581	17	BG6746	BG6746	C 321	24	43.6	226	14	BE174114
C 249	24	43.6	586	17	AQ320497	AQ320497	C 322	24	43.6	237	9	AG911529
C 250	24	43.6	594	12	BG571816	BG571816	C 323	24	43.6	246	9	AG911529
C 251	24	43.6	599	10	BE150678	BE150678	C 324	24	43.6	253	13	BE150678
C 252	24	43.6	604	13	BE1548229	BE1548229	C 325	24	43.6	258	14	BE1548229
C 253	24	43.6	608	17	BG68414	BG68414	C 326	24	43.6	261	14	BE1548229
C 254	24	43.6	614	9	AA552907	AA552907	C 327	24	43.6	264	9	AA552907
C 255	24	43.6	617	10	AA552907	AA552907	C 328	24	43.6	264	14	AA552907
C 256	24	43.6	623	17	AQ380505	AQ380505	C 329	24	43.6	264	14	AA552907
C 257	24	43.6	628	14	BM991214	BM991214	C 330	24	43.6	268	9	AG911529
C 258	24	43.6	629	17	AQ560385	AQ560385	C 331	24	43.6	282	13	BE150678
C 259	24	43.6	631	9	AA056108	AA056108	C 332	24	43.6	282	13	BE150678
C 260	24	43.6	631	13	BM504006	BM504006	C 333	24	43.6	290	13	BE150678
C 261	24	43.6	631	17	AQ150345	AQ150345	C 334	24	43.6	290	13	BE150678
C 262	24	43.6	635	10	AW747980	AW747980	C 335	24	43.6	303	9	AA552907
C 263	24	43.6	637	17	AQ102493	AQ102493	C 336	24	43.6	303	9	AA552907
C 264	24	43.6	652	17	AQ348813	AQ348813	C 337	24	43.6	320	12	BG057766
C 265	24	43.6	656	10	AW820619	AW820619	C 338	24	43.6	325	9	AA05517
C 266	24	43.6	658	9	AA126519	AA126519	C 339	24	43.6	327	9	AA05517
C 267	24	43.6	660	9	AL705934	AL705934	C 340	24	43.6	327	9	AA05517
C 268	24	43.6	664	10	BE178471	BE178471	C 341	24	43.6	334	10	AA584474
C 269	24	43.6	665	17	AQ150986	AQ150986	C 342	24	43.6	335	9	AA584474
C 270	24	43.6	672	17	AQ092869	AQ092869	C 343	24	43.6	335	9	AA584474
C 271	24	43.6	684	17	AG166450	AG166450	C 344	24	43.6	343	10	AA584474
C 272	24	43.6	685	17	AG109125	AG109125	C 345	24	43.6	346	10	AA584474
C 273	24	43.6	686	17	AG118963	AG118963	C 346	24	43.6	346	10	AA584474
C 274	24	43.6	690	12	BE910659	BE910659	C 347	24	43.6	346	10	AA584474
C 275	24	43.6	691	17	AG186101	AG186101	C 348	24	43.6	350	9	AA551413
C 276	24	43.6	693	17	AG114428	AG114428	C 349	24	43.6	350	9	AA551413
C 277	24	43.6	699	17	AG095566	AG095566	C 350	24	43.6	351	14	AA551413
C 278	24	43.6	700	17	AQ013879	AQ013879	C 351	24	43.6	351	14	AA551413
C 279	24	43.6	702	17	AQ062195	AQ062195	C 352	24	43.6	351	14	AA551413
C 280	24	43.6	706	17	AG186101	AG186101	C 353	24	43.6	357	10	BE146697
C 281	24	43.6	707	17	AG094472	AG094472	C 354	24	43.6	357	10	BE146697
C 282	24	43.6	715	17	AG118483	AG118483	C 355	24	43.6	366	17	AQ099316
C 283	24	43.6	721	12	BG540436	BG540436	C 356	24	43.6	367	17	AQ263757
C 284	24	43.6	728	9	AL596676	AL596676	C 357	24	43.6	371	9	AQ263757
C 285	24	43.6	730	14	BQ183112	BQ183112	C 358	24	43.6	371	9	AQ263757
C 286	24	43.6	733	17	B92010	CIT-HSP-217	C 359	24	43.6	371	9	AQ263757
C 287	24	43.6	736	10	AV721604	AV721604	C 360	24	43.6	371	9	AQ263757
C 288	24	43.6	746	17	AG031300	AG031300	C 361	24	43.6	374	10	AA584599
C 289	24	43.6	761	17	B95257	CIT-HSP-217	C 362	24	43.6	374	10	AA584599
C 290	24	43.6	772	17	AQ029113	AQ029113	C 363	24	43.6	375	17	AQ412819
C 291	24	43.6	773	17	AQ740481	AQ740481	C 364	24	43.6	375	17	AQ412819
C 292	24	43.6	776	14	BQ000500	UI-H-DPO-	C 365	24	43.6	378	9	AA535902
C 293	24	43.6	784	17	AV757536	AV757536	C 366	24	43.6	382	9	AA568433
C 294	24	43.6	788	13	BM007944	BM007944	C 367	24	43.6	382	9	AA568433
C 295	24	43.6	793	14	BQ212207	BQ212207	C 368	24	43.6	386	14	H62292
C 296	24	43.6	805	17	AQ986115	AQ986115	C 369	24	43.6	386	14	H62292
C 297	24	43.6	811	17	AQ780945	AQ780945	C 370	24	43.6	388	10	BE088635
C 298	24	43.6	846	12	BE739933	BE739933	C 371	24	43.6	388	10	BE088635
C 299	24	43.6	846	12	BE739933	BE739933	C 372	24	43.6	390	14	R98443
C 300	24	43.6	846	12	BE739933	BE739933	C 373	24	43.6	390	14	R98443
C 301	24	43.6	846	12	BE739933	BE739933	C 374	24	43.6	401	9	AA084782
C 302	24	43.6	846	12	BE739933	BE739933	C 375	24	43.6	401	9	AA084782
C 303	24	43.6	846	12	BE739933	BE739933	C 376	24	43.6	403	12	BF881703
C 304	24	43.6	846	12	BE739933	BE739933	C 377	24	43.6	403	12	BF881703
C 305	24	43.6	846	12	BE739933	BE739933	C 378	24	43.6	403	12	BF881703
C 306	24	43.6	846	12	BE739933	BE739933	C 379	24	43.6	405	12	BF881703
C 307	24	43.6	846	12	BE739933	BE739933	C 380	24	43.6	405	12	BF881703
C 308	24	43.6	846	12	BE739933	BE739933	C 381	24	43.6	405	12	BF881703
C 309	24	43.6	846	12	BE739933	BE739933	C 382	24	43.6	405	12	BF881703
C 310	24	43.6	846	12	BE739933	BE739933	C 383	24	43.6	405	12	BF881703
C 311	24	43.6	846	12	BE739933	BE739933	C 384	24	43.6	405	12	BF881703
C 312	24	43.6	846	12	BE739933	BE739933	C 385	24	43.6	405	12	BF881703
C 313	24	43.6	846	12	BE739933	BE739933	C 386	24	43.6	405	12	BF881703
C 314	24	43.6	846	12	BE739933	BE739933	C 387	24	43.6	405	12	BF881703
C 315	24	43.6	846	12	BE739933	BE739933	C 388	24	43.6	405	12	BF881703
C 316	24	43.6	846	12	BE739933	BE739933	C 389	24	43.6	405	12	BF881703
C 317	24	43.6	846	12	BE739933	BE739933	C 390	24	43.6	405	12	BF881703
C 318	24	43.6	846	12	BE739933	BE739933	C 391	24	43.6	405	12	BF881703
C 319	24	43.6	846	12	BE739933	BE739933	C 392	24	43.6	405	12	BF881703
C 320	24	43.6	846	12	BE739933	BE739933	C 393	24	43.6	405	12	BF881703
C 321	24	43.6	846	12	BE739933	BE739933	C 394	24	43.6	405	12	BF881703
C 322	24	43.6	846	12	BE739933	BE739933	C 395	24	43.6	405	12	BF881703
C 323	24	43.6	846	12	BE739933	BE739933	C 396	24	43.6	405	12	BF881703
C 324	24	43.6	846	12	BE739933	BE739933	C 397	24	43.6	405	12	BF881703
C 325	24	43.6	846	12	BE739933	BE739933	C 398	24	43.6	405	12	BF881703
C 326	24	43.6	846	12	BE739933	BE739933	C 399	24	43.6	405	12	BF881703
C 327	24	43.6	846	12	BE739933	BE739933	C 400	24	43.6	405	12	BF881703
C 328	24	43.6	846	12	BE739933	BE739933	C 401	24	43.6	405	12	BF881703
C 329	24	43.6	846	12	BE739933	BE739933	C 402					

C 372	23	41.8	448	17	AQ634562	RPCI-11-4	C 445	23	41.8	687	12	BG718011	BG718011	602696017
C 373	23	41.8	449	10	AV721585	AV721585	C 446	23	41.8	689	14	BQ021292	BQ021292	UI-H-DH1-
C 374	23	41.8	450	17	AQ412211	RPCI-11-1	C 447	23	41.8	691	17	AQ835107	AQ835107	HS_4822_A
C 375	23	41.8	452	17	AQ663990	AQ663990 HS_2277_B	C 448	23	41.8	692	17	AG173673	AG173673	Pan trogl
C 376	23	41.8	455	9	AA523834	AA523834 n150906.s	C 449	23	41.8	695	17	AQ344988	AQ344988	RPCI-11-1
C 377	23	41.8	456	17	AQ263210	AQ263210 CITBI-E1-	C 450	23	41.8	701	17	AG014803	AG014803	AV764198
C 378	23	41.8	459	14	BQ181460	UI-H-EUO-	C 451	23	41.8	701	17	AG014803	AG014803	Homo sapi
C 379	23	41.8	463	17	AQ021152	CIT-HSP-2	C 452	23	41.8	706	17	AG014804	AG014804	Homo sapi
C 380	23	41.8	467	17	AQ527122	CITBI-E1-	C 453	23	41.8	712	17	AG177809	AG177809	Pan trogl
C 381	23	41.8	468	14	N22428	YW39e06.s1	C 454	23	41.8	719	14	BM721278	BM721278	UI-E-BO1-
C 382	23	41.8	476	9	AA227360	AA227360 z17b04.r	C 455	23	41.8	720	17	AQ395438	AQ395438	CITBI-E1-
C 383	23	41.8	476	10	AW269690	AW269690 xv55d04.x	C 456	23	41.8	740	13	BI517589	BI517589	603041887
C 384	23	41.8	476	14	H58653	H58653 Yr20a06.s1	C 457	23	41.8	741	17	AG173270	AG173270	Pan trogl
C 385	23	41.8	476	14	W04193	W04193 za57e10.r1	C 458	23	41.8	751	12	BF669330	BF669330	602120614
C 386	23	41.8	479	17	AQ286120	RPCI-11-89	C 459	23	41.8	772	10	AV761968	AV761968	AV761968
C 387	23	41.8	491	17	AQ828509	AQ828509 HS_5255_B	C 460	23	41.8	775	9	AL700165	AL700165	DKF2p686J
C 388	23	41.8	496	14	H63390	H63390 Yr53b02.s1	C 461	23	41.8	804	17	AQ752317	AQ752317	HS_5565_B
C 389	23	41.8	497	17	AQ522229	AQ522229 HS_5221_A	C 462	23	41.8	855	17	AQ746225	AQ746225	HS_2276_A
C 390	23	41.8	498	17	AQ583170	AQ583170 RPCI-11-4	C 463	23	41.8	872	12	BF382089	BF382089	601814829
C 391	23	41.8	502	17	AQ172790	AQ172790 HS_3195_B	C 464	23	41.8	891	14	BQ220253	BQ220253	AGENCOURT
C 392	23	41.8	504	17	AQ175961	AQ175961 HS_3214_B	C 465	23	41.8	901	12	BF674663	BF674663	602137887
C 393	23	41.8	518	13	BG998514	BG998514 PM4-HT130	C 466	23	41.8	942	9	AL515364	AL515364	AL515364
C 394	23	41.8	518	17	AQ331615	AQ331615 HS_5006_A	C 467	23	41.8	966	12	BG387516	BG387516	602412327
C 395	23	41.8	520	12	BF853910	BF853910 MR3-EN008	C 468	23	41.8	969	14	BQ220750	BQ220750	AGENCOURT
C 396	23	41.8	520	17	AQ251736	AQ251736 HS_3202_B	C 469	23	41.8	989	14	BQ223101	BQ223101	AGENCOURT
C 397	23	41.8	525	9	AA461163	AA461163 zx70a06.s	C 470	22	40.0	100	10	AW809210	AW809210	MR4-ST011
C 398	23	41.8	525	12	BF751908	BF751908 RC3-EN003	C 471	22	40.0	145	10	AW809262	AW809262	MR4-ST011
C 399	23	41.8	526	12	BF699338	BF699338 602125906	C 472	22	40.0	145	10	AW809283	AW809283	MR4-ST011
C 400	23	41.8	527	17	AQ542658	AQ542658 RPCI-11-3	C 473	22	40.0	190	10	BE178921	BE178921	RC3-HT061
C 401	23	41.8	528	17	AQ314944	AQ314944 RPCI-11-94	C 474	22	40.0	218	10	AW440677	AW440677	hc88c03.x
C 402	23	41.8	534	17	AQ277751	AQ277751 CITBI-E1-	C 475	22	40.0	221	9	AI377441	AI377441	tc23f01.x
C 403	23	41.8	535	9	A1912588	A1912588 wt1d10.x	C 476	22	40.0	224	10	AW833129	AW833129	RC3-TT000
C 404	23	41.8	537	17	AQ708354	AQ708354 HS_5569_A	C 477	22	40.0	229	14	R97049	R97049	YQ74905.s1
C 405	23	41.8	550	14	BQ287956	BQ287956 IK37f107.x	C 478	22	40.0	284	14	N72436	N72436	YV4909.r1
C 406	23	41.8	552	12	BF850673	BF850673 PM4-EN006	C 479	22	40.0	284	13	BI028338	BI028338	CM4-MT028
C 407	23	41.8	552	17	B48639	B48639 RPCI-11-2M15	C 480	22	40.0	282	17	AQ424457	AQ424457	CITBI-E1-
C 408	23	41.8	556	9	AL134615	AL134615 DKF2p547F	C 481	22	40.0	293	10	AW801998	AW801998	IL5-UM007
C 409	23	41.8	557	12	BG289272	BG289272 602384280	C 482	22	40.0	298	13	BI026936	BI026936	CM3-TT029
C 410	23	41.8	566	9	AU158610	AU158610 AU158610	C 483	22	40.0	307	9	AA699307	AA699307	zi32h07.s
C 411	23	41.8	573	17	AQ307838	AQ307838 HS_2199_A	C 484	22	40.0	329	12	BF945347	BF945347	PMO-NN117
C 412	23	41.8	573	17	AQ415110	AQ415110 RPCI-11-2	C 485	22	40.0	356	10	AW890526	AW890526	QV4-NT004
C 413	23	41.8	575	9	AL692058	AL692058 DKF2p313M	C 486	22	40.0	356	10	AW890454	AW890454	QV4-NT004
C 414	23	41.8	577	17	AZ516938	AZ516938 RPCI-11-8	C 487	22	40.0	363	13	BI003322	BI003322	PMO-HN007
C 415	23	41.8	580	10	AW394122	MR2-TT001	C 488	22	40.0	367	10	AW088656	AW088656	xdl0908.x
C 416	23	41.8	581	10	AW248498	AW248498 2820490.3	C 489	22	40.0	367	12	BF900888	BF900888	IL2-TT017
C 417	23	41.8	582	13	BG996815	BG996815 PMO-HT116	C 490	22	40.0	368	10	AW693769	AW693769	AV693769
C 418	23	41.8	582	17	AQ427274	AQ427274 CITBI-E1-	C 491	22	40.0	370	10	AW695089	AW695089	AV695089
C 419	23	41.8	594	12	BF130220	BF130220 601818246	C 492	22	40.0	375	10	AW689521	AW689521	AV689521
C 420	23	41.8	594	17	AG016678	AG016678 Homo sapi	C 493	22	40.0	376	12	BG996294	BG996294	HOA29-1-A
C 421	23	41.8	597	12	BG777139	BG777139 602664355	C 494	22	40.0	377	9	AA705566	AA705566	zj92g12.s
C 422	23	41.8	597	14	W27004	W27004 19h3 Human	C 495	22	40.0	377	10	AA695098	AA695098	AV695098
C 423	23	41.8	617	9	AL037258	AL037258 DKF2p564A	C 496	22	40.0	377	10	AW814002	AW814002	RC6-ST019
C 424	23	41.8	627	14	BQ417413	BQ417413 IK37f107.y	C 497	22	40.0	380	10	AW695096	AW695096	AV695096
C 425	23	41.8	629	10	AW977942	AW977942 EST390051	C 498	22	40.0	381	10	AW692912	AW692912	AV692912
C 426	23	41.8	635	17	AG017087	AG017087 Homo sapi	C 499	22	40.0	381	13	BI003337	BI003337	PMO-HN007
C 427	23	41.8	642	17	AG084074	AG084074 Pan trogl	C 500	22	40.0	384	9	AI202789	AI202789	qi39b10.x
C 428	23	41.8	642	17	AG178478	AG178478 Pan trogl	C 501	22	40.0	389	9	AI053562	AI053562	qi68e04.x
C 429	23	41.8	645	17	AG136634	AG136634 Pan trogl	C 502	22	40.0	391	9	AI253439	AI253439	ap85h07.x
C 430	23	41.8	648	10	AW993287	AW993287 RC2-EN003	C 503	22	40.0	395	17	AQ060869	AQ060869	CIT-HSP-2
C 431	23	41.8	655	12	BG720278	BG720278 602692341	C 504	22	40.0	397	14	H49353	H49353	YQ18d11.s1
C 432	23	41.8	657	17	AG017098	AG017098 Homo sapi	C 505	22	40.0	399	12	BF763656	BF763656	CMO-CS004
C 433	23	41.8	660	17	AG157820	AG157820 Pan trogl	C 506	22	40.0	411	9	AA676553	AA676553	zi38d09.s
C 434	23	41.8	664	17	AG107524	AG107524 Pan trogl	C 507	22	40.0	415	9	AA508070	AA508070	ng93a04.s
C 435	23	41.8	665	14	BQ672640	BQ672640 AGENCOURT	C 508	22	40.0	416	17	AQ212371	AQ212371	HS_3002_B
C 436	23	41.8	665	17	AG084035	AG084035 Pan trogl	C 509	22	40.0	417	13	BI026661	BI026661	PMI-WT019
C 437	23	41.8	667	12	BF669424	BF669424 602120124	C 510	22	40.0	425	10	AW833911	AW833911	QV0-TT000
C 438	23	41.8	670	10	AV752038	AV752038 AV752038	C 511	22	40.0	426	9	AA648957	AA648957	ns30g05.s
C 439	23	41.8	671	13	BI597240	BI597240 603250517	C 512	22	40.0	428	17	AQ278208	AQ278208	CITBI-E1-
C 440	23	41.8	672	12	BG492997	BG492997 602537443	C 513	22	40.0	429	17	AQ493975	AQ493975	HS_5134_B
C 441	23	41.8	672	14	BQ000216	BQ000216 UI-H-DIO-	C 514	22	40.0	433	10	AW683048	AW683048	AV683048
C 442	23	41.8	676	17	AQ630943	AQ630943 RPCI-11-4	C 515	22	40.0	433	10	AW698172	AW698172	AV698172
C 443	23	41.8	677	17	AQ284240	AQ284240 RPCI-11-79	C 516	22	40.0	433	10	AW698174	AW698174	AV698174
C 444	23	41.8	685	17	AG014842	AG014842 Homo sapi	C 517	22	40.0	433	10	AV698212	AV698212	AV698212

C 518	22	40.0	435	9	AA262463	zsl6h08.r	591	21	38.2	158	12	BF805831	BF805831 QV4-C1015
C 519	22	40.0	439	10	AW195152	xm66f03.x	C 592	21	38.2	163	13	BI016061	BI016061 PMO-ET025
C 520	22	40.0	444	10	BE144030	MRO-HT016	593	21	38.2	168	10	AW893063	AW893063 CM3-NN000
C 521	22	40.0	446	9	A1620103	tu92e11.x	594	21	38.2	172	10	BE004691	BE004691 CM1-BN011
C 522	22	40.0	462	14	H61613	yr23b01.r1	595	21	38.2	173	12	BF858536	BF858536 RCL-F7019
C 523	22	40.0	464	17	AQ266993	RPC111-71	596	21	38.2	192	9	AA434346	AA434346 aa83a11.r
C 524	22	40.0	464	17	AQ266993	RPC111-71	C 597	21	38.2	193	12	EG013063	EG013063 PM1-GN030
C 525	22	40.0	470	14	H89771	yu82b01.r1	598	21	38.2	197	17	B65546	B65546 CIT-HSP-202
C 526	22	40.0	476	17	BI010330	MR2-EN009	599	21	38.2	207	13	BI036762	BI036762 RC6-NT015
C 527	22	40.0	477	13	BI010330	MR2-EN009	600	21	38.2	207	14	F23326	F23326 HSPD13217 H
C 528	22	40.0	477	13	BI010330	MR2-EN009	601	21	38.2	210	9	AA371898	AA371898 EST83754
C 529	22	40.0	480	10	BE246739	TECAPD14	C 602	21	38.2	219	13	EG991569	EG991569 MR3-HT113
C 530	22	40.0	480	14	BQ363256	MR3-ST019	C 603	21	38.2	225	9	A1950671	A1950671 wx52g10.x
C 531	22	40.0	484	17	AQ833576	HS 5304_B	C 604	21	38.2	229	12	BF872623	BF872623 IL3-ET011
C 532	22	40.0	489	17	AQ476669	CITBI-E1	605	21	38.2	229	12	BF874288	BF874288 IL3-ET011
C 533	22	40.0	491	12	BF821084	MR1-RT004	606	21	38.2	231	14	F18187	F18187 HSPD02762 H
C 534	22	40.0	493	17	AQ354205	CITBI-E1	C 607	21	38.2	235	9	AA809413	AA809413 ob71f08.s
C 535	22	40.0	495	17	AQ036334	CIT-HSP-2	C 608	21	38.2	241	12	EG54636	EG54636 i042c06.x
C 536	22	40.0	496	9	A100747	z191h04.r	C 609	21	38.2	244	12	BF858528	BF858528 RCL-F7019
C 537	22	40.0	501	10	AW820917	RC2-ST030	610	21	38.2	249	17	AQ194922	AQ194922 RPC111-59
C 538	22	40.0	502	17	AQ140180	HS 3109_B	C 611	21	38.2	250	9	AA077870	AA077870 7H13G09_C
C 539	22	40.0	511	14	W02850	W02850 za05b06.r1	612	21	38.2	252	17	AQ263585	AQ263585 CITBI-E1
C 540	22	40.0	518	10	AW813432	MR3-ST019	613	21	38.2	252	17	AQ280701	AQ280701 CITBI-E1
C 541	22	40.0	525	12	BE878288	601A88005	C 614	21	38.2	253	9	AA680253	AA680253 ac86b08.s
C 542	22	40.0	534	17	AQ481386	RPC111-2	C 615	21	38.2	254	9	A1535853	A1535853 jun2.F02r
C 543	22	40.0	534	17	AQ318992	RPC111-10	C 616	21	38.2	259	14	BQ353144	BQ353144 PMO-HT091
C 544	22	40.0	546	9	AA088714	z189a12.r	617	21	38.2	259	17	AQ088982	AQ088982 HS 2200_B
C 545	22	40.0	547	9	AL702622	DKF2p686K	C 618	21	38.2	263	9	A1242994	A1242994 qh46h12.x
C 546	22	40.0	548	17	AQ314262	RPC111-96	C 619	21	38.2	265	17	AQ362933	AQ362933 CITBI-E1
C 547	22	40.0	551	17	AQ356084	RPC111-4	620	21	38.2	267	12	BF907766	BF907766 IL2-UT007
C 548	22	40.0	563	17	AQ427704	CITBI-E1	C 621	21	38.2	270	13	BI020263	BI020263 IL3-WT026
C 549	22	40.0	575	10	AV747043	AV747043	C 622	21	38.2	270	14	H40191	H40191 yps59e05.r1
C 550	22	40.0	591	14	BM819135	K-EST0086	623	21	38.2	271	9	AA339780	AA339780 EST44919
C 551	22	40.0	592	17	AQ625967	CITBI-E1	C 624	21	38.2	272	9	AU147947	AU147947 AU147947
C 552	22	40.0	598	17	AQ712466	HS 2118_A	625	21	38.2	272	12	BF921835	BF921835 CM3-NT017
C 553	22	40.0	604	10	AW851224	IL3-CT022	626	21	38.2	273	17	AQ417534	AQ417534 RPCI-11-1
C 554	22	40.0	604	10	AW851361	IL3-CT022	627	21	38.2	274	10	AW085882	AW085882 xc60c06.x
C 555	22	40.0	614	13	BI115316	602863111	628	21	38.2	275	17	AQ103532	AQ103532 HS 3070_A
C 556	22	40.0	633	10	BE156176	QV0-HT036	C 629	21	38.2	279	9	AA224238	AA224238 zr14g10.s
C 557	22	40.0	642	12	BG482973	602502986	630	21	38.2	281	17	AQ461035	AQ461035 HS 5183_A
C 558	22	40.0	647	17	AG104223	Pan trogl	C 631	21	38.2	286	10	AW884576	AW884576 QV3-OT006
C 559	22	40.0	650	12	EG570337	602590764	632	21	38.2	288	9	AA868763	AA868763 ak52f08.s
C 560	22	40.0	662	10	BE156181	QV0-HT036	C 633	21	38.2	291	9	AA374958	AA374958 EST87225
C 561	22	40.0	663	17	AQ351794	CITBI-E1	634	21	38.2	292	17	AQ634620	AQ634620 RPCI-11-4
C 562	22	40.0	668	17	AG033573	Pan trogl	635	21	38.2	298	9	AA610702	AA610702 np32a07.s
C 563	22	40.0	672	17	AQ345321	RPC111-12	636	21	38.2	302	9	AA366269	AA366269 EST77198
C 564	22	40.0	692	17	AG180755	Pan trogl	C 637	21	38.2	303	10	AW078904	AW078904 xl19e06.x
C 565	22	40.0	698	10	AG362331	AV696231	C 638	21	38.2	304	9	AA480783	AA480783 ne86c12.s
C 566	22	40.0	701	17	AG011324	Homo sapi	639	21	38.2	305	17	AQ276159	AQ276159 CITBI-E1
C 567	22	40.0	702	17	AQ343621	RPC111-12	640	21	38.2	310	9	AA092605	AA092605 116269.se
C 568	22	40.0	703	10	AV697319	AV697319	C 641	21	38.2	310	13	BG995013	BG995013 MR4-HT105
C 569	22	40.0	704	10	AV683192	AV683192	C 642	21	38.2	311	9	A1198718	A1198718 qf78b02.x
C 570	22	40.0	708	10	AV684276	AV684276	643	21	38.2	313	10	AV754619	AV754619 AV754619
C 571	22	40.0	708	17	AQ740332	HS 5501_A	C 644	21	38.2	315	9	A1300628	A1300628 q021c11.x
C 572	22	40.0	712	12	EG569919	602590562	C 645	21	38.2	324	9	A1343421	A1343421 nc19d08.s
C 573	22	40.0	713	10	AV696227	AV696227	646	21	38.2	324	9	AA226620	AA226620 nc19d08.s
C 574	22	40.0	716	17	AG011336	Homo sapi	C 647	21	38.2	331	9	A1147087	A1147087 ok33e12.s
C 575	22	40.0	717	10	AV697321	AV697321	C 648	21	38.2	332	13	BG977421	BG977421 PM1-C1015
C 576	22	40.0	725	17	AG011323	Homo sapi	C 649	21	38.2	332	17	AQ531074	AQ531074 RPCI-11-3
C 577	22	40.0	734	17	AG102918	Pan trogl	650	21	38.2	335	14	M78032	M78032 EST01619.H1
C 578	22	40.0	734	17	AG102918	Pan trogl	C 651	21	38.2	338	17	AQ088667	AQ088667 HS 22335_B
C 579	22	40.0	735	17	AG144447	Pan trogl	C 652	21	38.2	340	14	H93453	H93453 yu57a12.r1
C 580	22	40.0	753	17	AQ896801	HS 3184_A	C 653	21	38.2	346	10	AV732537	AV732537 AV732537
C 581	22	40.0	890	14	BQ230601	AGENCYCOURT	C 654	21	38.2	353	17	AQ552922	AQ552922 RPCI-11-4
C 582	22	40.0	908	12	BG181036	602329141	C 655	21	38.2	355	12	BF842194	BF842194 RC6-HT084
C 583	22	40.0	942	13	BI113842	602861073	C 656	21	38.2	356	12	BF903107	BF903107 CM3-WT019
C 584	22	40.0	1011	14	BQ943906	AGENCYCOURT	C 657	21	38.2	357	14	H91361	H91361 yu87e03.r1
C 585	22	40.0	1712	11	AF119914	Homo sapi	C 658	21	38.2	357	14	R64046	R64046 y122b04.r1
C 586	21	38.2	107	9	AA564523	nh21e12.s	659	21	38.2	358	12	BF871414	BF871414 IL3-ET011
C 587	21	38.2	119	13	BG985326	PMO-CN015	660	21	38.2	358	17	AQ665179	AQ665179 HS 5344_B
C 588	21	38.2	127	12	BF856443	RCO-FN020	661	21	38.2	359	9	AA640359	AA640359 nr21h12.s
C 589	21	38.2	127	14	BQ345849	PMO-WT031	C 662	21	38.2	361	12	BF897181	BF897181 IL2-WT017
C 590	21	38.2	155	10	BE085073	RC5-BT066	663	21	38.2	361	17	AQ111390	AQ111390 CIT-HSP-2

664	21	38.2	363	17	AQ084492	AQ084492 HS 2252.A	737	21	38.2	443	17	BH141050	BH141050 UP 310-11
665	21	38.2	365	17	AQ349192	AQ349192 RC111-13	738	21	38.2	443	17	AQ589759	AQ589759 HS 2117.B
666	21	38.2	366	14	EQ328821	EQ328821 QV4-EN004	739	21	38.2	444	13	BI481020	BI481020 HZPE-087
667	21	38.2	367	14	H54457	H54457 YQ91907.s1	740	21	38.2	444	17	AQ218824	AQ218824 HS 2004.A
668	21	38.2	368	17	AQ132644	AQ132644 HS 3057.A	741	21	38.2	445	9	AI038726	AI038726 ox35f10.s
669	21	38.2	369	9	A1699049	A1699049 tx74d06.x	742	21	38.2	445	9	AA460924	AA460924 xz61b09.s
670	21	38.2	370	9	AA347382	AA347382 EST53673	743	21	38.2	446	9	AL700830	AL700830 DKZ2p661
671	21	38.2	371	9	AA230159	AA230159 nc38d10.s	744	21	38.2	447	9	AI433833	AI433833 til7a07.x
672	21	38.2	372	17	B93239	B93239 CIT-HSP-217	745	21	38.2	448	17	BH367106	BH367106 UP 295-16
673	21	38.2	373	10	AW276741	AW276741 xp65c09.x	746	21	38.2	449	9	AI471480	AI471480 ta20g06.x
674	21	38.2	374	9	A1224619	A1224619 qw36g09.x	747	21	38.2	451	9	AI096395	AI096395 qb91g08.x
675	21	38.2	375	9	A1494488	A1494488 qz16d03.x	748	21	38.2	451	9	AI650702	AI650702 wb25f10.x
676	21	38.2	376	17	B90423	B90423 CIT-HSP-216	749	21	38.2	453	17	AQ020765	AQ020765 CIT-HSP-2
677	21	38.2	377	9	AA569315	AA569315 nm31h05.s	750	21	38.2	454	10	AW834472	AW834472 MR2-TT001
678	21	38.2	378	17	AQ214890	AQ214890 HS 3059.B	751	21	38.2	455	17	AQ242743	AQ242743 HS 2058.B
679	21	38.2	379	12	BF915728	BF915728 MR3-UT012	752	21	38.2	456	14	R97987	R97987 YQ75b01.s1
680	21	38.2	380	14	H51593	H51593 YQ32g02.r1	753	21	38.2	457	17	AQ040970	AQ040970 CIT-HSP-2
681	21	38.2	381	14	T26396	T26396 AB164F4R In	754	21	38.2	458	9	AI791137	AI791137 ab95c08.x
682	21	38.2	382	14	BO693971	BO693971 1000114.H	755	21	38.2	460	9	AA158787	AA158787 zo63c11.s
683	21	38.2	383	9	AA714733	AA714733 nw30a08.s	756	21	38.2	462	9	AA658863	AA658863 nt84b07.s
684	21	38.2	384	17	AQ342425	AQ342425 RPC111-11	757	21	38.2	463	14	H30475	H30475 yo58c01.r1
685	21	38.2	385	17	AQ411300	AQ411300 HS 5071.B	758	21	38.2	463	17	AQ765103	AQ765103 HS 3153.B
686	21	38.2	386	17	F23264	F23264 HSPD13207.H	759	21	38.2	463	17	AQ637211	AQ637211 RPC1-11-4
687	21	38.2	387	9	AA525522	AA525522 ni33d09.s	760	21	38.2	465	9	AA721998	AA721998 zh17e05.s
688	21	38.2	388	10	AV655267	AV655267 AV655267	761	21	38.2	469	17	AQ729762	AQ729762 HS 2133.A
689	21	38.2	389	14	R99851	R99851 YQ69h11.r1	762	21	38.2	470	17	AQ524022	AQ524022 HS 5224.A
690	21	38.2	390	10	EQ946252	EQ946252 AGENCOURT	763	21	38.2	473	14	R99852	R99852 yq69h11.s1
691	21	38.2	391	13	BI049547	BI049547 IL5-NG024	764	21	38.2	473	14	AI016881	AI016881 HS 3213.A
692	21	38.2	392	17	AQ093299	AQ093299 HS 3018.A	765	21	38.2	473	17	AQ588668	AQ588668 CITBI-E1
693	21	38.2	393	17	AQ630254	AQ630254 RPC1-11-4	766	21	38.2	475	17	B50249	B50249 CIT-HSP-247
694	21	38.2	394	17	AQ531108	AQ531108 RPC1-11-3	767	21	38.2	476	17	AQ147453	AQ147453 HS 3070.A
695	21	38.2	395	17	AQ166650	AQ166650 HS 3148.A	768	21	38.2	477	12	BG164052	BG164052 G02341071
696	21	38.2	396	9	AA406668	AA406668 zv09g11.s	769	21	38.2	477	13	BI013263	BI013263 PM4-ET015
697	21	38.2	397	17	AQ495244	AQ495244 HS 5143.B	770	21	38.2	480	17	R44148	R44148 HS -1058-B2-
698	21	38.2	398	10	AA350087	AA350087 EST57440	771	21	38.2	481	14	R98221	R98221 YQ75b01.r1
699	21	38.2	399	10	AA080057	AA080057 xg48b07.x	772	21	38.2	482	14	N26037	N26037 yx89c01.s1
700	21	38.2	400	9	AA806405	AA806405 oc27b12.s	773	21	38.2	482	17	AQ712614	AQ712614 HS 2134.A
701	21	38.2	401	9	AA827756	AA827756 ob59g01.s	774	21	38.2	483	13	BM312571	BM312571 ig76c08.y
702	21	38.2	402	17	AQ153556	AQ153556 HS 2242.B	775	21	38.2	483	17	AQ734019	AQ734019 HS 2151.A
703	21	38.2	403	12	BF934706	BF934706 IL2-NT020	776	21	38.2	484	14	N67821	N67821 za04h11.s1
704	21	38.2	404	14	N24668	N24668 yx90f11.s1	777	21	38.2	484	17	AQ393054	AQ393054 CITBI-E1
705	21	38.2	405	17	AQ889852	AQ889852 HS 2199.B	778	21	38.2	487	17	B72461	B72461 RPC111-8P13
706	21	38.2	406	13	BI024433	BI024433 CM3-MT029	779	21	38.2	492	12	BE888651	BE888651 G01513046
707	21	38.2	407	10	AV759911	AV759911 AV759911	780	21	38.2	495	17	AQ531096	AQ531096 RPC1-11-3
708	21	38.2	408	9	AA640990	AA640990 nr27g08.r	781	21	38.2	496	10	AW156911	AW156911 au89e03.x
709	21	38.2	409	9	AA6461227	AA6461227 xz61b09.r	782	21	38.2	499	13	BM142609	BM142609 QV3-KT001
710	21	38.2	410	10	AW300650	AW300650 xk03d12.x	783	21	38.2	500	12	BF736906	BF736906 QV3-KT001
711	21	38.2	411	17	B63136	B63136 CIT978SK-A-	784	21	38.2	501	14	N74620	N74620 za55b06.s1
712	21	38.2	412	17	BF741641	BF741641 CM4-HS002	785	21	38.2	501	17	AQ417519	AQ417519 RPC1-11-1
713	21	38.2	413	12	BF741641	BF741641 CM4-HS002	786	21	38.2	501	17	N70251	N70251 za55c10.s1
714	21	38.2	414	17	AQ039353	AQ039353 CIT-HSP-2	787	21	38.2	503	14	AQ727945	AQ727945 HS 5438.B
715	21	38.2	415	10	AW571685	AW571685 xx36c04.x	788	21	38.2	503	17	BQ037756	BQ037756 HS 5056.B
716	21	38.2	416	9	AA074096	AA074096 zf78a06.s	789	21	38.2	504	14	BQ025859	BQ025859 UT-1-BB1P
717	21	38.2	417	10	AA074096	AA074096 zf78a06.s	790	21	38.2	504	14	BH152879	BH152879 UP 297-17
718	21	38.2	418	14	H99483	H99483 YX25c02.s1	791	21	38.2	506	17	AQ590149	AQ590149 HS 2126.A
719	21	38.2	419	17	AQ165554	AQ165554 HS 3011.B	792	21	38.2	508	14	H81519	H81519 yu61h04.r1
720	21	38.2	420	17	AQ147452	AQ147452 HS 3070.A	793	21	38.2	508	17	AQ622943	AQ622943 HS 5351.A
721	21	38.2	421	17	AA693988	AA693988 z148a09.s	794	21	38.2	509	9	AI523959	AI523959 tg98f09.x
722	21	38.2	422	17	AQ787447	AQ787447 HS 3224.B	795	21	38.2	509	10	AV718842	AV718842 CIT-HSP-2
723	21	38.2	423	14	H93454	H93454 yu57a12.s1	796	21	38.2	509	17	AQ062552	AQ062552 CIT-HSP-2
724	21	38.2	424	17	AQ059328	AQ059328 CIT-HSP-2	797	21	38.2	509	17	AQ771989	AQ771989 HS 5413.B
725	21	38.2	425	17	AA135488	AA135488 zo28g06.s	798	21	38.2	509	17	AQ264678	AQ264678 CITBI-E1
726	21	38.2	426	9	AI135488	AI135488 zo28g06.s	799	21	38.2	509	17	AA171399	AA171399 zp33a05.s
727	21	38.2	427	9	AI1700365	AI1700365 wd07b04.x	800	21	38.2	513	9	AA171399	AA171399 zp33a05.s
728	21	38.2	428	10	AW977899	AW977899 EST390008	801	21	38.2	514	17	AQ721134	AQ721134 HS 5557.A
729	21	38.2	429	10	AQ311458	AQ311458 CITBI-E1	802	21	38.2	516	17	AQ214501	AQ214501 HS 3243.B
730	21	38.2	430	17	AA854903	AA854903 PM0-CT026	803	21	38.2	517	17	AQ581110	AQ581110 RPC1-11-4
731	21	38.2	431	10	AI004740	AI004740 ou04f03.x	804	21	38.2	517	17	AQ691287	AQ691287 HS 5358.A
732	21	38.2	432	9	AI004740	AI004740 ou04f03.x	805	21	38.2	518	17	AQ760344	AQ760344 HS 3028.A
733	21	38.2	433	17	AQ088547	AQ088547 HS 3000.A	806	21	38.2	518	17	AQ880778	AQ880778 HS 5059.A
734	21	38.2	434	17	AQ227371	AQ227371 HS 2017.B	807	21	38.2	520	17	AQ186785	AQ186785 HS 3109.B
735	21	38.2	435	17	B89067	B89067 CIT-HSP-217	808	21	38.2	520	17	AW375925	AW375925 RC2-CT020
736	21	38.2	436	17	B65515	B65515 CIT-HSP-202	809	21	38.2	525	10	BQ640757	BQ640757 hs32g10.y

810	21	38.2	532	17	AQ019256	CIT-HSP-2	AQ019256	CIT-HSP-2	883	21	38.2	682	17	AG075285	AG075285 Pan trogl
C 811	21	38.2	536	13	B1017697	MR4-ET013	B1017697	MR4-ET013	884	21	38.2	684	17	AG170364	AG170364 Pan trogl
C 812	21	38.2	539	9	A1091278	owG2b10.x	A1091278	owG2b10.x	885	21	38.2	687	17	AG154132	AG154132 Pan trogl
C 813	21	38.2	539	17	AQ429382	CITBI-E1-	AQ429382	CITBI-E1-	886	21	38.2	688	17	AG062661	AG062661 Pan trogl
C 814	21	38.2	540	17	AQ679599	HS 5346.A	AQ679599	HS 5346.A	887	21	38.2	692	10	BE397160	BE397160 60120852
C 815	21	38.2	541	10	BE390700		BE390700		888	21	38.2	696	17	AG159631	AG159631 Pan trogl
C 816	21	38.2	541	17	AQ719752	HS 5544.A	AQ719752	HS 5544.A	889	21	38.2	704	17	AG092502	AG092502 Pan trogl
C 817	21	38.2	543	10	AW376024	RC2-CT020	AW376024	RC2-CT020	890	21	38.2	704	17	AG085773	AG085773 Pan trogl
C 818	21	38.2	545	10	AW835295	QV0-LT001	AW835295	QV0-LT001	C 891	21	38.2	709	17	AQ379867	AQ379867 RPiC11-16
C 819	21	38.2	546	9	A1903466	RC-BT029-	A1903466	RC-BT029-	C 892	21	38.2	710	17	AG002493	AG002493 Homo sapi
C 820	21	38.2	548	9	A1903342	RC-BT029-	A1903342	RC-BT029-	C 893	21	38.2	711	17	AG002492	AG002492 Homo sapi
C 821	21	38.2	549	17	AQ673632	HS 5481.B	AQ673632	HS 5481.B	C 894	21	38.2	711	17	AG144362	AG144362 Pan trogl
C 822	21	38.2	550	17	AQ779553	HS 3001.A	AQ779553	HS 3001.A	C 895	21	38.2	714	14	BM979083	BM979083 UI-CF-DU1
C 823	21	38.2	553	13	B1014701		B1014701		896	21	38.2	728	17	AG139892	AG139892 Pan trogl
C 824	21	38.2	560	9	AA207152	zq84b04.s	AA207152	zq84b04.s	897	21	38.2	729	9	A1133721	A1133721 HA2346.Hu
C 825	21	38.2	561	10	AW851451		AW851451		898	21	38.2	730	17	AV708236	AV708236 AV708236
C 826	21	38.2	561	17	AQ391161	CITBI-E1-	AQ391161	CITBI-E1-	899	21	38.2	736	17	AG104187	AG104187 Pan trogl
C 827	21	38.2	562	17	AQ311380		AQ311380		900	21	38.2	737	17	AQ888919	AQ888919 HS 3100.A
C 828	21	38.2	565	17	AQ231371	HS 2027.B	AQ231371	HS 2027.B	901	21	38.2	742	12	BG402743	BG402743 602418407
C 829	21	38.2	566	17	AQ514219	HS 5184.B	AQ514219	HS 5184.B	902	21	38.2	745	17	AG031599	AG031599 Pan trogl
C 830	21	38.2	566	17	AQ542989	RPCI-11-3	AQ542989	RPCI-11-3	903	21	38.2	746	12	BE877847	BE877847 601489324
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C 834	21	38.2	582	17	AQ632117	RPCI-11-4	AQ632117	RPCI-11-4	907	21	38.2	766	17	AQ749899	AQ749899 HS 5573.A
C 835	21	38.2	584	17	AQ552982		AQ552982		C 908	21	38.2	768	9	AI903408	AI903408 RC-BT029-
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C 838	21	38.2	592	17	AQ771958	HS 5413.B	AQ771958	HS 5413.B	C 911	21	38.2	776	13	BI333658	BI333658 602999118
C 839	21	38.2	593	12	EG484873		EG484873		912	21	38.2	788	13	BI870254	BI870254 603393756
C 840	21	38.2	595	17	AQ380872	RPCI11-16	AQ380872	RPCI11-16	C 913	21	38.2	789	9	AI903449	AI903449 RC-BT029-
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C 844	21	38.2	602	17	B58317		B58317		C 917	21	38.2	815	12	EG400842	EG400842 602464065
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C 848	21	38.2	608	17	AQ563385	HS 5302.A	AQ563385	HS 5302.A	921	21	38.2	897	12	BG533381	BG533381 601860768
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C 851	21	38.2	621	17	AQ881021		AQ881021		924	21	38.2	918	12	EG403431	EG403431 602419116
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C 853	21	38.2	625	9	AL523643		AL523643		C 926	21	38.2	924	13	BI772030	BI772030 603058885
C 854	21	38.2	627	14	BQ712185	AGENCOURT	BQ712185	AGENCOURT	927	21	38.2	927	17	AQ743709	AQ743709 HS 5507.A
C 855	21	38.2	631	17	AQ237934		AQ237934		928	21	38.2	931	12	BF031034	BF031034 601558911
C 856	21	38.2	635	17	AG133268		AG133268		C 929	21	38.2	941	14	BQ710423	BQ710423 AGENCOURT
C 857	21	38.2	636	17	AG066329		AG066329		930	21	38.2	955	14	BQ999033	BQ999033 AGENCOURT
C 858	21	38.2	638	13	BM007682		BM007682		931	21	38.2	976	14	BQ956832	BQ956832 AGENCOURT
C 859	21	38.2	638	17	AQ768775		AQ768775		C 932	21	38.2	985	14	BQ883445	BQ883445 AGENCOURT
C 860	21	38.2	643	17	AG122019	Pan trogl	AG122019	Pan trogl	933	21	38.2	1002	13	BM473164	BM473164 AGENCOURT
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C 863	21	38.2	644	17	AG017592	Homo sapi	AG017592	Homo sapi	936	21	38.2	1154	12	BG112891	BG112891 602285093
C 864	21	38.2	648	12	BG484168		BG484168		C 937	21	38.2	1236	14	BQ432831	BQ432831 AGENCOURT
C 865	21	38.2	649	17	AG017591	Homo sapi	AG017591	Homo sapi	938	21	38.2	1520	13	BM558118	BM558118 AGENCOURT
C 866	21	38.2	649	17	AG017593	Homo sapi	AG017593	Homo sapi	939	21	38.2	2871	11	BC026029	BC026029 Homo sapi
C 867	21	38.2	649	17	AG064568		AG064568		C 940	20	36.4	108	10	BE244605	BE244605 TCBA2E08
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C 870	21	38.2	655	17	AQ284316		AQ284316		C 943	20	36.4	140	12	BF901310	BF901310 IL2-WT017
C 871	21	38.2	658	17	AG088933	Pan trogl	AG088933	Pan trogl	944	20	36.4	160	13	BI030697	BI030697 IL5-WT026
C 872	21	38.2	660	14	BQ020061		BQ020061		C 945	20	36.4	173	13	BI029484	BI029484 IL5-WT026
C 873	21	38.2	662	17	AG149255	Pan trogl	AG149255	Pan trogl	C 946	20	36.4	180	14	F05220	F05220 HSC04B121.n
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C 875	21	38.2	663	17	AG080702		AG080702		948	20	36.4	192	9	AI255004	AI255004 qv48c12.x
C 876	21	38.2	664	17	AQ062179		AQ062179		C 949	20	36.4	196	13	BI003351	BI003351 PM0-HN007
C 877	21	38.2	668	17	AQ261203	CITBI-E1-	AQ261203	CITBI-E1-	C 950	20	36.4	201	9	AA218911	AA218911 zq15f05.s
C 878	21	38.2	671	9	AA630096		AA630096		951	20	36.4	209	10	AW864296	AW864296 PM4-SN001
C 879	21	38.2	672	17	AQ110663	CIT-HSP-2	AQ110663	CIT-HSP-2	C 952	20	36.4	212	9	AL044042	AL044042 DKFZp434K
C 880	21	38.2	673	13	BI160652		BI160652		C 953	20	36.4	215	12	BF923476	BF923476 IL0-WT023
C 881	21	38.2	675	17	AQ378745		AQ378745		954	20	36.4	230	12	BF996130	BF996130 RC3-GN004
C 882	21	38.2	680	10	AV700695	AV700695	AV700695	AV700695	955	20	36.4	231	9	AA528570	AA528570 nf01h03.s

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960 20 36.4 237 10 BE068256 MR0-BT0037
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965 20 36.4 255 12 BF838567 IL5-HT099
966 20 36.4 256 9 AA806212 oe29e01.s
967 20 36.4 273 9 AA669706 ac23c11.s
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978 20 36.4 283 17 AQ390852 CITBI-E1-
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989 20 36.4 309 13 BI492411 df23g11.w
990 20 36.4 314 17 AQ091805 HS-2208.A
991 20 36.4 316 12 BF80764 QV3-ET017
992 20 36.4 324 9 AA745191 nw15f10.s
993 20 36.4 327 17 AQ087044 HS-2236.A
994 20 36.4 329 12 BF900875 IL2-MT017
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ALIGNMENTS

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RESULT 1
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LOCUS 60240986P1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4537892 5',
DEFINITION mRNA sequence.
ACCESSION BG284780
VERSION BG284780.1 GI:13036079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 388)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DFP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10463 row: 1 column: 21
High quality sequence stop: 388.
Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 118 a 96 c 107 g 67 t
ORIGIN
Query Match 65.5%; Score 36; DB 12; Length 388;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
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Db 141 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 176
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LOCUS UI-HF-BNO-akt-d-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
DEFINITION IMAGE:3078210 5', mRNA sequence.
ACCESSION AW503185
VERSION AW503185.1 GI:7118344
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
The following repetitive elements were found in this cDNA
sequence:
7-205, >ALU 123-412, >ALU
Seq primer: M13 Forward.
Location/Qualifiers
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/lab_host="DH10B (LTI)"
/note="vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de

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BASE COUNT      103 a 108 c 124 g 77 t
ORIGIN
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RESULT 3
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LOCUS      AQ582126          574 bp      DNA      linear      GSS 07-JUN-1999
DEFINITION      RPCI-11-460L9-TV RPCI-11 Homo sapiens genomic clone RPCI-11-460L9,
                DNA sequence.
ACCESSION      AQ582126
VERSION      AQ582126.1 GI:5009236
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 574)
AUTHORS      Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                J.C.
TITLE      Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                Map Building
JOURNAL      Unpublished (1997)
COMMENT      Other GSSs: RPCI-11-460L9.TJ
                Contact: Shaying Zhao, William Nierman, Mark Adams
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Dr., Rockville, MD 20850
                Tel: 301 838 0200
                Fax: 301 838 0208
                Email: hbe@tigr.org
                Clones are derived from the human BAC library RPCI-11. For BAC
                library availability, please contact Pieter de Jong
                (pieter@jeong.med.buffalo.edu). Clones may be purchased from
                BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
                Research Genet cs (info@resgen.com). BAC end search page:
                http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
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                Class: BAC ends.
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BASE COUNT      176 a 127 c 116 g 155 t
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    Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 239 TGAGGTGAGGAATTCGAGATCAGCTGGCCCAACATG 274

RESULT 4
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LOCUS      AU119400          814 bp      mRNA      linear      EST 01-AUG-2002
DEFINITION      HRI human cDNA project
                Unpublished (2000)
                Contact: Takao Isogai
                Genomics Laboratory
                Helix Research Institute
                1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                Tel: 81-438-52-3975
                Fax: 81-438-52-3986
                Email: genomics@hri.co.jp
                HRI human cDNA project
                Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
                Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                Isogai,T.
TITLE      HRI human cDNA project
JOURNAL      Unpublished (2000)
COMMENT      Contact: Takao Isogai
                Genomics Laboratory
                Helix Research Institute
                1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                Tel: 81-438-52-3975
                Fax: 81-438-52-3986
                Email: genomics@hri.co.jp
                HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

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DEFINITION      AU119400 HEMBA1 Homo sapiens cDNA clone HEMBA1005720 5', mRNA
                sequence.
ACCESSION      AU119400
VERSION      AU119400.1 GI:10934635
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 814)
AUTHORS      Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
                Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                Isogai,T.
TITLE      HRI human cDNA project
JOURNAL      Unpublished (2000)
COMMENT      Contact: Takao Isogai
                Genomics Laboratory
                Helix Research Institute
                1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                Tel: 81-438-52-3975
                Fax: 81-438-52-3986
                Email: genomics@hri.co.jp
                HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
                Research Institute; cDNA library construction: Department of
                Virology, Institute of Medical Science, University of Tokyo, and
                Helix Research Institute.
FEATURES             Location/Qualifiers
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                /clone_lib="HEMBA1"
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                /dev_stage="embryo, 10 weeks"
                /note="Vector: pME18SFL3"
BASE COUNT      218 a 186 c 225 g 181 t
ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 5.2e-07;
    Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTGAGGAATTCGAGATCAGCTGGCCCAACATG 53
    |||||||
Db 583 TGAGGTGAGGAATTCGAGATCAGCTGGCCCAACATG 618

RESULT 5
AU119141
LOCUS      AU119141 HEMBA1 Homo sapiens cDNA clone HEMBA1005123 5', mRNA
DEFINITION      AU119141 HEMBA1 Homo sapiens cDNA clone HEMBA1005123 5', mRNA
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ACCESSION      AU119141
VERSION      AU119141.1 GI:10934376
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 824)
AUTHORS      Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
                Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                Isogai,T.
TITLE      HRI human cDNA project
JOURNAL      Unpublished (2000)
COMMENT      Contact: Takao Isogai
                Genomics Laboratory
                Helix Research Institute
                1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                Tel: 81-438-52-3975
                Fax: 81-438-52-3986
                Email: genomics@hri.co.jp
                HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

```

Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers

1. .824
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1005123"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mainly head"
/dev_stages="embryo, 10 weeks"
/note="Vector: pME185FL3"
227 a 185 c 226 g 183 t 3 others

BASE COUNT

227 a 185 c 226 g 183 t 3 others

ORIGIN

Query Match 65.5%; Score 36; DB 9; Length 824;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
|||||

Db 583 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 618
|||||

RESULT 6

LOCUS

BO643665 933 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8302262 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6271131
5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L10M2447 row: g column: 04
High quality sequence stop: 432.

FEATURES

source

1. .933
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6271131"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT

257 a 204 c 244 g 226 t 2 others

ORIGIN

Query Match 65.5%; Score 36; DB 14; Length 933;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
|||||

Db 624 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 659
|||||

RESULT 7

LOCUS

AQ460151 528 bp DNA linear GSS 23-APR-1999
HS 5125_B2_C04_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=701 Col=8 Row=F, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 528)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

JOURNAL

MEDLINE

COMMENT

93380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>)
or from Resear h Genetics (inforesgen.com). BAC end Web Server:
<http://www.htsc.washington.edu>
Plate: 701 row: F column: 8
Seq primer: T7
Class: BAC ends

FEATURES

source

High quality sequence stop: 528.
Location/Qualifiers
1. .528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=701 Col=8 Row=F"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

BASE COUNT 168 a 113 c 138 g 107 t 2 others

ORIGIN

Query Match 58.2%; Score 32; DB 17; Length 528;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTCAGGAATTCGAGATCAGCTGGCCCA 49
|||||

Db 193 TGAGGTCAGGAATTCGAGATCAGCTGGCCCA 224
|||||

RESULT 8

LOCUS

AQ298954 569 bp DNA linear GSS 15-DEC-1998
HS 3171_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3171 Col=12 Row=N, DNA sequence.

```

ACCESSION AQ298954
VERSION AQ298954.1 GI:4016133
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 569)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 9380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3171 row: N column: 12
Class: BAC ends
High quality sequence stop: 569.
Location/Qualifiers
1..569
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_plate="3171 Col=12 Row=N"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli 'DH10B'"

BASE COUNT 165 a 113 c 143 g 140 t 8 others
ORIGIN

Query Match 58.2%; Score 32; DB 17; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GTCAGGAATTCGAGATCAGCTGCGCAACATG 53
|||||
Db 172 GTCAGGAATTCGAGATCAGCTGCGCAACATG 203
|||||

RESULT 9
BE279465/c
LOCUS BE279465 751 bp mRNA linear EST 13-JUL-2000
DEFINITION 601158078F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504906 5',
mRNA sequence.
ACCESSION BE279465
VERSION BE279465.1 GI:9154458
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 751)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM80 row: k column: 19
High quality sequence stop: 618.

```

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FEATURES
source
Location/Qualifiers
1..751
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3504906"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 166 a 168 c 211 g 206 t
ORIGIN

Query Match 58.2%; Score 32; DB 10; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGTCAGGAATTCGAGATCAGCTGG 45
|||||
Db 532 CACTTGAGTCAGGAATTCGAGATCAGCTGG 501
|||||

RESULT 10
BF927015
LOCUS BF927015 465 bp mRNA linear EST 19-JAN-2001
DEFINITION CM2-NT0192-051200-577-el0 NT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF927015
VERSION BF927015.1 GI:12324871
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 465)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NT0192-
051200-577-el0&t3=2000-12-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 103
High quality sequence stop: 461.
Location/Qualifiers
1..465
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0192"
/dev_stage="Adult"
/note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products

```

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
ORIGIN

148 a 109 c 112 g 96 t

Query Match 56.4%; Score 31; DB 12; Length 465;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGTTCAGGAATTCGAGATCAGCTGGCCA 48
Db 369 TGAGTTCAGGAATTCGAGATCAGCTGGCCA 399

RESULT 11
LOCUS AW834360/c 361 bp mRNA linear EST 18-MAY-2000
DEFINITION MR2-TT0013-211199-017-a08 TT0013 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW834360
VERSION AW834360.1 GI:7928334
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 361)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.U. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
PROC Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL 20202663
MEDLINE
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR2-TT0013-211199-017-a08&t3=1999-11-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 124.

FEATURES
source
1. 361
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="TT0013"
/dev_stages="Adult"
/note="Organ: testis; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 91 a 98 c 84 g 88 t

ORIGIN

Query Match 54.5%; Score 30; DB 10; Length 361;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTCAGGTTCAGGAATTCGAGATCAGCCT 43
Db 78 CACTTCAGGTTCAGGAATTCGAGATCAGCCT 49

RESULT 12

LOCUS BE395693 625 bp mRNA linear EST 21-JUL-2000

DEFINITION 601309693F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631223 5', mRNA sequence.

ACCESSION BE395693

VERSION BE395693.1 GI:9341058

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 625)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov

Source Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LNCM320 row: j column: 24

High quality sequence stop: 614.

FEATURES

source
1. 625

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3631223"

/clone_lib="NIH_MGC_44"

/tissue_type="endometrium, adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 168 a 140 c 179 g 138 t

ORIGIN

Query Match 52.7%; Score 29; DB 10; Length 625;

Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGTTCAGGAATTCGAGATCAGCCTGGC 46

Db 549 TGAGTTCAGGAATTCGAGATCAGCCTGGC 577

RESULT 13

LOCUS BQ331585 108 bp mRNA linear EST 17-MAY-2002

DEFINITION PM3-ET0262-070501-017-e04_1 ET0262 Homo sapiens cDNA, mRNA

ACCESSION BQ331585

VERSION BQ331585.1 GI:20972750

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 108)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM3&t2=PM3-ET0262-070501-017-e04.l&t3=2001-05-07&t4=1>)

Seq primer: pUC18 forward.

FEATURES

source

1..108
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0262"
/dev_stage="Adult"

/note="Organ: lung_tumor; Vector: puc18; Site1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

31 a 27 c 31 g 19 t

ORIGIN

Query Match 50.9%; Score 28; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

26 GGAATTCGAGATCAGCTGGCCACATG 53

|||||

Db

22 GGAATTCGAGATCAGCTGGCCACATG 49

RESULT 14

AQ467676

LOCUS

DEFINITION HS 5203 B1 A05 SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic_clone Plate=779 Col=9 Row=B, DNA sequence.

ACCESSION

AQ467676

VERSION

GSS.

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

MEDLINE

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

<http://www.htsc.washington.edu>

Plate: 779 row: B column: 9

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 175.

Location/Qualifiers

source

1..175

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate=779 Col=9 Row=B"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="vector: pBAC3.6; Site1: EcoRI; Site 2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBAC3.6 vector at EcoRI sites"

52 a 38 c 46 g 39 t

BASE COUNT

ORIGIN

Query Match 50.9%; Score 28; DB 17; Length 175;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GAGCAGGCGAGCAGCTTGAGGTCAGGA 28

|||||

Db

104 GAGCAGGCGAGCAGCTTGAGGTCAGGA 131

RESULT 15

AQ412104/c

LOCUS

DEFINITION

RPCI-11-198P7.TV RPCI-11 Homo sapiens genomic clone RPCI-11-198P7,

DNA sequence.

ACCSSION

AQ412104

VERSION

AQ412104.1 GI:4471592

KEYWORDS

GSS;

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 302)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready

Map Building

Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@igr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.

Seg primer: T7

Class: BAC ends.

Location/Qualifiers

1..302

/organism="Homo sapiens"

/db_xref="GDB:7576014"

```

/db_xref="taxon:9606"
/clone="RPCI-11-198P7"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC111 Human Male BAC Library"
BASE COUNT      82 a      71 c      60 g      89 t
ORIGIN
Query Match      50.9%; Score 28; DB 17; Length 302;
Best Local Similarity 100.0%; Pred.No: 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GAGCAGGCAGACACTTGAGGTCAGGA 28
      |||||
Db      141 GAGCAGGCAGACACTTGAGGTCAGGA 114
Search completed: June 17, 2003, 06:23:23
Job time : 116.75 secs

```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 42.3809 Seconds
(without alignments)
15794.017 Million cell updates/sec

Title: US-09-513-888c-1_COPY_4451_4473

Perfect score: 23

Sequence: 1 cagccaggcatggtgacagtggt 23

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	23	100.0	9108	9	AF123653	AF123653 Homo sapi
2	23	100.0	173264	2	AC025853	AC025853 Homo sapi
C 3	23	100.0	177568	9	HS388M5	Z97055 Human DNA s
4	22	95.7	1821	9	AB046623	AB046623 Macaca fa
5	22	95.7	2787	9	AB052149	AB052149 Macaca fa
C 6	22	95.7	4913	9	AL451072	AL451072 Human DNA
7	22	95.7	39151	9	AP000535	AP000535 Homo sapi
8	22	95.7	39668	9	AP000536	AP000536 Homo sapi
9	22	95.7	40102	9	AC010647	AC010647 Homo sapi
10	22	95.7	41159	9	AC004755	AC004755 Homo sapi
11	22	95.7	41576	9	HSN128A12	Z75407 Human DNA s
12	22	95.7	44767	9	AL669893	AL669893 Human DNA
C 13	22	95.7	54154	9	AL583845	AL583845 Human DNA
14	22	95.7	56652	2	AC027427	AC027427 Homo sapi
15	22	95.7	62833	2	AC107942	AC107942 Homo sapi
16	22	95.7	68035	9	AL158199	AL158199 Human DNA
17	22	95.7	69415	2	AC107916	AC107916 Homo sapi
18	22	95.7	70384	2	AC084263	AC084263 Homo sapi
19	22	95.7	77027	9	AL161792	AL161792 Human DNA
C 20	22	95.7	77237	2	AC022599	AC022599 Homo sapi
C 21	22	95.7	79018	9	AL627107	AL627107 Human DNA
C 22	22	95.7	82732	9	AL512347	AL512347 Human DNA
C 23	22	95.7	83750	9	AL359390	AL359390 Human DNA
24	22	95.7	84657	9	AL136378	AL136378 Human DNA
25	22	95.7	85490	2	AC022957	AC022957 Homo sapi
26	22	95.7	87636	9	AL139039	AL139039 Human DNA
C 27	22	95.7	89429	2	AL356304	AL356304 Homo sapi
28	22	95.7	96669	9	AC055720	AC055720 Homo sapi
29	22	95.7	96717	9	AL359182	AL359182 Human DNA
C 30	22	95.7	102714	9	AP000692	AP000692 Homo sapi
31	22	95.7	104660	9	AP000347	AP000347 Homo sapi
32	22	95.7	110000	2	AC008576_1	Continuation (2 of)
33	22	95.7	110000	2	AC008576_2	Continuation (3 of)
C 34	22	95.7	110000	2	AC079517_2	Continuation (3 of)
C 35	22	95.7	111122	2	AC097105	AC097105 Homo sapi
C 36	22	95.7	111187	2	AC009283	AC009283 Homo sapi
C 37	22	95.7	111370	9	AC067815	AC067815 Homo sapi
38	22	95.7	114600	9	HS477H23	AL033538 Human DNA
C 39	22	95.7	115371	9	AC004918	AC004918 Homo sapi
C 40	22	95.7	117000	9	AC117475	AC117475 Homo sapi
C 41	22	95.7	117628	9	AC008891	AC008891 Homo sapi
C 42	22	95.7	120029	2	HSJ282H10	AL132672 Homo sapi
C 43	22	95.7	122889	9	HSDA204F4	AL121878 Human DNA
C 44	22	95.7	124540	9	AL353600	AL353600 Human DNA
45	22	95.7	125780	9	CNS01DWK	AL137229 Human chr
C 46	22	95.7	130753	9	HS510L9	AL022098 Homo sapi
C 47	22	95.7	134362	2	AC084853	AC084853 Homo sapi
C 48	22	95.7	134577	2	AC015680	AC015680 Homo sapi
C 49	22	95.7	135417	9	HSJ412I7	AL132795 Human DNA
C 50	22	95.7	136327	2	AC005845	AC005845 Homo sapi
C 51	22	95.7	137077	9	AC007562	AC007562 Homo sapi
52	22	95.7	137682	9	AC023274	AC023274 Homo sapi
53	22	95.7	138817	2	AC090148	AC090148 Homo sapi
54	22	95.7	140335	9	AC018645	AC018645 Homo sapi
C 55	22	95.7	141220	2	AC024238	AC024238 Homo sapi
C 56	22	95.7	141450	9	CNS05TBX	AL352978 Human chr
57	22	95.7	143968	9	AL138744	AL138744 Human DNA
C 58	22	95.7	145726	2	AC021807	AC021807 Homo sapi
59	22	95.7	145966	9	AC006451	AC006451 Homo sapi
60	22	95.7	146698	2	AC105039	AC105039 Homo sapi
61	22	95.7	146877	2	AC026487	AC026487 Homo sapi
C 62	22	95.7	147492	9	AL358781	AL358781 Human DNA
63	22	95.7	147974	2	AC076970	AC076970 Homo sapi
C 64	22	95.7	148876	9	AC011455	AC011455 Homo sapi
65	22	95.7	149546	9	AC087256	AC087256 Homo sapi

66	22	95.7	150937	9	AL445243	Human DNA	139	22	95.7	210957	2	AL392188	Homo sapi
67	22	95.7	152876	2	AC099488	Homo sapi	140	22	95.7	211748	9	AC010146	Homo sapi
68	22	95.7	152966	9	AL359713	Human DNA	c 141	22	95.7	212505	2	AC027220	Homo sapi
69	22	95.7	154939	9	AC022537	Homo sapi	c 142	22	95.7	215962	9	AC010615	Homo sapi
70	22	95.7	155290	9	AL359175	Human DNA	143	22	95.7	217117	2	AC116438	Pan trogl
71	22	95.7	155226	2	AC013371	Homo sapi	c 144	22	95.7	225428	2	AC115115	Homo sapi
72	22	95.7	155702	9	AC013271	Homo sapi	c 145	22	95.7	226035	9	CNS01DVX	Human chr
73	22	95.7	155786	2	AC027721	Homo sapi	c 146	22	95.7	263839	9	AC117380	Homo sapi
74	22	95.7	156955	9	AL157886	Human DNA	147	22	95.7	284671	2	AC106710	Homo sapi
75	22	95.7	157921	2	AC027726	Homo sapi	c 148	22	95.7	305000	9	HSXDP4	Homo sapi
76	22	95.7	157968	2	AC023438	Homo sapi	c 149	22	95.7	340000	9	AP001725	Homo sapi
77	22	95.7	159384	2	AL356110	Homo sapi	150	21	91.3	51	6	AX159173	Sequence
78	22	95.7	159859	2	AC074010	Homo sapi	151	21	91.3	51	6	AX159174	Sequence
79	22	95.7	161487	2	AC119571	Pan trogl	c 152	21	91.3	170	6	AX322336	Sequence
80	22	95.7	161494	2	AC110495	Homo sapi	153	21	91.3	401	6	AX270245	Sequence
81	22	95.7	161699	9	AC113435	Pan trogl	154	21	91.3	401	6	AX270246	Sequence
82	22	95.7	162208	2	AC073321	Homo sapi	155	21	91.3	401	6	AX270247	Sequence
83	22	95.7	164423	2	AC026828	Homo sapi	156	21	91.3	401	6	AX270248	Sequence
84	22	95.7	164916	9	AC021305	Homo sapi	157	21	91.3	401	6	AX271776	Sequence
85	22	95.7	165090	9	AC010655	Homo sapi	158	21	91.3	401	6	AX271777	Sequence
86	22	95.7	165854	9	AC073043	Homo sapi	159	21	91.3	401	6	AX271778	Sequence
87	22	95.7	166164	2	AC023188	Homo sapi	160	21	91.3	401	6	AX271779	Sequence
88	22	95.7	166186	2	AC109815	Homo sapi	161	21	91.3	441	11	HUMUT5200A	L31121 Human STS U
89	22	95.7	167021	9	AC079414	Homo sapi	162	21	91.3	463	11	HUMUT5408	L18699 Human chrom
90	22	95.7	167195	9	AC009044	Homo sapi	163	21	91.3	476	9	AF512806	Homo sapi
91	22	95.7	168227	9	AC021868	Homo sapi	164	21	91.3	527	6	AX388834	Sequence
92	22	95.7	169342	9	AL136991	Human DNA	165	21	91.3	558	6	AX389815	Sequence
93	22	95.7	170026	2	AC013627	Homo sapi	166	21	91.3	558	6	AX391031	Sequence
94	22	95.7	170520	2	AL358172	Homo sapi	167	21	91.3	581	6	AX390832	Sequence
95	22	95.7	171360	2	AC068543	Homo sapi	168	21	91.3	581	11	G63668	SHGC-141466
96	22	95.7	171731	2	AC091659	Papio cyn	169	21	91.3	1552	9	HO09384S10	AF218898 Homo sapi
97	22	95.7	172573	9	AC007276	Homo sapi	c 170	21	91.3	1561	9	BC007023	Homo sapi
98	22	95.7	173135	9	AC092018	Homo sapi	c 171	21	91.3	1675	9	AK097604	Homo sapi
99	22	95.7	173456	9	AL158198	Human DNA	c 172	21	91.3	1764	9	AK092844	Homo sapi
100	22	95.7	174826	9	AC116562	Homo sapi	c 173	21	91.3	1879	9	AK021739	Homo sapi
101	22	95.7	175064	2	AC012230	Homo sapi	c 174	21	91.3	2049	9	AK094063	Homo sapi
102	22	95.7	175236	2	AC108938	Homo sapi	c 175	21	91.3	2107	9	AB050434	Macaca fa
103	22	95.7	175339	9	AC005772	Homo sapi	c 176	21	91.3	2130	9	F187967S01	AF187967 Homo sapi
104	22	95.7	175403	9	AC093268	Homo sapi	c 177	21	91.3	2443	9	AK055262	Homo sapi
105	22	95.7	175835	2	AC024074	Homo sapi	c 178	21	91.3	2580	9	AK094213	Homo sapi
106	22	95.7	175952	9	AL391872	Human DNA	c 179	21	91.3	2611	9	AK074364	Homo sapi
107	22	95.7	176182	9	AC010845	Homo sapi	c 180	21	91.3	2783	9	D50134	D50134 Homo sapien
108	22	95.7	176544	2	AL138877	Homo sapi	c 181	21	91.3	2852	9	AK092611	Homo sapi
109	22	95.7	178500	2	AL135926	Homo sapi	c 182	21	91.3	2893	9	BC020558	Homo sapi
110	22	95.7	178771	2	AF267168	Homo sapi	c 183	21	91.3	2968	9	HSU52154	U52154 Human G pro
111	22	95.7	179040	2	AC022732	Homo sapi	c 184	21	91.3	2975	9	BC008816	Homo sapi
112	22	95.7	179064	9	AL353807	Human DNA	c 185	21	91.3	2975	9	BC011631	BC011631 Homo sapi
113	22	95.7	181302	9	AC091619	Papio cyn	c 186	21	91.3	3085	9	HUM114D	D55653 Human mRNA
114	22	95.7	182178	9	AL138711	Human DNA	c 187	21	91.3	3172	6	AX330716	Sequence
115	22	95.7	182617	9	AC007731	Homo sapi	c 188	21	91.3	3172	6	AX331138	Sequence
116	22	95.7	184560	2	AC021124	Homo sapi	c 189	21	91.3	3172	9	HSU23942	U23942 Human lanos
117	22	95.7	185279	9	AC007338	Homo sapi	c 190	21	91.3	3180	9	HSU800659	HSU800659
118	22	95.7	188023	10	AL645543	Mouse DNA	c 191	21	91.3	3324	9	AK090602	Homo sapi
119	22	95.7	188622	2	AL359258	Human DNA	c 192	21	91.3	3514	9	AK091323	Homo sapi
120	22	95.7	188736	9	CNS00M8M	Human chr	c 193	21	91.3	3521	9	HUM36DC32	L80203 Homo sapien
121	22	95.7	188833	9	HS268H5	Human DNA	c 194	21	91.3	4337	9	AK096349	Homo sapi
122	22	95.7	189317	9	HS190J20	Human DNA	c 195	21	91.3	4463	9	HUMGUSBA	M65002 Human beta-
123	22	95.7	189610	9	AC104301	Homo sapi	c 196	21	91.3	4734	9	HSPDBACG7	AF157816 Homo sapi
124	22	95.7	190998	9	AC019181	Homo sapi	c 197	21	91.3	5119	9	AF082937	AF082937 Homo sapi
125	22	95.7	191774	2	AC025648	Homo sapi	c 198	21	91.3	5759	9	HUMFEN1GNA	L19896 Human fibri
126	22	95.7	192592	9	AC005500	Homo sapi	c 199	21	91.3	5880	9	AB070559	AB070559 Homo sapi
127	22	95.7	192670	9	AC008592	Homo sapi	c 200	21	91.3	6222	9	AY028318S2	AY028318 Homo sapi
128	22	95.7	195634	2	AC013464	Homo sapi	c 201	21	91.3	6283	9	AY033055S2	AY033055 Homo sapi
129	22	95.7	196541	2	AC091622	Homo sapi	c 202	21	91.3	6306	9	AY028320S2	AY028321 Homo sapi
130	22	95.7	196817	9	AC019209	Homo sapi	c 203	21	91.3	9839	9	HS295622	HS295622 Homo sapi
131	22	95.7	196993	9	CNS01D7T	Human chr	c 204	21	91.3	10315	9	AC104526	AC104526 Homo sapi
132	22	95.7	197310	2	AF254981	Homo sapi	c 205	21	91.3	10318	9	AL662877	AL662877 Human DNA
133	22	95.7	197455	9	AC005701	Homo sapi	c 206	21	91.3	12206	9	HS169F7A	Z69649 Human DNA s
134	22	95.7	197992	2	AC020715	Homo sapi	c 207	21	91.3	12293	6	AX409505	AX409505 Sequence
135	22	95.7	201305	2	AC120051	Homo sapi	c 208	21	91.3	12293	9	HUMC201	L09706 Homo sapien
136	22	95.7	202768	2	AC092345	Homo sapi	c 209	21	91.3	13288	9	AC119795	AC119795 Homo sapi
137	22	95.7	206399	9	AC090376	Homo sapi	c 210	21	91.3	15469	2	AC009067	Homo sapi
138	22	95.7	207767	2	AP001497	Homo sapi	c 211	21	91.3	16090	9	AL354812	Human DNA

C 212	21	91.3	16342	9	HSN85E10	268758 Human DNA s	C 285	21	91.3	40451	9	AL139802	Human DNA
C 213	21	91.3	17429	9	AL445253	AL445253 Human DNA	C 286	21	91.3	40491	9	AC002116	Human DNA
C 214	21	91.3	18228	9	AL772153	AL772153 Human DNA	C 287	21	91.3	40883	9	AC005776	Homo sapi
C 215	21	91.3	20125	9	AC094079	AC094079 Homo sapi	C 288	21	91.3	40962	2	AC006189	Homo sapi
C 216	21	91.3	20539	9	HS349E10	AL022341 Human DNA	C 289	21	91.3	41219	2	AC005382	Homo sapi
C 217	21	91.3	20938	9	AL589942	AL589942 Human DNA	C 290	21	91.3	41300	2	AC003097	Homo sapi
C 218	21	91.3	21249	2	AC004105	AC004105 Homo sapi	C 291	21	91.3	41518	9	AC010515	Homo sapi
C 219	21	91.3	22050	9	AC087243	AC087243 Homo sapi	C 292	21	91.3	41572	9	AC006132	Homo sapi
C 220	21	91.3	24019	9	AL359184	AL359184 Human DNA	C 293	21	91.3	41630	9	AC005785	Homo sapi
C 221	21	91.3	24747	9	AL136990	AL136990 Human DNA	C 294	21	91.3	41669	9	AL138821	Human DNA
C 222	21	91.3	24869	2	AC083996	AC083996 Homo sapi	C 295	21	91.3	42301	9	AC005944	Homo sapi
C 223	21	91.3	24935	9	AC092423	AC092423 Homo sapi	C 296	21	91.3	42304	9	AL355881	Human DNA s
C 224	21	91.3	25031	9	HSJ917C11	AL078642 Human DNA	C 297	21	91.3	42749	9	HSU42H12	Human DNA s
C 225	21	91.3	26226	9	AL136180	AL136180 Human DNA	C 298	21	91.3	42863	9	AB065617	Homo sapi
C 226	21	91.3	26356	9	AC092001	AC092001 Homo sapi	C 299	21	91.3	42863	9	AB065617	Homo sapi
C 227	21	91.3	26855	2	AL391984	AL391984 Homo sapi	C 300	21	91.3	43058	6	AX332810	Sequence
C 228	21	91.3	27182	9	AC007093	AC007093 Homo sapi	C 301	21	91.3	43058	6	AX333047	Sequence
C 229	21	91.3	27213	9	AP000291	AP000291 Homo sapi	C 302	21	91.3	43058	6	AX411306	Sequence
C 230	21	91.3	27927	9	AC103879	AC103879 Homo sapi	C 303	21	91.3	43058	9	HSJG1	Human DNA s
C 231	21	91.3	28428	9	AY057059S2	AY057060 Homo sapi	C 304	21	91.3	43527	9	AC006293	Homo sapi
C 232	21	91.3	28519	9	AL512565	AL512565 Human DNA	C 305	21	91.3	43661	9	AC004493	Homo sapi
C 233	21	91.3	29021	9	AL356477	AL356477 Human DNA	C 306	21	91.3	43735	9	AC108209	Homo sapi
C 234	21	91.3	29103	9	HSJ165D7	Z58273 Human DNA s	C 307	21	91.3	43746	9	AC093641	Homo sapi
C 235	21	91.3	31501	9	HSJ6216	AC006216 Homo sapi	C 308	21	91.3	44118	9	AC006165	Homo sapi
C 236	21	91.3	31671	9	AC009977	AC009977 Homo sapi	C 309	21	91.3	44621	9	AP001873	Homo sapi
C 237	21	91.3	31686	9	AC117422	AC117422 Homo sapi	C 310	21	91.3	45292	9	AC114957	Homo sapi
C 238	21	91.3	32360	9	AL607067	AL607067 Human DNA	C 311	21	91.3	45911	9	AC005688	Homo sapi
C 239	21	91.3	32360	9	AC005339	AC005339 Homo sapi	C 312	21	91.3	45980	2	U82206	Homo sapien
C 240	21	91.3	32887	9	AC118535	AC118535 Homo sapi	C 313	21	91.3	46166	2	AC104253	Homo sapi
C 241	21	91.3	33795	6	AX409537	AX409537 Sequence	C 314	21	91.3	46251	9	AD000671	Homo sapi
C 242	21	91.3	33795	9	AF253417	AF253417 Homo sapi	C 315	21	91.3	46324	9	AC093818	Homo sapi
C 243	21	91.3	33917	9	AC004410	AC004410 Homo sapi	C 316	21	91.3	46894	9	AC114729	Homo sapi
C 244	21	91.3	33931	9	AC022156	AC022156 Homo sapi	C 317	21	91.3	46912	9	AC011557	Homo sapi
C 245	21	91.3	34068	9	HS312E8	AL032819 Human DNA	C 318	21	91.3	47673	2	AC083879	Homo sapi
C 246	21	91.3	34359	9	AL596307	AL596307 Human DNA	C 319	21	91.3	47834	9	HSJ834A16	Human DNA
C 247	21	91.3	34507	9	AL591895	AL591895 Human DNA	C 320	21	91.3	48133	9	AL359700	Human DNA
C 248	21	91.3	35001	9	AP002892	AP002892 Homo sapi	C 321	21	91.3	48289	9	AC067729	Homo sapi
C 249	21	91.3	35120	9	AL590112	AL590112 Human DNA	C 322	21	91.3	48522	2	AC105112	Homo sapi
C 250	21	91.3	35587	9	AC005763	AC005763 Homo sapi	C 323	21	91.3	48623	2	AC130469	Homo sapi
C 251	21	91.3	35688	9	AC073417	AC073417 Homo sapi	C 324	21	91.3	48677	9	AC108465	Homo sapi
C 252	21	91.3	35730	9	HSN74G7	Z69715 Human DNA s	C 325	21	91.3	48698	9	AL592171	Human DNA
C 253	21	91.3	36029	9	U73479	U73479 Homo sapien	C 326	21	91.3	48860	9	AL136461	Human DNA
C 254	21	91.3	36413	2	AC097272	AC097272 Hylobates	C 327	21	91.3	49351	2	AC068148	Homo sapi
C 255	21	91.3	36428	9	AC110000	AC110000 Homo sapi	C 328	21	91.3	49362	2	AL355875	Human DNA
C 256	21	91.3	36431	9	AC068499	AC068499 Homo sapi	C 329	21	91.3	49831	9	AC104063	Homo sapi
C 257	21	91.3	36437	9	HSU138B7	Z78422 Human DNA s	C 330	21	91.3	51700	9	AL157763	Human DNA
C 258	21	91.3	36534	9	U73167	U73167 Homo sapien	C 331	21	91.3	51705	9	AC092589	Homo sapi
C 259	21	91.3	36552	9	HSU90094	U90094 Human chrom	C 332	21	91.3	51953	2	AC083779	Homo sapi
C 260	21	91.3	36558	9	HSU81834	U81834 Human cosmi	C 333	21	91.3	52273	2	AC068690	Homo sapi
C 261	21	91.3	36565	9	HSU73648	U73648 Human chrom	C 334	21	91.3	52597	2	HSJ421120	Human DNA
C 262	21	91.3	36594	9	HUMTPA	K03021 Human tissu	C 335	21	91.3	52737	2	AC007800	Homo sapi
C 263	21	91.3	37219	9	HSN11D4	Z68285 Human DNA s	C 336	21	91.3	52813	9	AC010991	Homo sapi
C 264	21	91.3	37239	9	AC096549	AC096549 Homo sapi	C 337	21	91.3	52835	2	AL356121	Human DNA
C 265	21	91.3	37448	9	AC006138	AC006138 Homo sapi	C 338	21	91.3	53047	2	AC104987	Homo sapi
C 266	21	91.3	37693	9	AP000522	AP000522 Homo sapi	C 339	21	91.3	53249	2	AC092688	Homo sapi
C 267	21	91.3	37852	9	AC124902	AC124902 Homo sapi	C 340	21	91.3	53542	6	AX247730	Sequence
C 268	21	91.3	37991	9	AC005101	AC005101 Homo sapi	C 341	21	91.3	53823	2	AC091642	Homo sapi
C 269	21	91.3	38080	9	HS429E7	AL031722 Human DNA	C 342	21	91.3	53987	2	AC091943	Homo sapi
C 270	21	91.3	38134	9	AC000040	AC000040 Homo sapi	C 343	21	91.3	54375	9	AC011377	Homo sapi
C 271	21	91.3	38250	2	AC012006	AC012006 Homo sapi	C 344	21	91.3	54395	2	AC011297	Homo sapi
C 272	21	91.3	38491	9	AC006049	AC006049 Homo sapi	C 345	21	91.3	54498	2	AC023815	Homo sapi
C 273	21	91.3	38684	2	AC108461	AC108461 Homo sapi	C 346	21	91.3	55448	9	AC084353	Homo sapi
C 274	21	91.3	38852	9	AC006261	AC006261 Homo sapi	C 347	21	91.3	56641	2	AL138833	Homo sapi
C 275	21	91.3	38974	2	AL450315	AL450315 Homo sapi	C 348	21	91.3	56716	2	AC105047	Homo sapi
C 276	21	91.3	39000	9	HSN86D4	Z82250 Human DNA s	C 349	21	91.3	56822	2	AC091084	Homo sapi
C 277	21	91.3	39132	9	AC005515	AC005515 Homo sapi	C 350	21	91.3	56827	9	HSJHC3A5	Human DNA s
C 278	21	91.3	39514	9	AC005594	AC005594 Homo sapi	C 351	21	91.3	56913	9	HS67C13	Sequence
C 279	21	91.3	39838	9	AC007766	AC007766 Homo sapi	C 352	21	91.3	57108	2	AC130297	Homo sapi
C 280	21	91.3	39856	9	AF241735	AF241735 Homo sapi	C 353	21	91.3	57121	2	AC084255	Homo sapi
C 281	21	91.3	39923	9	AL627082	AL627082 Human DNA	C 354	21	91.3	57821	9	AC073595	Homo sapi
C 282	21	91.3	40179	9	AC004036	AC004036 Homo sapi	C 355	21	91.3	58917	9	AC004819	Homo sapi
C 283	21	91.3	40351	9	AC005620	AC005620 Homo sapi	C 356	21	91.3	59065	6	AR183260	Sequence
C 284	21	91.3	40439	9	AF442963	AF442963 Homo sapi	C 357	21	91.3	59406	9	AP001171	Homo sapi

358	21	91.3	59427	9	AC079882	AC079882 Homo sapi	431	21	91.3	71903	9	AL607035	Human DNA
C 359	21	91.3	59586	9	HS449017	Z98749 Human DNA s	C 432	21	91.3	72022	9	AC084430	Homo sapi
C 360	21	91.3	60149	9	AL135925	AL135925 Homo sapi	C 433	21	91.3	72305	2	AC076975	Homo sapi
C 361	21	91.3	60455	9	AP000264	AP000264 Homo sapi	C 434	21	91.3	72402	2	AC089924	Human DNA
C 362	21	91.3	60694	2	AC087827	AC087827 Homo sapi	C 435	21	91.3	72485	2	AC083792	Homo sapi
C 363	21	91.3	60725	9	AL669983	AL669983 Homo sapi	C 436	21	91.3	72533	2	AC083792	Homo sapi
C 364	21	91.3	60834	2	AC087472	AC087472 Homo sapi	C 437	21	91.3	72665	2	AC026981	Homo sapi
C 365	21	91.3	60901	9	AL160406	AL160406 Homo sapi	C 438	21	91.3	72665	2	AC026981	Homo sapi
C 366	21	91.3	61079	9	AC105202	AC105202 Homo sapi	C 439	21	91.3	72978	9	AL359759	Human DNA
C 367	21	91.3	61228	9	AC106706	AC106706 Homo sapi	C 440	21	91.3	73386	2	AC129501	Homo sapi
C 368	21	91.3	61913	9	AL671966	AL671966 Homo sapi	C 441	21	91.3	73469	2	AC117575	Mus muscu
C 369	21	91.3	61991	2	AC131282	AC131282 Homo sapi	C 442	21	91.3	73503	2	AC013586	Homo sapi
C 370	21	91.3	62078	2	AC013711	AC013711 Homo sapi	C 443	21	91.3	74102	9	AL356316	Human DNA
C 371	21	91.3	62078	2	AC013711	AC013711 Homo sapi	C 444	21	91.3	74129	2	AC073167	Homo sapi
C 372	21	91.3	62147	9	AC093251	AC093251 Homo sapi	C 445	21	91.3	74274	2	AC087717	Homo sapi
C 373	21	91.3	62287	2	AC115104	AC115104 Homo sapi	C 446	21	91.3	74581	9	AL391235	Human DNA
C 374	21	91.3	62288	9	AC005571	AC005571 Homo sapi	C 447	21	91.3	75184	9	AC005218	Homo sapi
C 375	21	91.3	62464	2	AC131572	AC131572 Homo sapi	C 448	21	91.3	75326	2	AC026999	Homo sapi
C 376	21	91.3	62747	2	AC087475	AC087475 Homo sapi	C 449	21	91.3	75440	9	AP000786	Homo sapi
C 377	21	91.3	63006	9	AL451166	AL451166 Homo sapi	C 450	21	91.3	75523	9	AL627233	Human DNA
C 378	21	91.3	63029	2	AC131288	AC131288 Homo sapi	C 451	21	91.3	76848	9	AC003041	Homo sapi
C 379	21	91.3	63090	9	AC087320	AC087320 Homo sapi	C 452	21	91.3	76982	9	AL731542	Human DNA
C 380	21	91.3	63522	2	AC040937	AC040937 Homo sapi	C 453	21	91.3	77239	9	AL583844	Human DNA
C 381	21	91.3	63528	2	AC091196	AC091196 Homo sapi	C 454	21	91.3	77322	2	AC021334	Homo sapi
C 382	21	91.3	63749	9	AC004694	AC004694 Homo sapi	C 455	21	91.3	77331	9	AL354983	Human DNA
C 383	21	91.3	63797	2	AC127453	AC127453 Homo sapi	C 456	21	91.3	77663	2	AL357131	Continuation (4 of
C 384	21	91.3	63955	9	AC108151	AC108151 Homo sapi	C 457	21	91.3	77691	9	AL357131	Continuation (4 of
C 385	21	91.3	64080	9	AL133217	AL133217 Homo sapi	C 458	21	91.3	77702	9	AL120118	Homo sapi
C 386	21	91.3	64323	9	AL356976	AL356976 Homo sapi	C 459	21	91.3	78359	9	AF314199S7	Human DNA
C 387	21	91.3	64650	2	AC068864	AC068864 Homo sapi	C 460	21	91.3	78359	9	AL125158	Homo sapi
C 388	21	91.3	64931	9	AC128716	AC128716 Homo sapi	C 461	21	91.3	78467	9	AC008078	Homo sapi
C 389	21	91.3	64952	9	AL359745	AL359745 Homo sapi	C 462	21	91.3	78643	9	AC004964	Homo sapi
C 390	21	91.3	65111	2	AC055857	AC055857 Homo sapi	C 463	21	91.3	79223	9	AL391114	Human DNA
C 391	21	91.3	65237	2	AC105208	AC105208 Homo sapi	C 464	21	91.3	79227	9	HS148E22	Human DNA
C 392	21	91.3	65356	2	AC090990	AC090990 Homo sapi	C 465	21	91.3	79319	9	AL512274	Human DNA
C 393	21	91.3	65413	2	AC116019	AC116019 Homo sapi	C 466	21	91.3	79422	2	AC022750	Homo sapi
C 394	21	91.3	65608	6	AX330738	AX330738 Sequence	C 467	21	91.3	79600	2	AL353657	Human DNA
C 395	21	91.3	65608	6	AX332242	AX332242 Sequence	C 468	21	91.3	80039	2	AC021290	Homo sapi
C 396	21	91.3	65608	6	AX335496	AX335496 Sequence	C 469	21	91.3	80119	9	AC111152	Homo sapi
C 397	21	91.3	65608	9	HS062293	HS062293 Human LIM-k	C 470	21	91.3	80272	2	HS0491C16	Human sapi
C 398	21	91.3	65821	2	AC087461	AC087461 Homo sapi	C 471	21	91.3	80318	2	AC016300	Homo sapi
C 399	21	91.3	66148	2	AC110017	AC110017 Homo sapi	C 472	21	91.3	80363	2	AC025805	Homo sapi
C 400	21	91.3	66235	2	AC016226	AC016226 Homo sapi	C 473	21	91.3	80515	9	AC011992	Homo sapi
C 401	21	91.3	66575	2	AC130324	AC130324 Homo sapi	C 474	21	91.3	80547	9	AC007382	Homo sapi
C 402	21	91.3	66981	2	AC023178	AC023178 Homo sapi	C 475	21	91.3	80565	9	AL357374	Human DNA
C 403	21	91.3	67046	9	HS063721	HS063721 Human elast	C 476	21	91.3	81001	6	AX063464	Sequence
C 404	21	91.3	67150	9	AC021651	AC021651 Homo sapi	C 477	21	91.3	81001	6	AX469876	Sequence
C 405	21	91.3	67326	2	AC073034	AC073034 Homo sapi	C 478	21	91.3	81674	9	HS722E9	Human DNA
C 406	21	91.3	67392	9	AC107220	AC107220 Homo sapi	C 479	21	91.3	81768	9	AL662825	Human DNA
C 407	21	91.3	67462	2	AC091595	AC091595 Homo sapi	C 480	21	91.3	81874	9	HS931E15	Human DNA
C 408	21	91.3	67674	2	AC090641	AC090641 Homo sapi	C 481	21	91.3	81914	9	HS0363M2	Human DNA
C 409	21	91.3	67709	9	AC104830	AC104830 Homo sapi	C 482	21	91.3	82279	2	AC010464	Homo sapi
C 410	21	91.3	67713	2	AC102796	AC102796 Homo sapi	C 483	21	91.3	82316	9	AL354726	Human DNA
C 411	21	91.3	68091	2	AC124094	AC124094 Homo sapi	C 484	21	91.3	82374	9	AL355001	Human DNA
C 412	21	91.3	68509	2	HSY313F4_3	Continuation (4 of	C 485	21	91.3	82700	2	AC015635	Homo sapi
C 413	21	91.3	68554	2	AC090387	Continuation (4 of	C 486	21	91.3	82806	9	AC007111	Homo sapi
C 414	21	91.3	68582	9	AB017652	AB017652 Homo sapi	C 487	21	91.3	82827	9	AC079395	Homo sapi
C 415	21	91.3	68582	9	AP000464	AP000464 Homo sapi	C 488	21	91.3	82938	9	AC079250	Homo sapi
C 416	21	91.3	68607	9	AC103887	AC103887 Homo sapi	C 489	21	91.3	83153	2	AC011417	Homo sapi
C 417	21	91.3	68843	9	AL450427	AL450427 Homo sapi	C 490	21	91.3	83552	9	AL157759	Human DNA
C 418	21	91.3	68914	2	AC024970	AC024970 Homo sapi	C 491	21	91.3	83705	9	AC025766	Homo sapi
C 419	21	91.3	69028	9	AC087493	AC087493 Homo sapi	C 492	21	91.3	83820	9	AL133264	Human DNA
C 420	21	91.3	69051	2	AC073171	AC073171 Homo sapi	C 493	21	91.3	83951	9	AL354824	Human DNA
C 421	21	91.3	69165	2	AC023465	AC023465 Homo sapi	C 494	21	91.3	84176	9	AL590782	Human DNA
C 422	21	91.3	69678	9	AC091573	AC091573 Homo sapi	C 495	21	91.3	84364	9	HS522J7	Z98885 Human DNA s
C 423	21	91.3	69901	9	HS694E4	AL031255 Human DNA	C 496	21	91.3	84477	2	AC015827	Human DNA
C 424	21	91.3	69918	9	AL441988	AL441988 Homo sapi	C 497	21	91.3	84570	9	AL359552	Human DNA
C 425	21	91.3	70043	9	AL157776	AL157776 Homo sapi	C 498	21	91.3	84678	2	AC087464	Homo sapi
C 426	21	91.3	70621	9	AL713971	AL713971 Homo sapi	C 499	21	91.3	84679	2	AC022571	Homo sapi
C 427	21	91.3	70849	2	AC090139	AC090139 Homo sapi	C 500	21	91.3	84881	9	AL390726	Human DNA
C 428	21	91.3	71117	9	HSJ132F21	AL079335 Human DNA	C 501	21	91.3	84971	9	AC092271	Homo sapi
C 429	21	91.3	71353	9	AF104455	AF104455 Homo sapi	C 502	21	91.3	85275	9	AC092180	Homo sapi
C 430	21	91.3	71864	2	AC103852	AC103852 Homo sapi	C 503	21	91.3	85275	9	AC092180	Homo sapi

504	21	91.3	85382	9	AL390793	Human DNA	577	21	91.3	96308	9	CNS08C90	AL749540	Human chr
505	21	91.3	85420	9	AC004672	Homo sapi	578	21	91.3	96387	2	HSJ600024	AL080247	Homo sapi
506	21	91.3	85500	9	HS199H16	Human DNA	579	21	91.3	96444	9	HSJ738116	AL049867	Human DNA
507	21	91.3	85550	9	AC104466	Homo sapi	580	21	91.3	96482	9	AC096739	AC096739	Homo sapi
508	21	91.3	85818	9	AL161640	Human DNA	581	21	91.3	96489	9	AC011395	AC011395	Homo sapi
509	21	91.3	85942	9	AC091971	Homo sapi	582	21	91.3	96559	9	AC079347	AC079347	Homo sapi
510	21	91.3	85977	9	AC094085	Homo sapi	583	21	91.3	96638	9	AC092545	AC092545	Homo sapi
511	21	91.3	86057	9	AC092112	Homo sapi	584	21	91.3	96951	9	AC026433	AC026433	Homo sapi
512	21	91.3	86077	9	AC073971	Homo sapi	585	21	91.3	96975	9	AC004975	AC004975	Homo sapi
513	21	91.3	86769	9	HSAP003626	Homo sapi	586	21	91.3	96978	9	AC024075	AC024075	Homo sapi
514	21	91.3	86825	9	AC006967	Homo sapi	587	21	91.3	97037	9	AC004973	AC004973	Homo sapi
515	21	91.3	87000	9	AC097103	Homo sapi	588	21	91.3	97112	9	AL353631	AL353631	Human DNA
516	21	91.3	87076	9	AC005918	Homo sapi	589	21	91.3	97129	9	HS292H14	AL008710	Human DNA
517	21	91.3	87323	9	AC006373	Homo sapi	590	21	91.3	97254	2	AC079517 ⁴	Continuation (5 of	
518	21	91.3	87350	2	AC009752	Homo sapi	591	21	91.3	97495	9	AC093014	AC093014	Homo sapi
519	21	91.3	87917	2	AC016261	Homo sapi	592	21	91.3	97556	9	AC079781	AC079781	Homo sapi
520	21	91.3	87973	9	AC009185	Homo sapi	593	21	91.3	97700	9	AL136079	AL136079	Human DNA
521	21	91.3	88347	2	AC104981	Homo sapi	594	21	91.3	97835	9	HS292E10	293930	Human DNA s
522	21	91.3	88520	9	AC097503	Homo sapi	595	21	91.3	98261	9	HS1054C24	AL035249	Human DNA
523	21	91.3	88528	9	AL356857	Human DNA	596	21	91.3	98404	2	AL355676	AL355676	Homo sapi
524	21	91.3	89153	9	AC026714	Homo sapi	597	21	91.3	98433	9	AC006365	AC006365	Homo sapi
525	21	91.3	89214	9	AC093009	Homo sapi	598	21	91.3	98638	9	CNS05TDO	AL356806	Human chr
526	21	91.3	89603	9	HSU63834	Human K.I.T p	599	21	91.3	98804	2	AC106723 ³	Continuation (4 of	
527	21	91.3	89871	9	AC092207	Homo sapi	600	21	91.3	98835	9	AC073195	AC073195	Homo sapi
528	21	91.3	90136	9	HS330012	Human DNA	601	21	91.3	98935	9	AC004935	AC004935	Homo sapi
529	21	91.3	90150	9	AC068576	Homo sapi	602	21	91.3	98955	9	AC008886	AC008886	Homo sapi
530	21	91.3	90244	9	AB023051	Homo sapi	603	21	91.3	99036	9	AC005773	AC005773	Homo sapi
531	21	91.3	90256	9	AP001582	Homo sapi	604	21	91.3	99227	9	AC114737	AC114737	Homo sapi
532	21	91.3	90331	9	AL353682	Human DNA	605	21	91.3	99370	9	AC005057	AC005057	Homo sapi
533	21	91.3	90422	9	AC023880	Homo sapi	606	21	91.3	99521	2	AC127700	AC127700	Homo sapi
534	21	91.3	90430	9	AC003100	Homo sapi	607	21	91.3	99611	9	AL591519	AL591519	Human DNA
535	21	91.3	90476	9	AC015910	Homo sapi	608	21	91.3	99859	2	AC025368	AC025368	Homo sapi
536	21	91.3	90815	9	AC002559	Homo sapi	609	21	91.3	99886	9	HS598F2	AL021579	Human DNA
537	21	91.3	90820	2	AC111155	Homo sapi	610	21	91.3	99995	9	AC010480	AC010480	Homo sapi
538	21	91.3	91071	2	AC022589	Homo sapi	611	21	91.3	100000	9	AP000035	AP000035	Homo sapi
539	21	91.3	91311	9	AC011230	Homo sapi	612	21	91.3	100000	9	AP000043	AP000043	Homo sapi
540	21	91.3	91323	9	AC106901	Homo sapi	613	21	91.3	100000	9	AP000101	AP000101	Homo sapi
541	21	91.3	91692	9	AC084253	Homo sapi	614	21	91.3	100000	9	AP000111	AP000111	Homo sapi
542	21	91.3	91832	2	AC114546	Homo sapi	615	21	91.3	100000	9	AP000177	AP000177	Homo sapi
543	21	91.3	91842	9	AC008392	Homo sapi	616	21	91.3	100000	9	AP000187	AP000187	Homo sapi
544	21	91.3	92068	2	AL672077	Homo sapi	617	21	91.3	100000	9	AP000210	AP000210	Homo sapi
545	21	91.3	92242	9	AF216668	Homo sapi	618	21	91.3	100000	9	AP000502	AP000502	Homo sapi
546	21	91.3	92460	9	AL136228	Human DNA	619	21	91.3	100000	9	AP000513	AP000513	Homo sapi
547	21	91.3	92472	9	HS181C9	Human DNA s	620	21	91.3	100000	17	AP000132	AP000132	Homo sapi
548	21	91.3	92487	9	AC068280	Homo sapi	621	21	91.3	100116	9	AL591178	AL591178	Human DNA
549	21	91.3	92636	9	AC005251	Homo sapi	622	21	91.3	100133	9	AC113342	AC113342	Homo sapi
550	21	91.3	92644	2	AF186995	Homo sapi	623	21	91.3	100139	9	AC021752	AC021752	Homo sapi
551	21	91.3	92807	9	HS1137F22	Human Chrom	624	21	91.3	100139	9	AC021752	AC021752	Homo sapi
552	21	91.3	92858	2	AC024959	Homo sapi	625	21	91.3	100267	9	HSMEHC3W36A	U89337	Homo sapi
553	21	91.3	92969	9	HSJ687F11	Human DNA	626	21	91.3	100493	9	AC091810	AC091810	Homo sapi
554	21	91.3	93033	2	AP000644	Homo sapi	627	21	91.3	100506	2	AP002020	AP002020	Homo sapi
555	21	91.3	93395	2	AC087882	Homo sapi	628	21	91.3	100521	9	AC119397	AC119397	Homo sapi
556	21	91.3	93403	9	AC073261	Homo sapi	629	21	91.3	100653	2	AC093215	AC093215	Homo sapi
557	21	91.3	93431	9	HUU95737	Human Chrom	630	21	91.3	100701	9	AC005911	AC005911	Homo sapi
558	21	91.3	93519	9	AC130458	Homo sapi	631	21	91.3	100791	9	CNS01R18	AL163011	Human chr
559	21	91.3	94224	9	HS661120	Human DNA	632	21	91.3	100808	9	AC108081	AC108081	Homo sapi
560	21	91.3	94296	2	AL160261	Homo sapi	633	21	91.3	101036	9	AC008711	AC008711	Homo sapi
561	21	91.3	94385	2	AL356673	Homo sapi	634	21	91.3	101077	2	AC024051	AC024051	Homo sapi
562	21	91.3	95084	9	AC010385	Homo sapi	635	21	91.3	101370	9	AC003962	AC003962	Homo sapi
563	21	91.3	95097	9	AL133232	Human DNA	636	21	91.3	101507	9	AP000359	AP000359	Homo sapi
564	21	91.3	95241	9	HS398B19	Human DNA	637	21	91.3	101652	9	AC079754	AC079754	Homo sapi
565	21	91.3	95345	9	AC007029	Homo sapi	638	21	91.3	101728	9	HS109088	AL033524	Human DNA
566	21	91.3	95375	9	HS228A9	Human DNA	639	21	91.3	101768	9	AC006465	AC006465	Homo sapi
567	21	91.3	95546	9	AC022816	Homo sapi	640	21	91.3	101880	9	AC021089	AC021089	Homo sapi
568	21	91.3	95648	9	AC090214	Homo sapi	641	21	91.3	101937	9	AC010221	AC010221	Homo sapi
569	21	91.3	95681	9	AL157890	Human DNA	642	21	91.3	102105	9	AL136166	AL136166	Human DNA
570	21	91.3	95926	9	AC106752	Homo sapi	643	21	91.3	102351	2	AL138848	AL138848	Homo sapi
571	21	91.3	95983	9	AC004874	Homo sapi	644	21	91.3	102370	9	HSJ976013	AL117354	Human DNA
572	21	91.3	96000	2	AC079684	Homo sapi	645	21	91.3	102446	9	AL662849	AL662849	Human DNA
573	21	91.3	96002	2	AC109326	Homo sapi	646	21	91.3	102718	9	AC107628	AC107628	Homo sapi
574	21	91.3	96146	9	AC095052	Homo sapi	647	21	91.3	102892	9	AL359813	AL359813	Human DNA
575	21	91.3	96280	9	AC006968	Homo sapi	648	21	91.3	102910	9	AF254822	AF254822	Homo sapi
576	21	91.3	96308	9	AF190465	Homo sapi	649	21	91.3	103009	9	AC087225	AC087225	Homo sapi

c 650	21	91.3 103023	9	AP000747	AP000747 Homo sapi	c 723	21	91.3 110000	2	AL683889	4	Continuation (5 of
c 651	21	91.3 103108	2	AC008718	AC008718 Homo sapi	724	21	91.3 110000	2	AL732359	0	AL732359 Homo sapi
c 652	21	91.3 103327	9	AL662830	AL662830 Human DNA	725	21	91.3 110000	2	AP002753	0	AP002753 Homo sapi
c 653	21	91.3 103370	9	AL61656	AL61656 Human DNA	726	21	91.3 110000	2	AP002753	1	Continuation (2 of
c 654	21	91.3 103476	9	AC123912	AC123912 Homo sapi	727	21	91.3 110000	2	AC024562	3	Continuation (4 of
c 655	21	91.3 103667	9	AL357073	AL357073 Human DNA	728	21	91.3 110000	9	AC005079	1	Continuation (2 of
c 656	21	91.3 103699	9	AC034305	AC034305 Homo sapi	c 729	21	91.3 110000	9	AF440620	2	Continuation (3 of
c 657	21	91.3 103765	9	AC096743	AC096743 Homo sapi	730	21	91.3 110000	9	AF491780	09	Continuation (10 of
c 658	21	91.3 103829	9	AP000665	AP000665 Homo sapi	731	21	91.3 110025	9	AP003699	0	AP003699 Homo sapi
c 659	21	91.3 104285	9	AC091729	AC091729 Homo sapi	732	21	91.3 110042	9	AL590788	0	AL590788 Human DNA
c 660	21	91.3 104289	2	HS104D14	AL035554 Homo sapi	c 733	21	91.3 110129	9	AC008956	0	AC008956 Homo sapi
c 661	21	91.3 104307	9	AL591845	AL591845 Human DNA	734	21	91.3 110130	9	AL360268	0	AL360268 Human DNA
c 662	21	91.3 104581	2	AF267908	AF267908 Homo sapi	735	21	91.3 110184	9	AC020906	0	AC020906 Homo sapi
c 663	21	91.3 104600	9	AP001166	AP001166 Homo sapi	c 736	21	91.3 110599	2	AC079343	0	AC079343 Homo sapi
c 664	21	91.3 104770	9	HSJ245M18	AL078584 Human DNA	737	21	91.3 110900	9	HSJ392M17	0	AL078584 Human DNA
c 665	21	91.3 104853	9	AC117444	AC117444 Homo sapi	c 738	21	91.3 111104	9	AC117389	0	AC117389 Homo sapi
c 666	21	91.3 104926	9	AC010168	AC010168 Homo sapi	c 739	21	91.3 111191	2	AC127525	0	AC127525 Homo sapi
c 667	21	91.3 104972	9	AC025176	AC025176 Homo sapi	740	21	91.3 111249	9	AP000343	0	AP000343 Homo sapi
c 668	21	91.3 105040	9	AC011229	AC011229 Homo sapi	c 741	21	91.3 111328	9	AP002755	0	AP002755 Homo sapi
c 669	21	91.3 105207	9	AC011594	AC011594 Homo sapi	c 742	21	91.3 111500	9	AC121344	0	AC121344 Homo sapi
c 670	21	91.3 105288	9	AC012330	AC012330 Homo sapi	743	21	91.3 111517	9	AC074366	0	AC074366 Homo sapi
c 671	21	91.3 105489	9	AC093894	AC093894 Homo sapi	c 744	21	91.3 111641	2	HS232N11	0	HS232N11 Homo sapi
c 672	21	91.3 105960	9	HS209A6	AL035401 Human DNA	c 745	21	91.3 111688	2	AC105020	0	AC105020 Homo sapi
c 673	21	91.3 106117	9	AC103564	AC103564 Homo sapi	746	21	91.3 111862	2	AL139143	0	AL139143 Homo sapi
c 674	21	91.3 106123	9	AL158015	AL158015 Human DNA	c 747	21	91.3 111996	9	AC093388	0	AC093388 Homo sapi
c 675	21	91.3 106208	2	AC130466	AC130466 Homo sapi	c 748	21	91.3 112031	9	AL445487	0	AL445487 Human DNA
c 676	21	91.3 106246	9	AC108721	AC108721 Homo sapi	749	21	91.3 112067	9	AC091485	0	AC091485 Homo sapi
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c 679	21	91.3 106650	9	AC007708	AC007708 Homo sapi	752	21	91.3 112208	9	AC093313	0	AC093313 Homo sapi
c 680	21	91.3 106696	9	HUAC003661	AC003661 Homo sapi	c 753	21	91.3 112389	2	AC003025	0	AC003025 Human Chr
c 681	21	91.3 106735	2	AC011381	AC011381 Homo sapi	c 754	21	91.3 112389	2	AC073598	0	AC073598 Homo sapi
c 682	21	91.3 106859	9	AL512626	AL512626 Human DNA	c 755	21	91.3 112501	9	AC092953	0	AC092953 Homo sapi
c 683	21	91.3 106859	9	AL512626	AL512626 Human DNA	c 756	21	91.3 112501	9	AC010240	0	AC010240 Homo sapi
c 684	21	91.3 106868	2	AC003023	AC003023 Homo sapi	c 757	21	91.3 112659	9	AC010677	0	AC010677 Homo sapi
c 685	21	91.3 107104	9	HS1179L24	AL096708 Human DNA	c 758	21	91.3 112697	2	AP005367	0	AP005367 Homo sapi
c 686	21	91.3 107226	9	AC010618	AC010618 Homo sapi	c 759	21	91.3 112748	9	AC007242	0	AC007242 Homo sapi
c 687	21	91.3 107427	9	HS481A17	Z82212 Human DNA s	c 760	21	91.3 112902	2	AC034211	0	AC034211 Homo sapi
c 688	21	91.3 107462	2	AC068208	AC068208 Homo sapi	c 761	21	91.3 113020	2	HS394I7	0	HS394I7 Homo sapi
c 689	21	91.3 107467	9	HS958B3	Z93023 Homo sapien	c 762	21	91.3 113036	9	AL158160	0	AL158160 Human DNA
c 690	21	91.3 107558	2	AC093252	AC093252 Homo sapi	c 763	21	91.3 113202	9	HSJ397H23	0	HSJ397H23 Homo sapi
c 691	21	91.3 107558	2	AC093252	AC093252 Homo sapi	c 764	21	91.3 113241	9	HUAC002425	0	HUAC002425 Homo sapi
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c 695	21	91.3 108205	9	AL138758	AL138758 Human DNA	c 768	21	91.3 113530	9	AC073216	0	AC073216 Homo sapi
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c 699	21	91.3 108813	9	AL138718	AL138718 Human DNA	772	21	91.3 113743	9	AC072023	0	AC072023 Homo sapi
c 700	21	91.3 108841	9	AL359185	AL359185 Human DNA	c 773	21	91.3 113810	9	AC068292	0	AC068292 Homo sapi
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c 703	21	91.3 109098	2	AF295013	AF295013 Homo sapi	776	21	91.3 113980	2	AP001540	0	AP001540 Homo sapi
c 704	21	91.3 109134	9	AC024571	AC024571 Homo sapi	777	21	91.3 113991	9	AC096742	0	AC096742 Homo sapi
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c 707	21	91.3 109445	9	AC008946	AC008946 Homo sapi	780	21	91.3 114202	2	AC103829	0	AC103829 Homo sapi
c 708	21	91.3 109523	2	AL844527	AL844527 Homo sapi	781	21	91.3 114349	9	AP000920	0	AP000920 Homo sapi
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c 710	21	91.3 109666	9	AP000838	AP000838 Homo sapi	c 783	21	91.3 114517	2	AL158152	0	AL158152 Human DNA
c 711	21	91.3 109933	2	AC093285	AC093285 Homo sapi	784	21	91.3 114657	9	AC097711	0	AC097711 Homo sapi
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c 713	21	91.3 110000	2	AC079517	Continuation (2 of	c 786	21	91.3 114809	2	AC083823	0	AC083823 Homo sapi
c 714	21	91.3 110000	2	AC091528	Continuation (3 of	787	21	91.3 114846	9	HS257I20	0	HS257I20 Human DNA
c 715	21	91.3 110000	2	AC011600	AC011600 Homo sapi	c 788	21	91.3 114972	9	AC016617	0	AC016617 Homo sapi
c 716	21	91.3 110000	2	AC106723	AC106723 Homo sapi	789	21	91.3 115174	9	AC003695	0	AC003695 Homo sapi
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c 718	21	91.3 110000	2	AC125232	Continuation (3 of	791	21	91.3 115408	2	AC068848	0	AC068848 Homo sapi
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c 720	21	91.3 110000	2	AL359456	AL359456 Homo sapi	793	21	91.3 115583	9	HSJ351K20	0	HSJ351K20 Human DNA
c 721	21	91.3 110000	2	AL359456	Continuation (4 of	794	21	91.3 115664	2	AC010324	0	AC010324 Homo sapi
c 722	21	91.3 110000	2	AL390202	Continuation (7 of	795	21	91.3 115762	2	AP000663	0	AP000663 Homo sapi

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797 21 91.3 115806 9 AL591363 Human DNA
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AC087253 Pan trogl
AL603882 Human DNA
AP000708 Homo sapi
AC008874 Homo sapi
AL136137 Human DNA
AC098583 Homo sapi
AP000682 Homo sapi
AC098828 Homo sapi
AC027796 Homo sapi
AC027796 Homo sapi
AC022095 Homo sapi
AC016888 Homo sapi
ZS5331 Human DNA
AC006236 Homo sapi
AC006236 Homo sapi
AL353135 Human DNA
AC023813 Homo sapi
AC108084 Homo sapi
AC130271 Homo sapi
AC092894 Homo sapi
AC105036 Homo sapi
AC025071 Homo sapi

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943 21 91.3 128206 2 AC008633
c 944 21 91.3 128266 9 AC008623 Homo sapi
945 21 91.3 128332 9 AC008657 Homo sapi
c 946 21 91.3 128411 2 AC091230 Homo sapi
947 21 91.3 128459 9 AC083849 Homo sapi
948 21 91.3 128639 2 AC013527 Homo sapi
c 949 21 91.3 128642 9 AC008838 Homo sapi
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c 952 21 91.3 128935 9 AC105243 Homo sapi
c 953 21 91.3 128978 9 AC002073 Human PAC
c 954 21 91.3 129036 9 AC005378 Homo sapi
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c 956 21 91.3 129261 2 AC068247 Homo sapi
c 957 21 91.3 129293 9 AC092289 Homo sapi
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ALIGNMENTS

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RESULT 1
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DEFINITION AF123653
ACCESSION AF123653
VERSION AF123653.1 GI:4572463
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9108)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 9108)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2338 10th street, Philadelphia, PA 19107, USA
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LQSNMWSLKALSFSDGSKLGHNKADKSPCVSRSPISDECSIQLEOKLLEREGA
LQKQSFKEKELASLAEYERPRRCDELEGPEPGKGLKQASQSKSQRAQVHLHQ
VLQOQKQKQLROELESMLKQDLLETUKLSYEREKTSFGPALEETQWEVCQSGEIS
LLKQOLKESQTEYNAKASEILGLKQDKTRGLELELTQDLEGALRTYGLLELYC
ENELQKQNEALLREKVNLLQELQELQAALADMGPTTFPDEVPALELELR
AELEERQGHQDMSSGFOHERLVWKEKEKVIQYQKQSQSYVAMYQRNQRLEKALQO
LARGDSAGEPLEVDLEGADIPYDIATETI"
BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others
ORIGIN
Query Match 100.0%; Score 23; DB 9; Length 9108;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CAGCAGGCATGTGGCAGGTGT 23
Db 4511 CAGCAGGCATGTGGCAGGTGT 4533
RESULT 2
AC025853
LOCUS AC025853 Homo sapiens chromosome 8 clone RP11-353K12 map 8, *** SEQUENCING
DEFINITION IN PROGRESS ***, 3 unordered pieces.
ACCESSION AC025853
VERSION AC025853.13 GI:21431202
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173264)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-353K12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173264)

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AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPeeters,R., Melidrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 173264)

REFERENCE

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Melidrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 17, 2002 this sequence version replaced gi:21321864.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web code: WTR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7454

Center clone name: 353_K_12

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 39461: contig of 39461 bp in length
* 39462 39561: gap of 100 bp

FEATURES

source

* 39562 108347: contig of 68786 bp in length
* 108348 108447: gap of 100 bp
* 108448 173264: contig of 64817 bp in length.

Location/Qualifiers
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BASE COUNT

ORIGIN

Query Match 100.0%; Score 23; DB 2; Length 173264;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGGTGGCAGGTGT 23

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Db 26751 CAGCCAGGCATGGTGGCAGGTGT 26773

RESULT 3

HS388M5/c

LOCUS

DEFINITION

HS388M5 177568 bp DNA linear PRI 12-DEC-1999
Human DNA sequence from clone RP3-388M5 on chromosome 22 Contains an RPL4 (60S Ribosomal Protein L4) pseudogene, the HMGI7L1 gene for high-mobility group (nonhistone chromosomal) protein 17-like 1, the gene for a novel Sulfotransferase (sulfokinase, EC 2.8.2.1) like protein, the gene for a GS2 like protein, ESTs, STSS, GSSs and four putative CpG islands, complete sequence.

ACCESSION

VERSION

297055.1 GI:2916859

HRG; 60S Ribosomal Protein L4; CpG island; GS2; HMGI7L1; RPL4;

Sulfokinase; Sulfotransferase.

SOURCE

ORGANISM

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 177568)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 28, 1998 this sequence version replaced gi:213438.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TRMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

<http://www.sanger.ac.uk/projects/Celegans/wormpep> This sequence

was generated from part of bacterial clone contigs of human

chromosome 22, constructed by the Sanger Centre Chromosome 22

Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr22>

RP3-388M5 is from the library RPI-3 constructed at the Roswell

Park Cancer Institute by the group of Pieter de Jong. For further

details see <http://bacpac.med.buffalo.edu/VECTOR: pCYPAC2>

This sequence is the entire insert of clone RP3-388M5 The start of

this sequence overlaps with sequence AL023654 The end of this
sequence overlaps with sequence AL023801.

FEATURES

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pseudogene)
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Em:X05217 Em:X05216 Em:L20868
match: proteins: Sw:Q28346 Sw:P09180 Sw:P36578 Wp:CE07669
Sw:P08429 Sw:P49165 Sw:P50878 Sw:P02385 Sw:P14117
Sw:P35679 Sw:P49691 Tr:O94253 Sw:P10664"
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repeat_region
25437..25970
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repeat_region
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29655..29759
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repeat_region
29971..31122
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32732..32972
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33894. .34201

Query Match 100.0%; Score 23; DB 9; Length 177568;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGGCATGTGGCAGGTGT 23
|||||
Db 155046 CAGCAGGCATGTGGCAGGTGT 155024

RESULT 4
AB046623 1821 bp mRNA linear PRI 01-AUG-2000
LOCUS Macaca fascicularis brain cDNA, clone QcCE-10576.
DEFINITION
AB046623
ACCESSION
AB046623.1 GI:9651056
VERSION
AB046623.1 GI:9651056
KEYWORDS
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone lib:macaque brain cDNA library QcCE clone:QcCE-10576.
SOURCE
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1 (sites)
Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
libraries
Unpublished
2 (bases 1 to 1821)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (28-JUL-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: pME18S-FL3 (Acc.No. AB009864)
R. Site2: DrIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DrIII sites of pME18S-FL3. XhoI sites just outside
the DrIII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing ( 5' end
primer [CTTCTGCTCTAAAGCTCGG]; 3' end primer [CGACCTGCAGCTCGACACA] ).

FEATURES
source
Location/Qualifiers
1. 1821
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QcCE-10576"
/sex="male"
/tissue_type="cerebellum cortex"
/clone_lib="macaque brain cDNA library QcCE"
/dev_stage="adult"
/codon_start=1
133..417
/product="hypothetical protein"
/protein_id="BAB03541.1"
/db_xref="GI:9651057"
/translation="MWTSLLPQPGIRGLCHANVLGNRSRSEAGSEIDLAKGRYVRS
GFUGRQISLGRKQRTFLMWSKCKSLVRVLEAVSSLSLEAFKKRLGRAR"

repeat_region /note="L185 repeat: matches 5265. .5313 of consensus"
33615. .33739
/note="L184 repeat: matches 5320. .5450 of consensus"
33740. .33864
/note="L185 repeat: matches 5313. .5587 of consensus"
33894. .34201

Query Match 100.0%; Score 23; DB 9; Length 177568;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGGCATGTGGCAGGTGT 23
|||||
Db 155046 CAGCAGGCATGTGGCAGGTGT 155024

RESULT 4
AB046623 1821 bp mRNA linear PRI 01-AUG-2000
LOCUS Macaca fascicularis brain cDNA, clone QcCE-10576.
DEFINITION
AB046623
ACCESSION
AB046623.1 GI:9651056
VERSION
AB046623.1 GI:9651056
KEYWORDS
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone lib:macaque brain cDNA library QcCE clone:QcCE-10576.
SOURCE
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1 (sites)
Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
libraries
Unpublished
2 (bases 1 to 1821)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (28-JUL-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: pME18S-FL3 (Acc.No. AB009864)
R. Site2: DrIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DrIII sites of pME18S-FL3. XhoI sites just outside
the DrIII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing ( 5' end
primer [CTTCTGCTCTAAAGCTCGG]; 3' end primer [CGACCTGCAGCTCGACACA] ).

FEATURES
source
Location/Qualifiers
1. 1821
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QcCE-10576"
/sex="male"
/tissue_type="cerebellum cortex"
/clone_lib="macaque brain cDNA library QcCE"
/dev_stage="adult"
/codon_start=1
133..417
/product="hypothetical protein"
/protein_id="BAB03541.1"
/db_xref="GI:9651057"
/translation="MWTSLLPQPGIRGLCHANVLGNRSRSEAGSEIDLAKGRYVRS
GFUGRQISLGRKQRTFLMWSKCKSLVRVLEAVSSLSLEAFKKRLGRAR"

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BASE COUNT 479 a 460 c 511 g 371 t
ORIGIN
Query Match 95.7%; Score 22; DB 9; Length 1821;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGGCATGTGGCAGGTGT 23
|||||
Db 538 AGCAGGCATGTGGCAGGTGT 559

RESULT 5
AB052149 2787 bp mRNA linear PRI 11-OCT-2001
LOCUS Macaca fascicularis brain cDNA, clone:QcCE-20783.
DEFINITION
AB052149
ACCESSION
AB052149.1 GI:11611578
VERSION
AB052149.1 GI:11611578
KEYWORDS
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone lib:macaque brain cDNA library QcCE clone:QcCE-20783.
SOURCE
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1
Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirata,M.,
Suto,Y., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
chromosomes
Gene 275 (1), 31-37 (2001)
21458551
2 (bases 1 to 2787)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (05-DEC-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)
Lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DrIII (CACCATGTG)
R. Site2: DrIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DrIII sites of pME18S-FL3. XhoI sites just outside
the DrIII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing
( 5' end primer [CTTCTGCTCTAAAGCTCGG];
3' end primer [CGACCTGCAGCTCGACACA] ).

FEATURES
source
Location/Qualifiers
1. 2787
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QcCE-20783"
/sex="male"
/tissue_type="cerebellum cortex"
/clone_lib="macaque brain cDNA library QcCE"
/dev_stage="adult"
380..1495
/codon_start=1
/product="hypothetical protein"
/protein_id="BAB19004.1"
/db_xref="GI:11611579"
/translation="MGTTATLRMENVVKEQWDELPRLPEETGVLLGSVEVDT
SSPNTLNENGAHKTKTLVADINLSLOSEGLSDDFLDPTDDLDINVDLETDP
ETLSLEFLNGNELEWGDDTPVYATKNMPCGSADLFGDTGTEGGAANGRLWRTVIIG
EQEHRIDLHMRPYMKVVTGHGYYGGLNAILVFAACFLPDSSLFPHYIMENFLVY

```

ISSLELLVAEDYMYVLNLTGATPRRRPGIGWLKKYOMIDRRRLKNLKLIIIVHPSWF
 IRTVLAISRPISVFKFNKYVHSLEDLQLPMEHVQIPDCVLOVEERLKRRES
 ARPOPEFMRSEKPKVAPVENSAPVTDQETMS"

BASE COUNT 657 a 832 c 772 g 526 t
 ORIGIN

Query Match 95.7%; Score 22; DB 9; Length 2787;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCGATGGTGGCAGGTGT 23

Db 2675 AGCCAGGCGATGGTGGCAGGTGT 2696

RESULT 6
 AL451072/c
 LOCUS
 DEFINITION Human DNA sequence from clone RPI-236H13 on chromosome 6, complete sequence.
 AL451072
 VERSION AL451072.14 GI:12666306
 KEYWORDS HTG.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 4913)

REFERENCE Donnelly,S.
 AUTHORS Direct Submission
 TITLE Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 JOURNAL requests: clonerequests@sanger.ac.uk

COMMENT On Feb 5, 2001 this sequence version replaced gi:12657210.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated repeat sequence elements. Where the sequence is
 ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em', EMBL; Sw', SWISSPROT; Tr', TREMBL; Wp', WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr6

RPI-236H13 is from the library RPCI-1 constructed by the group of
 Pieter de Jong. For further details see
 http://www.chori.org/bacpac/home.htm
 VECTOR: pcIPAC2

IMPORTANT: This sequence is not the entire insert of clone
 RPI-236H13 it may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true left end of clone RPI-297M16 is at 4814 in this sequence.
 The true right end of clone RPI1-613F7 is at 100 in this sequence.

FEATURES
 Location/Qualifiers
 source
 1..4913
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RPI-236H13"
 /clone_lib="RPCI-1"
 repeat_region 2..140
 repeat_region /note="L1M4 repeat: matches 25..164 of consensus"
 143..494

/note="L1M4 repeat: matches 2911..3262 of consensus"
 878..1208
 /note="L1M2 repeat: matches 5800..6142 of consensus"
 1209..1522
 /note="AluSp repeat: matches 1..309 of consensus"
 1523..1999
 /note="L1M2 repeat: matches 5374..5800 of consensus"
 2000..2299
 /note="AluX repeat: matches 1..300 of consensus"
 2300..2538
 /note="L1M2 repeat: matches 5127..5374 of consensus"
 2555..2659
 /note="U6 repeat: matches 1..107 of consensus"
 2751..2934
 /note="MER5A repeat: matches 1..189 of consensus"
 3050..3149
 /note="L2 repeat: matches 2466..2560 of consensus"
 3150..3454
 /note="AluX repeat: matches 1..303 of consensus"
 3455..3624
 /note="L2 repeat: matches 2560..2749 of consensus"
 3646..3701
 /note="28 copies 2 mer aa 69% conserved"
 4127..4418
 /note="AluJo repeat: matches 3..290 of consensus"
 4445..4472
 /note="14 copies 2 mer tg 100% conserved"
 4473..4757
 /note="AluX repeat: matches 1..286 of consensus"
 BASE COUNT 1383 a 997 c 949 g 1584 t
 ORIGIN

Query Match 95.7%; Score 22; DB 9; Length 4913;

Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCGATGGTGGCAGGTG 22

Db 3320 CAGCCAGGCGATGGTGGCAGGTG 3299

RESULT 7

LOCUS AP000535

DEFINITION Homo sapiens genomic DNA, chromosome 22q11.2, Cat Eye Syndrome
 region, clone: c58F10.

ACCESSION AP000535 BA000006

VERSION AP000535.1 GI:5931513

KEYWORDS

SOURCE Homo sapiens EB transformed lymphoblast cell line:CH91-157

DNA, clone_lib:Keio Cat Eye Syndrome Cosmid library clone:c58F10.

ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Location/Qualifiers

source

1..39151

/organism="Homo sapiens"

/db_xref="taxon:9606"

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/map="22q11.2"
/clone="c58f10"
/cell_line="EB transformed lymphoblast cell"
/clone_lib="Keio Cat Eye Syndrome Cosmid library"
complement(2930..3218)
/evidence=not_experimental
/rpt_family="AluSc"
complement(3282..3702)
/evidence=not_experimental
/rpt_family="L1p"
4685..4977
/evidence=not_experimental
/rpt_family="AluSg"
complement(6229..6313)
/evidence=not_experimental
/rpt_family="L1MA7"
6331..6481
/evidence=not_experimental
/rpt_family="L1MB3A"
complement(6665..6835)
/evidence=not_experimental
/rpt_family="L1MA8"
complement(6944..7147)
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complement(7168..7281)
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complement(7284..7469)
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complement(7574..7984)
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complement(7985..9000)
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/rpt_family="L1"
complement(8996..10089)
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complement(10081..10238)
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10250..10373
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complement(10459..10755)
/evidence=not_experimental
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complement(11085..11264)
/evidence=not_experimental
/rpt_family="AluSg"
11273..11306
/evidence=not_experimental
/rpt_family="(TTTG)n"
complement(11307..11527)
/evidence=not_experimental
/rpt_family="AluY"
complement(11528..11662)
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/rpt_family="AluSg"
complement(12100..13667)
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complement(14009..14478)
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14491..16655
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complement(17097..17424)

repeat_region
/evidence=not_experimental
/rpt_family="L1M2"
17950..18046
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/rpt_family="MIR"
18072..18093
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/rpt_family="AT_rich"
18433..19005
/evidence=not_experimental
/rpt_family="TAR1"
19030..19050
/evidence=not_experimental
/rpt_family="AT_rich"
19141..19334
/evidence=not_experimental
/rpt_family="(TTAGGG)n"
complement(19343..19783)
/evidence=not_experimental
/rpt_family="L1"
complement(21304..21520)
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complement(21521..21685)
/evidence=not_experimental
/rpt_family="FRAM"
complement(21686..22059)
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/rpt_family="L1M4"
23644..23791
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/rpt_family="L1PBA"
23792..27636
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/rpt_family="L1PBA"
27640..27810
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/rpt_family="AluSp"
27815..28541
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/rpt_family="L1"
28545..28881
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complement(28984..34339)
/evidence=not_experimental
/rpt_family="L1p"
34353..34521
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/rpt_family="L2"
34522..34822
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/rpt_family="AluSg"
34856..35227
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/rpt_family="L2"
35235..35511
/evidence=not_experimental
/rpt_family="AluY"
35512..35561
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35636..35720
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/rpt_family="MIR"
36404..36465
/evidence=not_experimental
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9048. .9322 /evidence=not_experimental
repeat_region /rpt_family="L2"
9603. .9709 /evidence=not_experimental
repeat_region /rpt_family="LTR5"
9905. .9930 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
9931. .10445 /evidence=not_experimental
repeat_region /rpt_family="MER3"
10446. .10480 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
10494. .10780 /evidence=not_experimental
repeat_region /rpt_family="AluSp"
complement(10798. .10989)
/evidence=not_experimental
repeat_region /rpt_family="L1MD2"
10990. .11018 /evidence=not_experimental
repeat_region /rpt_family="(TA)n"
complement(11019. .11088)
/evidence=not_experimental
repeat_region /rpt_family="L1MD2"
complement(11125. .11558)
/evidence=not_experimental
repeat_region /rpt_family="L1MD2"
11712. .11965 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
11971. .12385 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
12386. .12600 /evidence=not_experimental
repeat_region /rpt_family="MER20"
12601. .12788 /evidence=not_experimental
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12789. .13094 /evidence=not_experimental
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13095. .13172 /evidence=not_experimental
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13181. .13671 /evidence=not_experimental
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13748. .14321 /evidence=not_experimental
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14355. .14724 /evidence=not_experimental
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14903. .14938 /evidence=not_experimental
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16330. .16368 /evidence=not_experimental
repeat_region /rpt_family="(CA)n"
16450. .16728 /evidence=not_experimental
repeat_region /rpt_family="AluY"
16742. .16859 /evidence=not_experimental
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17135. .17157 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
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/evidence=not_experimental
repeat_region /rpt_family="AluSx"
18223. .19013 /evidence=not_experimental
repeat_region /rpt_family="L1PA2"
19467. .19487 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
19596. .19657 /evidence=not_experimental
repeat_region /rpt_family="(CATATA)n"
complement(20389. .20420)
/evidence=not_experimental
repeat_region /rpt_family="L2"
20458. .20754 /evidence=not_experimental

Query Match 95.7%; Score 22; DB 9; Length 39668;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 AGCAGGCATGTCGCGAGTGT 23
Db 714 AGCAGGCATGTCGCGAGTGT 735
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RESULT 9
AC010647 AC010647 40102 bp DNA linear PRI 12-DEC-2001
LOCUS Homo sapiens chromosome 19 clone LLNLR-279F8, complete sequence.
DEFINITION AC010647
ACCESSION AC010647
VERSION AC010647.5 GI:17530703
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
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```
REFERENCE 1 (bases 1 to 40102)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 40102)
DOE Joint Genome Institute.
AUTHORS Direct Submission
TITLE Submitted (16-SEP-1999)
JOURNAL Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
```

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REFERENCE 3 (bases 1 to 40102)
DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS Direct Submission
JOURNAL Submitted (12-DEC-2001)
DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 12, 2001 this sequence version replaced gi:8576044.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
```

```
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 45kb). It is clipped at the overlap with AC020895. The
number of bases overlapped is 5950.
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FEATURES
source
1. .40102
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="LLNLR-279F8"
BASE COUNT 9903 a 9289 c 9373 g 11537 t
ORIGIN
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Query Match 95.7%; Score 22; DB 9; Length 40102;
Best Local Similarity 100.0%; Pred. No. 0.0046;
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/note="BLASTN similarity to Z65958 (1..269); match: 0.98,
score: 1.0e-90; database searched: nt; H.sapiens CpG DNA,
clone 69d1, reverse read cpg69d1.rt1a."
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/note="BLASTN similarity to Z65957 (13..213); match: 0.97,
score: 8.4e-71; database searched: nt; H.sapiens CpG DNA,
clone 69d1, forward read cpg69d1.ft1a."
misc_feature
    9351..9498
/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 66.000"
repeat_region
    10096..10160
repeat_region
    /rpt_family="GA)n"
repeat_region
    10360..10445
repeat_region
    /rpt_family="CA)n"
repeat_region
    10449..10574
repeat_region
    /rpt_family="CA)n"
repeat_region
    10796..11097
repeat_region
    /rpt_family="AluSg"
repeat_region
    10796..11095
repeat_region
    /rpt_family="Alu"
repeat_region
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repeat_region
    10796..11095
repeat_region
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repeat_region
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repeat_region
    /rpt_family="Alu"
repeat_region
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repeat_region
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repeat_region
    complement(11213..11464)
repeat_region
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repeat_region
    11803..11903
repeat_region
    /rpt_family="FLAM_C"
repeat_region
    11803..11899
repeat_region
    /rpt_family="Alu"
repeat_region
    11803..11899
repeat_region
    /rpt_family="Alu"
repeat_region
    11949..11995
repeat_region
    /rpt_family="CA)n"
misc_feature
    12173..12491
/note="DDS similarity to AA587610 nm95a11.s1 NCI CGAP Co9
Homo sapiens cDNA clone IMAGE:1075964; (462..144); 100%
identity."
repeat_region
    12467..12547
repeat_region
    /rpt_family="GA)n"
misc_feature
    12542..12684
/note="DDS similarity to AA587610 nm95a11.s1 NCI CGAP Co9
Homo sapiens cDNA clone IMAGE:1075964; (143..1); 99%
identity."
repeat_region
    12650..12691
repeat_region
    /rpt_family="POLY_A"
misc_feature
    complement(14148..14217)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 62.000"
repeat_region
    14398..14698
repeat_region
    /rpt_family="AluY"
repeat_region
    14403..14697
repeat_region
    /rpt_family="Alu"
repeat_region
    14403..14697
repeat_region
    /rpt_family="Alu"
misc_feature
    15157..15522
/note="BLASTN similarity to:
AA922094 (4..369); match: 0.99, score: 6.6e-144; database
searched: month.na; omale09.s1 Soares_NFL_T_GBC_S1 Homo
sapiens cDNA clone IMAGE:1543624 3'~(15178..15466)
AA927168 (1..289); match: 0.98, score: 3.3e-110; database
    95.7%; Score 22; DB 9; Length 41159;
Query Match
Best Local Similarity 100.0%; Pred.No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 AGCCAGGCATGGTGGCAGGTGT 23
    |||||
Db 20977 AGCCAGGCATGGTGGCAGGTGT 20998
```

```
RESULT 11
HSN128A12
LOCUS
DEFINITION
    HSN128A12          41576 bp      DNA          linear      PRI 12-DEC-1999
    Human DNA sequence from clone LL22NC03-128A12 on chromosome 22
    Contains STSs, GSSs and a CpG Island, complete sequence.
VERSION
    275407
KEYWORDS
    HTG; CpG Island.
SOURCE
    Homo sapiens.
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 41576)
REFERENCE
    Hunt,A.
    Direct Submission
    Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
    CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
    requests: clonerequest@sanger.ac.uk
    On Dec 13, 1999 this sequence version replaced gi:1418824.
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.
    This sequence has been finished according to sequence map criteria
    as follows. An attempt is made to resolve all sequencing problems,
    such as compressions and repeats, but not necessarily within known
    annotated human repeat sequence elements (e.g. Alu). Where the
    sequence is ambiguous, there is an annotation using the 'unsure'
    feature key.
    The following abbreviations are used to associate primary accession
    numbers given in the feature table with their source databases:
    Em.: EMBL; SW.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information
    on the WORMPEP database can be found at
    http://www.sanger.ac.uk/projects/C-elegans/wormpep This sequence
    was generated from part of bacterial clone contigs of human
    chromosome 22, constructed by the Sanger Centre Chromosome 22
    Mapping Group. Further information can be found at
    http://www.sanger.ac.uk/HGP/Chr22
    LL22NC03-128A12 is from the human chromosome 22-specific cosmid
    library LL22NC03, constructed at the Biomedical Sciences Division,
    Lawrence Livermore National Laboratory, Livermore, CA 94550 under
    the auspices of the National Laboratory Gene Library Project
    sponsored by the US Department of Energy. The source of the flow
    sorted chromosomes was a human/hamster hybrid containing
    chromosomes Y, 22 and 9. VECTOR: lawrist16
    This sequence is the entire insert of clone LL22NC03-128A12.
FEATURES
    Location/Qualifiers
        1..41576
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="22"
            /clone="LL22NC03-128A12"
            /clone_lib="LL22NC03"
            /notes="4 copies 15 mer 98 conserved"
        repeat_region
            972..1031
            /notes="49 copies 2 mer gg 61 conserved"
        misc_feature
            2836..4733
            /note="CpG island"
            /evidence=not_experimental
        repeat_region
            4555..4656
            /notes="17 copies 6 mer ggcggg 66 conserved"
        repeat_region
            4559..4656
            /notes="THE1B repeat: matches 1..154 of consensus"
        repeat_region
            4923..5228
            /notes="AluX repeat: matches 1..306 of consensus"
        repeat_region
            5685..5866
            /notes="THE1B repeat: matches 1..154 of consensus"
        repeat_region
            5867..6172
            /note="AluY repeat: matches 1..306 of consensus"
        repeat_region
            6173..6373
            /note="THE1B repeat: matches 154..364 of consensus"
        repeat_region
            6484..6713
```

repeat_region /note="MER72 repeat: matches 1. .218 of consensus"
6737. .7214
repeat_region /note="MER72 repeat: matches 136. .668 of consensus"
7361. .7885
repeat_region /note="LTR45 repeat: matches 1. .525 of consensus"
8926. .8973
repeat_region /note="8 copies 6 mer tgata 81 conserved"
9371. .9757
repeat_region /note="L1MD repeat: matches -17. .368 of consensus"
9758. .11291
repeat_region /note="L1MB6 repeat: matches 4553. .6175 of consensus"
11281. .11751
repeat_region /note="L1MD1 repeat: matches 1922. .4386 of consensus"
11752. .12057
repeat_region /note="AluSg repeat: matches 1. .308 of consensus"
12058. .12203
repeat_region /note="L1MD1 repeat: matches 4386. .4529 of consensus"
12204. .12631
repeat_region /note="WSTB repeat: matches 1. .426 of consensus"
12632. .12665
repeat_region /note="L1MD1 repeat: matches 4529. .4561 of consensus"
12666. .12961
repeat_region /note="AluSx repeat: matches 1. .296 of consensus"
12962. .14295
repeat_region /note="L1MD1 repeat: matches 4561. .5893 of consensus"
14296. .14578
repeat_region /note="AluSx repeat: matches 1. .283 of consensus"
14687. .14973
repeat_region /note="L1MD1 repeat: matches 5920. .6216 of consensus"
14986. .15313
repeat_region /note="AluJo repeat: matches 1. .312 of consensus"
15601. .15637
repeat_region /note="L1MD1 repeat: matches 511. .547 of consensus"
15665. .15848
repeat_region /note="L2 repeat: matches 1824. .1986 of consensus"
15849. .16071
repeat_region /note="L1PB1 repeat: matches 5926. .6155 of consensus"
16072. .16405
repeat_region /note="L2 repeat: matches 1411. .1824 of consensus"
16522. .16827
repeat_region /note="AluSg repeat: matches 1. .306 of consensus"
17599. .17757
repeat_region /note="SVA repeat: matches 1. .152 of consensus"
17986. .18184
repeat_region /note="AluSg/x repeat: matches 123. .298 of consensus"
18434. .18795
repeat_region /note="L1M4 repeat: matches 2291. .2620 of consensus"
18796. .19023
repeat_region /note="AluSg/x repeat: matches 67. .293 of consensus"
19024. .19663
repeat_region /note="L1M4 repeat: matches 1831. .2291 of consensus"
19667. .19977
repeat_region /note="AluSx repeat: matches 1. .312 of consensus"
19978. .20108
repeat_region /note="AluJo/FLAM repeat: matches 2. .133 of consensus"
20109. .20421
repeat_region /note="L1M4 repeat: matches 1547. .1831 of consensus"
20672. .21063
repeat_region /note="L1 repeat: matches 4963. .5391 of consensus"
21121. .21439
repeat_region /note="AluSx repeat: matches 1. .311 of consensus"
21666. .22198
repeat_region /note="HAL1 repeat: matches 1024. .1566 of consensus"
complement(21836. .22251)
misc_feature /note="match: GSS: Em:AQ029230; match: STS: Em:G52064"
complement(22209. .22781)
misc_feature /note="match: GSS: Em:AQ233552"
complement(22300. .22783)
misc_feature /note="match: STS: Em:B14416; match: GSS: Em:B14416"
complement(22321. .22783)
misc_feature /note="match: GSS: Em:B13995; match: STS: Em:B13995"
22401. .22516
repeat_region /note="HAL1 repeat: matches 662. .776 of consensus"

misc_feature complement(22566. .22776)
/note="match: GSS: Em:AQ108444"
22714. .22925
repeat_region /note="MER92B repeat: matches 216. .418 of consensus"
22926. .23229
repeat_region /note="AluSg repeat: matches 1. .305 of consensus"
23230. .23437
repeat_region /note="MER92B repeat: matches 418. .628 of consensus"
24404. .24700
repeat_region /note="AluSx repeat: matches 12. .300 of consensus"
24735. .24826
repeat_region /note="MLT1A1 repeat: matches 316. .547 of consensus"
25273. .25582
repeat_region /note="AluSg repeat: matches 1. .306 of consensus"
25609. .26309
repeat_region /note="MER21B repeat: matches 14. .794 of consensus"
26305. .26395
repeat_region /note="MER21B repeat: matches 704. .787 of consensus"
27337. .27637
repeat_region /note="AluSg repeat: matches 1. .310 of consensus"
28507. .28812
repeat_region /note="AluJo repeat: matches 1. .293 of consensus"
28890. .28954
repeat_region /note="MIR repeat: matches 83. .148 of consensus"
29596. .29838
repeat_region /note="L2 repeat: matches 1814. .2071 of consensus"
complement(29957. .30503)
misc_feature /note="match: STS: Em:AL021681; match: STS: Em:HS990A23T"
29977. .30271
repeat_region /note="AluSg repeat: matches 1. .296 of consensus"
31074. .31376
repeat_region /note="AluSg repeat: matches 1. .310 of consensus"
31589. .31847
repeat_region /note="MIR repeat: matches 4. .261 of consensus"
32326. .33013
repeat_region /note="match: GSS: Em:AQ057087"
33138. .33351
repeat_region /note="MIR repeat: matches 15. .242 of consensus"
33456. .33907
misc_feature /note="match: GSS: Em:AQ143587"
34031. .34336
repeat_region /note="AluSp repeat: matches 1. .312 of consensus"
34362. .34654
repeat_region /note="AluSx repeat: matches 1. .298 of consensus"
34559. .34922
repeat_region /note="L2 repeat: matches 2359. .2639 of consensus"
34944. .35120
repeat_region /note="MIR repeat: matches 40. .230 of consensus"
35349. .35410
repeat_region /note="31 copies 2 mer ca 88 conserved"
35363. .35410
repeat_region /note="8 copies 6 mer cacaca 100 conserved"
35431. .35526
repeat_region /note="MIR repeat: matches 47. .146 of consensus"
35565. .35901
repeat_region /note="MLT1A1 repeat: matches 1. .362 of consensus"

Query Match 95.7%; Score 22; DB 9; Length 41576;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGGTGGCAGGTGT 23

Db 11887 AGCCAGGCATGGTGGCAGGTGT 11908

RESULT 12

AL669893 AL669893 44767 bp DNA linear PRI 31-JAN-2002
LOCUS Human DNA sequence from clone RP11-122F10 on chromosome 9, complete
DEFINITION sequence.
ACCESSION AL669893 AC026643
VERSION AL669893.4 GI:18477441

KEYWORDS: HTG.
SOURCE: Homo sapiens
ORGANISM: human.

REFERENCE: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE: Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS: 1 (bases 1 to 44767)
JOURNAL: Skuce,C.

REFERENCE: Direct Submission
TITLE: Submitted (31-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
AUTHORS: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
JOURNAL: Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
COMMENT: On Feb 1, 2002 this sequence version replaced gi:18477022.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw.,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-122F10 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6

FEATURES
source
1..44767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-122F10"
/clone_lib="RPCI-11.1"
BASE COUNT 13104 a 8997 c 8942 g 13724 t

Query Match 95.7%; Score 22; DB 9; Length 44767;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 6357 AGCCAGGCATGGTGGCAGGTGT 6378

RESULT 13
AL583845/c 54154 bp DNA linear PRI 08-FEB-2002
LOCUS Human DNA sequence from clone RP11-211A7 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL583845
VERSION AL583845.16 GI:18643768
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE: Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS: 1 (bases 1 to 56652)
JOURNAL: Skuce,C.

REFERENCE: Direct Submission
TITLE: Submitted (08-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
AUTHORS: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
JOURNAL: Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
COMMENT: On Feb 10, 2002 this sequence version replaced gi:18476654.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw.,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-211A7 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6

FEATURES
Location/Qualifiers
1..54154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-211A7"
/clone_lib="RPCI-11.1"
BASE COUNT 17287 a 10487 c 11029 g 15351 t

Query Match 95.7%; Score 22; DB 9; Length 54154;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 47921 AGCCAGGCATGGTGGCAGGTGT 47900

RESULT 14
AC027427 56652 bp DNA linear HTG 28-NOV-2001
LOCUS Homo sapiens chromosome 1 clone RP11-211A7 map 1, LOW-PASS SEQUENCE
DEFINITION SAMPLING.
ACCESSION AC027427
VERSION AC027427.3 GI:17048288
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE: Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS: 1 (bases 1 to 56652)
JOURNAL: Skuce,C.

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 1, clone RP11-211A7
Unpublished
2 (bases 1 to 5652)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,
Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S.,
Dodgson, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galligan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, J., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lanazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrum, J., Menes, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2001 this sequence version replaced gi:13443233.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE
JOURNAL
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7689
Center clone name: 211_A7

NOTE: This record contains 72 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.

1 712: contig of 712 bp in length
713 812: gap of 100 bp
813 1523: contig of 711 bp in length
1524 1623: gap of 100 bp
1624 2334: contig of 711 bp in length
2335 2434: gap of 100 bp
2435 3148: contig of 714 bp in length
3149 3248: gap of 100 bp
3249 3930: contig of 682 bp in length
3931 4030: gap of 100 bp
4031 4745: contig of 715 bp in length
4746 4845: gap of 100 bp
4846 5529: contig of 684 bp in length
5530 5629: gap of 100 bp
5630 6323: contig of 694 bp in length
6324 6423: gap of 100 bp
6424 7118: contig of 695 bp in length
7119 7218: gap of 100 bp
7219 7899: contig of 681 bp in length
7900 7999: gap of 100 bp
8000 8652: contig of 653 bp in length

8653 8752: gap of 100 bp
8753 9447: contig of 695 bp in length
9448 9547: gap of 100 bp
9548 10205: contig of 658 bp in length
10206 10305: gap of 100 bp
10306 11002: contig of 697 bp in length
11003 11102: gap of 100 bp
11103 11798: contig of 696 bp in length
11799 11898: gap of 100 bp
11899 12566: contig of 668 bp in length
12567 12666: gap of 100 bp
12667 13340: contig of 674 bp in length
13341 13440: gap of 100 bp
13441 14129: contig of 689 bp in length
14130 14239: gap of 100 bp
14239 14893: contig of 664 bp in length
14894 14993: gap of 100 bp
14994 15682: contig of 689 bp in length
15683 15782: gap of 100 bp
15783 16482: contig of 700 bp in length
16483 16582: gap of 100 bp
16583 17273: contig of 691 bp in length
17274 17373: gap of 100 bp
17374 18075: contig of 702 bp in length
18076 18175: gap of 100 bp
18176 18861: contig of 686 bp in length
18862 18961: gap of 100 bp
18962 19639: contig of 678 bp in length
19640 19739: gap of 100 bp
19740 20424: contig of 685 bp in length
20425 20524: gap of 100 bp
20525 21176: contig of 652 bp in length
21177 21276: gap of 100 bp
21277 21958: contig of 682 bp in length
21959 22058: gap of 100 bp
22059 22759: contig of 701 bp in length
22760 22859: gap of 100 bp
22860 23533: contig of 674 bp in length
23534 23633: gap of 100 bp
23634 24340: contig of 707 bp in length
24341 24440: gap of 100 bp
24441 25127: contig of 687 bp in length
25128 25227: gap of 100 bp
25228 25930: contig of 703 bp in length
25931 26030: gap of 100 bp
26031 26715: contig of 685 bp in length
26716 26815: gap of 100 bp
26816 27509: contig of 694 bp in length
27510 27609: gap of 100 bp
27610 28313: contig of 704 bp in length
28314 28413: gap of 100 bp
28414 29109: contig of 696 bp in length
29110 29209: gap of 100 bp
29210 29881: contig of 672 bp in length
29882 29981: gap of 100 bp
29982 30652: contig of 671 bp in length
30653 30752: gap of 100 bp
30753 31432: contig of 680 bp in length
31433 31532: gap of 100 bp
31533 32233: contig of 701 bp in length
32234 32333: gap of 100 bp
32334 32995: contig of 662 bp in length
32996 33095: gap of 100 bp
33096 33776: contig of 681 bp in length
33777 33876: gap of 100 bp
33877 34564: contig of 688 bp in length
34565 34664: gap of 100 bp
34665 35363: contig of 699 bp in length
35364 35463: gap of 100 bp
35464 36128: contig of 663 bp in length
36127 36228: gap of 100 bp
36227 36928: contig of 702 bp in length
36929 37028: gap of 100 bp

```

* 37029 37716: contig of 688 bp in length
* 37717 37816: gap of 100 bp
* 37817 38600: contig of 784 bp in length
* 38601 38700: gap of 100 bp
* 38701 39373: contig of 673 bp in length
* 39374 39473: gap of 100 bp
* 39474 40161: contig of 688 bp in length
* 40162 40261: gap of 100 bp
* 40262 40943: contig of 682 bp in length
* 40944 41043: gap of 100 bp
* 41044 41702: contig of 659 bp in length
* 41703 41802: gap of 100 bp
* 41803 42450: contig of 648 bp in length
* 42451 42550: gap of 100 bp
* 42551 43244: contig of 694 bp in length
* 43245 43344: gap of 100 bp
* 43345 44030: contig of 686 bp in length
* 44031 44130: gap of 100 bp
* 44131 44816: contig of 686 bp in length
* 44817 44916: gap of 100 bp
* 44917 45588: contig of 672 bp in length
* 45589 45688: gap of 100 bp
* 45689 46396: contig of 708 bp in length
* 46397 46496: gap of 100 bp
* 46497 47180: contig of 684 bp in length
* 47181 47280: gap of 100 bp
* 47281 47986: contig of 706 bp in length
* 47987 48086: gap of 100 bp
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* 48864 49540: contig of 677 bp in length
* 49541 49640: gap of 100 bp
* 49641 50321: contig of 681 bp in length
* 50322 50421: gap of 100 bp
* 50422 51103: contig of 682 bp in length
* 51104 51203: gap of 100 bp
* 51204 51872: contig of 669 bp in length
* 51873 51972: gap of 100 bp
* 51973 52660: contig of 688 bp in length
* 52661 52760: gap of 100 bp
* 52761 53474: contig of 714 bp in length
* 53475 53574: gap of 100 bp
* 53575 54281: contig of 707 bp in length

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Query Match 95.7%; Score 22; DB 2; Length 56652;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23

Db 7296 AGCCAGGCATGGTGGCAGGTGT 7317

RESULT 15

AC107942

LOCUS

DEFINITION Homo sapiens chromosome 8 clone RP11-241L13 map 8, LOW-PASS

AC107942 62833 bp DNA linear HTG 24-JAN-2002

VERSION AC107942.1 GI:18308669

KEYWORDS HTG; HTGS PHASE0.

SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1. (bases 1 to 62833)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 8, clone RP11-241L13

Unpublished

2. (bases 1 to 62833)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Rett, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center Project name: L24036

Center Clone name: 241_L_13

* NOTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 4884 5605: contig of 722 bp in length
* 5606 5705: gap of 100 bp
* 5706 6443: contig of 738 bp in length
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* 6544 7263: contig of 720 bp in length
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* 18904 19003: gap of 100 bp
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* 22168 22267: gap of 100 bp
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* 54584 55279: contig of 696 bp in length
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Query Match 95.7%: Score 22; DB 2; Length 62833;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAGCCAGGCATGGTGGCAGGTG 22
| | | | | | | | | | | | | | | | | | | | | |
Db 27542 CAGCCAGGCATGGTGGCAGGTG 27563

Search completed: June 17, 2003, 03:57:01
Job time : 87.3809 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 4.06039 Seconds
(without alignments)
12756.396 Million cell updates/sec

Title: US-09-513-888C-1_COPY_4451_4473
Perfect score: 23
Sequence: 1 cagccagcagtggtgagcaggtgt 23

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	23	100.0	9048	21	AAAG4507 Nucleotide sequenc
2	22	95.7	204	21	AACT5023 Human secreted pro
3	22	95.7	389	23	ABV39095 Human prostate exp
4	22	95.7	440	23	ABV11210 Human prostate exp
5	22	95.7	477	23	ABV05712 Human prostate exp
6	22	95.7	478	23	ABV32356 Human prostate exp
7	22	95.7	478	23	ABV41286 Human prostate exp
8	22	95.7	495	23	ABV15013 Human prostate exp
9	22	95.7	506	23	ABV32243 Human prostate exp

521	23	ABV05844	Human prostate exp
557	23	ABV21254	Human prostate exp
557	23	ABV21288	Human prostate exp
557	23	ABV21292	Human prostate exp
557	23	ABV23638	Human prostate exp
557	23	ABV23898	Human prostate exp
557	23	ABV27022	Human prostate exp
557	23	ABV27075	Human prostate exp
557	23	ABV27107	Human prostate exp
557	23	ABV27111	Human prostate exp
557	23	ABV29498	Human prostate exp
557	23	ABV29567	Human prostate exp
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572	23	ABV14881	Human prostate exp
576	23	ABV14992	Human prostate exp
576	23	ABV44881	Human prostate exp
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639	23	ABV41174	Human prostate exp
639	23	ABV41242	Human prostate exp
639	23	ABV41281	Human prostate exp
639	23	ABV44755	Human prostate exp
639	23	ABV44861	Human prostate exp
850	23	ABV11097	Human prostate exp
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104	22	AAK71042	Human immune/haema
164	22	AAK71115	Human immune/haema
164	22	AAK80860	Human immune/haema
164	22	AAK81552	Human immune/haema
164	22	AAK81744	Human immune/haema
164	22	AAK85684	Human immune/haema
166	22	AAK84501	Human immune/haema
170	24	AAI69073	Activated T-cell d
186	22	AAS32543	Human genomic DNA
186	22	AAK81883	Human immune/haema
278	22	AAS27850	DNA encoding novel
278	22	AAS27651	DNA encoding novel
352	22	AAK97571	Human neuroregulin g
378	22	AAK67025	Human immune/haema
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401	22	AAK97570	Human neuroregulin g
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401	22	AAK97573	Human neuroregulin g
422	22	ABA07807	Human ovarian and
422	22	AAU03606	Human reproductive
504	22	AAK84322	Human immune/haema
525	23	ABV53372	Human prostate exp
527	23	ABN63795	Human cancer relat
534	23	ABV50306	Human prostate exp
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558	24	ABN65992	Human cancer relat
561	22	AAI23014	Human breast cancer
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663	22	AAI14152	Human immune/haema
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715	22	AAK81417	Human immune/haema
748	21	AAC66449	Human secreted pro
763	22	AAI24053	Human breast cancer
824	21	AAC59548	Human secreted pro
1057	22	ABAI18567	Human nervous syst
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83	21	91.3	1154	21	AAH51628	Human g35018 cdna	156	21	91.3	32248	22	ABA20412	Human nervous syst
84	21	91.3	1301	21	AAH51627	Human g35018 cdna	c 157	21	91.3	32248	22	AA137122	Human musculoskele
85	21	91.3	1386	21	AAH51631	Human g35018 cdna	c 158	21	91.3	32248	22	AA526795	Human genomic DNA
86	21	91.3	1378	24	ABA02154	Human signalase I	c 159	21	91.3	33795	24	ABN95686	Gene #184 used to
87	21	91.3	1643	22	ABAI19995	Human nervous syst	c 160	21	91.3	34269	22	AAK85168	Human immune/haema
88	21	91.3	1643	22	ABAI19996	Human nervous syst	c 161	21	91.3	34269	22	AAK85168	Human immune/haema
89	21	91.3	1699	24	ABU92345	Human secreted pro	c 162	21	91.3	36933	22	AAK66362	Human immune/haema
90	21	91.3	1847	21	AA26311	Human secreted pro	c 163	21	91.3	33058	22	ABN97455	Gene #3953 used to
91	21	91.3	1879	22	AAH17119	Human cdna sequenc	c 164	21	91.3	43058	24	ABL64982	Lung cancer relate
92	21	91.3	2509	21	AAAI6679	Human secreted pro	c 165	21	91.3	43058	24	ABL65219	Lung cancer relate
93	21	91.3	2646	22	AAI61012	Human polynucleoti	c 166	21	91.3	43938	22	AAK77216	Human immune/haema
94	21	91.3	2946	22	AAK68591	Human immune/haema	c 167	21	91.3	43938	22	AAK77217	Human immune/haema
95	21	91.3	3172	24	ABL62888	Breast cancer rela	c 168	21	91.3	52616	22	AAK70459	Human immune/haema
96	21	91.3	3172	24	ABL63310	Breast cancer rela	c 169	21	91.3	52616	22	AAK78930	Human immune/haema
97	21	91.3	3209	23	AA586285	DNA encoding novel	c 170	21	91.3	53552	22	AAK13655	Genomic DNA sequen
98	21	91.3	3591	23	AA586915	DNA encoding novel	c 171	21	91.3	56743	22	AAK68202	Human immune/haema
99	21	91.3	4733	22	ABA07211	Human pancreatic c	c 172	21	91.3	56743	22	AAK81760	Human immune/haema
100	21	91.3	4733	22	AAK89843	Human digestive sy	c 173	21	91.3	59065	24	ABL42416	Human serine/threo
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102	21	91.3	5054	22	AAK35968	Human musculoskele	c 175	21	91.3	65608	24	ABL62910	Breast cancer rela
103	21	91.3	6496	22	AAK72255	Human immune/haema	c 176	21	91.3	65608	24	ABL64414	Stomach cancer rel
104	21	91.3	7157	22	ABAI19506	Human nervous syst	c 177	21	91.3	65608	24	ABL67668	Oesophagus cancer
105	21	91.3	7330	22	AAK65121	Human immune/haema	c 178	21	91.3	81001	22	AAF30035	Human apolipoprote
106	21	91.3	7428	22	ABA07164	Human pancreatic c	c 179	21	91.3	84495	24	AA520588	Human methionine a
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109	21	91.3	8272	22	AA528433	Genomic sequence #	c 182	21	91.3	121724	24	ABO88143	Human osteoblast d
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130	21	91.3	8272	22	AA528433	Genomic sequence #	c 203	21	91.3	126512	24	ABN83429	Human transporter
131	21	91.3	8272	22	AA528433	Genomic sequence #	c 204	21	91.3	126512	24	ABN83429	Human transporter
132	21	91.3	8272	22	AA528433	Genomic sequence #	c 205	21	91.3	126512	24	ABN83429	Human transporter
133	21	91.3	8272	22	AA528433	Genomic sequence #	c 206	21	91.3	126512	24	ABN83429	Human transporter
134	21	91.3	8272	22	AA528433	Genomic sequence #	c 207	21	91.3	126512	24	ABN83429	Human transporter
135	21	91.3	8272	22	AA528433	Genomic sequence #	c 208	21	91.3	126512	24	ABN83429	Human transporter
136	21	91.3	8272	22	AA528433	Genomic sequence #	c 209	21	91.3	126512	24	ABN83429	Human transporter
137	21	91.3	8272	22	AA528433	Genomic sequence #	c 210	21	91.3	126512	24	ABN83429	Human transporter
138	21	91.3	8272	22	AA528433	Genomic sequence #	c 211	21	91.3	126512	24	ABN83429	Human transporter
139	21	91.3	8272	22	AA528433	Genomic sequence #	c 212	21	91.3	126512	24	ABN83429	Human transporter
140	21	91.3	8272	22	AA528433	Genomic sequence #	c 213	21	91.3	126512	24	ABN83429	Human transporter
141	21	91.3	8272	22	AA528433	Genomic sequence #	c 214	21	91.3	126512	24	ABN83429	Human transporter
142	21	91.3	8272	22	AA528433	Genomic sequence #	c 215	21	91.3	126512	24	ABN83429	Human transporter
143	21	91.3	8272	22	AA528433	Genomic sequence #	c 216	21	91.3	126512	24	ABN83429	Human transporter
144	21	91.3	8272	22	AA528433	Genomic sequence #	c 217	21	91.3	126512	24	ABN83429	Human transporter
145	21	91.3	8272	22	AA528433	Genomic sequence #	c 218	21	91.3	126512	24	ABN83429	Human transporter
146	21	91.3	8272	22	AA528433	Genomic sequence #	c 219	21	91.3	126512	24	ABN83429	Human transporter
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148	21	91.3	8272	22	AA528433	Genomic sequence #	c 221	21	91.3	126512	24	ABN83429	Human transporter
149	21	91.3	8272	22	AA528433	Genomic sequence #	c 222	21	91.3	126512	24	ABN83429	Human transporter
150	21	91.3	8272	22	AA528433	Genomic sequence #	c 223	21	91.3	126512	24	ABN83429	Human transporter
151	21	91.3	8272	22	AA528433	Genomic sequence #	c 224	21	91.3	126512	24	ABN83429	Human transporter
152	21	91.3	8272	22	AA528433	Genomic sequence #	c 225	21	91.3	126512	24	ABN83429	Human transporter
153	21	91.3	8272	22	AA528433	Genomic sequence #	c 226	21	91.3	126512	24	ABN83429	Human transporter
154	21	91.3	8272	22	AA528433	Genomic sequence #	c 227	21	91.3	126512	24	ABN83429	Human transporter
155	21	91.3	8272	22	AA528433	Genomic sequence #	c 228	21	91.3	126512	24	ABN83429	Human transporter

c 229	19	82.6	232	22	AA832771	Human genomic DNA	302	19	82.6	1495	20	AA224848	Human secreted pro
c 230	19	82.6	233	21	AA804872	Human secreted pro	303	19	82.6	1656	22	AAI80590	Human polynucleoti
c 231	19	82.6	234	21	AA818108	Human immune/haema	c 304	19	82.6	1719	22	AAI06358	Human reproductive
c 232	19	82.6	244	21	AA814071	Human secreted pro	305	19	82.6	1739	22	AAH15160	Human cDNA sequenc
c 233	19	82.6	287	24	ABU84027	Human ovarian canc	306	19	82.6	1746	20	AAH41403	Human normal pancr
c 234	19	82.6	292	22	AA818103	Human immune/haema	307	19	82.6	1851	22	AAH17054	Human cDNA sequenc
c 235	19	82.6	295	22	AA818104	Human immune/haema	308	19	82.6	1886	21	AAI069532	Human secreted pro
c 236	19	82.6	296	22	AA839695	Genomic sequence #	309	19	82.6	2049	22	AAH14874	Human cDNA sequenc
c 237	19	82.6	296	22	AA890038	Human digestive sy	310	19	82.6	2129	24	ABL69992	Pancreas cancer re
c 238	19	82.6	298	22	AAK73170	Human immune/haema	311	19	82.6	2129	24	AAD28256	Human pancreatic t
c 239	19	82.6	305	22	ABAI5810	Human nervous syst	312	19	82.6	2155	22	AAK72886	Human immune/haema
c 240	19	82.6	305	22	ABAI5810	Human nervous syst	313	19	82.6	2155	22	AAK72886	Human immune/haema
c 241	19	82.6	317	24	ABU84024	Human ovarian canc	314	19	82.6	2168	22	AAK94515	Human full-length
c 242	19	82.6	322	21	AA805361	Human secreted pro	315	19	82.6	2515	22	AAI17444	Human granulocyte
c 243	19	82.6	324	23	ABV53523	Human prostate exp	316	19	82.6	2557	22	AAH18475	Human cDNA sequenc
c 244	19	82.6	336	21	AA828935	Human secreted pro	317	19	82.6	2620	22	AAH18417	Human cDNA sequenc
c 245	19	82.6	360	22	AAK62217	Human immune/haema	c 318	19	82.6	2620	22	AAH18417	Human cDNA sequenc
c 246	19	82.6	362	21	AA813772	Human secreted pro	319	19	82.6	2863	22	AAU07837	Human secreted pro
c 247	19	82.6	362	21	AA814578	Human secreted pro	c 320	19	82.6	2969	24	ABL62909	Breast cancer rela
c 248	19	82.6	365	24	ABU84760	Human ovarian canc	321	19	82.6	3139	22	AAK71190	Human immune/haema
c 249	19	82.6	394	22	AA866101	Novel human polynu	c 322	19	82.6	3142	22	AAH17357	Human cDNA sequenc
c 250	19	82.6	401	22	AA865965	Novel human polynu	323	19	82.6	3144	22	AAH13942	Human cDNA sequenc
c 251	19	82.6	403	21	AA800508	Human secreted pro	324	19	82.6	3148	22	AAH17290	Human cDNA sequenc
c 252	19	82.6	409	24	ABN62750	Human cancer relat	c 325	19	82.6	3185	22	AAH57528	Human pancreas cel
c 253	19	82.6	412	24	ABN62750	Human cancer relat	326	19	82.6	3309	23	AA872615	DNA encoding novel
c 254	19	82.6	439	23	ABV05075	Human ovarian canc	327	19	82.6	3323	22	AA832820	Human genomic DNA
c 255	19	82.6	443	21	AAAI6023	Human prostate exp	328	19	82.6	3807	22	AA810456	Human stem cell fa
c 256	19	82.6	455	23	ABV14244	Human colon cancer	329	19	82.6	3807	22	AAH411340	Human stem cell f
c 257	19	82.6	478	23	ABV35337	Human prostate exp	330	19	82.6	3807	22	AA804120	Human genomic SCF
c 258	19	82.6	478	23	ABV44168	Human prostate exp	331	19	82.6	3807	22	AA804221	Human genomic SCF
c 259	19	82.6	485	23	ABV46908	Human prostate exp	332	19	82.6	3807	22	AA823898	Human genomic SCF
c 260	19	82.6	496	22	AAH04570	Human cDNA clone (333	19	82.6	3807	22	AA8F89100	Human stem cell fa
c 261	19	82.6	496	22	AAH04570	Human cancer relat	334	19	82.6	3807	22	AA835473	Human stem cell fa
c 262	19	82.6	507	22	AAK92960	Human cDNA 3'-end	335	19	82.6	4063	12	AAQ11540	Human Stem Cell fa
c 263	19	82.6	511	24	ABN63173	Human cancer relat	336	19	82.6	4412	22	AAH57372	Human heart cell s
c 264	19	82.6	543	23	ABV57782	Human prostate exp	c 337	19	82.6	4544	22	ABA15386	Human nervous syst
c 265	19	82.6	548	22	AAH09088	Human cDNA clone (338	19	82.6	4864	22	ABA09670	Human bone marrow
c 266	19	82.6	554	22	AAH09895	Human cDNA clone (339	19	82.6	5069	22	AAK67404	Human immune/haema
c 267	19	82.6	559	22	AAH10571	Human cDNA clone (c 340	19	82.6	5075	22	ABA16701	Human nervous syst
c 268	19	82.6	573	22	AA835984	Human cardiovascular	c 341	19	82.6	5076	22	ABA16699	Human nervous syst
c 269	19	82.6	576	24	ABN65904	Human cancer relat	c 342	19	82.6	5101	22	AA811960	Human immune/haema
c 270	19	82.6	579	24	ABN65230	Human cancer relat	c 343	19	82.6	5107	22	AAK81959	Human immune/haema
c 271	19	82.6	583	22	AA8F93607	cDNA isolated from	c 344	19	82.6	5118	22	AAK81958	Human immune/haema
c 272	19	82.6	584	24	ABN64986	Human cancer relat	345	19	82.6	5351	22	AA831466	Human DNA for a no
c 273	19	82.6	601	23	ABV53883	Human prostate exp	346	19	82.6	5351	24	ABQ66790	Human polynucleoti
c 274	19	82.6	619	22	AAK79318	Human immune/haema	347	19	82.6	5646	22	AAI03136	Human reproductive
c 275	19	82.6	620	22	AAK79317	Human immune/haema	348	19	82.6	5864	22	AA810458	Human stem cell fa
c 276	19	82.6	622	23	ABV51983	Human prostate exp	349	19	82.6	5864	22	AAH41342	Human stem cell fa
c 277	19	82.6	625	24	ABQ57233	Human colon cancer	350	19	82.6	5864	22	AA804122	Human SCF (stem ce
c 278	19	82.6	644	22	AA834255	Human cDNA encodin	351	19	82.6	5864	22	AA804223	Human SCF (stem ce
c 279	19	82.6	669	24	ABN62557	Human cancer relat	352	19	82.6	5864	22	AAH23900	Human SCF (stem ce
c 280	19	82.6	700	22	AAH92707	Human inflammatory	353	19	82.6	5864	22	AA8F89102	Human stem cell fa
c 281	19	82.6	708	22	AAH17113	Human prostate exp	c 354	19	82.6	5864	24	AA835475	Human stem cell fa
c 282	19	82.6	713	21	AA810667	Human secreted pro	c 355	19	82.6	5917	24	ABK84584	Human cDNA differe
c 283	19	82.6	750	20	AA817166	Human gene express	356	19	82.6	6235	21	AA8229169	Human G-CSF genomi
c 284	19	82.6	753	24	ABQ89117	Human prostate exp	357	19	82.6	6437	22	AAK82889	Human immune/haema
c 285	19	82.6	754	21	AA802212	Human colon cancer	358	19	82.6	6461	22	AA831467	Human DNA for a no
c 286	19	82.6	764	20	AA215768	Human gene express	359	19	82.6	6461	24	ABQ66791	Human polynucleoti
c 287	19	82.6	764	20	AA215768	Human gene express	c 360	19	82.6	6579	22	AAK70497	Human immune/haema
c 288	19	82.6	777	22	AAH04994	Human cDNA clone (361	19	82.6	6670	21	AAI02846	Human reproductive
c 289	19	82.6	796	21	AAAI3767	Human stem cell fa	362	19	82.6	6679	21	AAI02846	Partial sequence o
c 290	19	82.6	798	16	AA804886	Human SCF genomic	363	19	82.6	6679	22	AAI17443	Human granulocyte
c 291	19	82.6	802	22	AA839814	Genomic sequence #	c 364	19	82.6	6767	22	AAK83499	Human immune/haema
c 292	19	82.6	802	22	AA839814	Human digestive sy	c 365	19	82.6	7032	23	ABK42542	Genomic sequence #
c 293	19	82.6	874	21	AA858898	cDNA sequence of a	366	19	82.6	7032	22	ABA20748	Human nervous syst
c 294	19	82.6	916	22	AAI93223	Human polynucleoti	367	19	82.6	7052	22	AAI37450	Human musculoskele
c 295	19	82.6	924	21	AA858888	cDNA sequence of a	368	19	82.6	7105	22	AAI37450	Human bradykinin r
c 296	19	82.6	1046	22	AAH18696	Human cDNA sequenc	369	19	82.6	7328	21	AA820874	Human bradykinin r
c 297	19	82.6	1089	22	AA807902	Human secreted pro	370	19	82.6	7328	21	AA820887	Human bradykinin r
c 298	19	82.6	1136	22	ABAI4624	Human nervous syst	371	19	82.6	7328	21	AA820887	Human bradykinin r
c 299	19	82.6	1238	22	AAK82426	Human immune/haema	372	19	82.6	7328	21	AAA34756	Human adenosine re
c 300	19	82.6	1238	22	AAK82427	Human immune/haema	373	19	82.6	7328	21	AAA34765	Human adenosine re
c 301	19	82.6	1238	22	AAK82428	Human immune/haema	374	19	82.6	7713	22	AAI02845	Human reproductive

375	19	82.6	8271	22	AAK78824	Human immune/haema	C 448	19	82.6	21535	22	AAS29814	Human cytoskeletal
C 376	19	82.6	8387	22	ABA14892	Human nervous syst	C 449	19	82.6	21535	22	AAS35081	DNA #31 encoding h
C 377	19	82.6	8418	22	AAK4548	Human immune/haema	C 450	19	82.6	22465	22	ABK42133	Genomic sequence #
C 378	19	82.6	8575	22	AAS41906	Genomic sequence #	451	19	82.6	22465	22	ABK86932	Human immune/haema
379	19	82.6	8575	23	ABL06019	Human reproductive	C 452	19	82.6	23802	22	AAK75632	Human immune/haema
380	19	82.6	8575	23	ABL98584	Human testicular a	C 453	19	82.6	24110	22	AAD16628	Human novel protei
C 381	19	82.6	8622	21	AAS95912	Human KIK-L3 gene.	C 454	19	82.6	25715	22	AAS33462	DNA encoding human
382	19	82.6	9058	22	AAS41691	Genomic sequence #	C 455	19	82.6	25806	22	AAK86766	Human immune/haema
C 383	19	82.6	9180	19	AAV57416	Tumour suppressor	C 456	19	82.6	26372	22	AAK77103	Human immune/haema
C 384	19	82.6	9180	24	ABN96964	Gene #3462 used to	C 457	19	82.6	27754	24	ABQ72998	Human transporter
385	19	82.6	9337	22	AAK76038	Human immune/haema	C 458	19	82.6	28313	22	AAL36829	Human musculoskele
386	19	82.6	9337	22	AAK78564	Human immune/haema	C 459	19	82.6	28444	24	ABK86948	Human gluthathione
387	19	82.6	9469	22	AAK79514	Human immune/haema	C 460	19	82.6	28690	22	AAK7718	Human IL4Ralpha ge
388	19	82.6	9780	22	AAK72360	Human immune/haema	C 461	19	82.6	29228	22	AAL36833	Human musculoskele
389	19	82.6	9969	22	AAL04217	Human reproductive	C 462	19	82.6	30110	22	AAK89230	Human digestive sy
390	19	82.6	10684	17	AAT33758	Control region iso	C 463	19	82.6	30620	22	AAK66931	Human immune/haema
C 391	19	82.6	10872	22	AAL03182	Human reproductive	C 464	19	82.6	31730	22	AAL37445	Human musculoskele
C 392	19	82.6	10926	22	AAK65370	Human immune/haema	C 465	19	82.6	31853	22	AAI98993	Human excretory re
C 393	19	82.6	11101	24	ABN83947	Human transporter	C 466	19	82.6	31853	22	AAI63343	Human kidney relat
C 394	19	82.6	11125	22	AAK66446	Human immune/haema	C 467	19	82.6	31934	22	AAS30619	DNA encoding novel
C 395	19	82.6	11150	22	ABA07766	Human ovarian and	C 468	19	82.6	31934	22	AAS28165	Genomic sequence #
C 396	19	82.6	11150	22	AAL03557	Human reproductive	C 469	19	82.6	32148	22	AAL04218	Human reproductive
397	19	82.6	11150	22	AAK68451	Human immune/haema	C 470	19	82.6	32169	22	ABA14358	Human nervous syst
C 398	19	82.6	11150	22	AAK72674	Human immune/haema	C 471	19	82.6	32173	22	ABA07767	Human ovarian and
C 399	19	82.6	11474	23	ABK42672	Genomic sequence #	C 472	19	82.6	32173	22	AAU03558	Human reproductive
C 400	19	82.6	11881	22	AAS36624	Human cardiovascular	C 473	19	82.6	32177	22	AAL36886	Human musculoskele
C 401	19	82.6	11881	22	AAS27691	DNA encoding novel	C 474	19	82.6	32177	22	AAL04279	Human reproductive
C 402	19	82.6	11881	22	AAS27693	DNA encoding novel	C 475	19	82.6	32191	22	AAL37009	Human musculoskele
403	19	82.6	12045	22	AAL07066	Human reproductive	C 476	19	82.6	32199	22	AAK90296	Human digestive sy
404	19	82.6	12267	22	AAK85733	Human immune/haema	C 477	19	82.6	32199	22	AAI57673	Human colorectal c
405	19	82.6	12555	22	ABA18329	Human nervous syst	C 478	19	82.6	32224	22	AAK89986	Human digestive sy
C 406	19	82.6	12638	22	AAK70641	Human immune/haema	C 479	19	82.6	32247	22	ABA19669	Human nervous syst
407	19	82.6	12904	22	AAK85382	Human immune/haema	C 480	19	82.6	33747	22	AAK69279	Human immune/haema
408	19	82.6	13209	22	AAK81554	Human digestive sy	C 481	19	82.6	33747	22	AAK73093	Human immune/haema
409	19	82.6	13273	22	AAK96568	Human digestive sy	C 482	19	82.6	33747	22	AAK73093	ATM complete genom
C 410	19	82.6	13287	22	ABA14431	Human nervous syst	C 483	19	82.6	36797	24	AAK26738	Human synaptosomal
411	19	82.6	13646	24	AAS20126	Human gene for ret	C 484	19	82.6	36797	24	AAD26738	Human synaptosomal
412	19	82.6	13646	24	AAS20128	Human gene for ret	C 485	19	82.6	36797	24	AAD26830	Human SNAP29 gene
C 413	19	82.6	13912	22	AAK82686	Human immune/haema	C 486	19	82.6	36797	24	AAD26830	Human SNAP29 gene
C 414	19	82.6	14543	24	ABK15798	Human of Hippel-L	C 487	19	82.6	38136	22	AAK82172	Human immune/haema
C 415	19	82.6	15929	22	ABA18496	Human nervous syst	C 488	19	82.6	38140	22	AAK82171	Human immune/haema
C 416	19	82.6	15929	22	ABA19020	Human nervous syst	C 489	19	82.6	38653	22	AAK72348	Human immune/haema
C 417	19	82.6	15964	22	ABA18497	Human nervous syst	C 490	19	82.6	38928	22	AAK68452	Human immune/haema
C 418	19	82.6	15964	22	ABA19021	Human nervous syst	C 491	19	82.6	39353	22	AAK65396	Human immune/haema
C 419	19	82.6	17509	24	ABN95599	Gene #2097 used to	C 492	19	82.6	39353	22	AAK67232	Human immune/haema
420	19	82.6	17672	22	ABA15809	Human nervous syst	C 493	19	82.6	39358	22	AAK65397	Human immune/haema
421	19	82.6	17672	22	ABA18641	Human nervous syst	C 494	19	82.6	39358	22	AAK67233	Human immune/haema
422	19	82.6	17687	22	AAS42069	Genomic sequence #	C 495	19	82.6	43680	24	ABK62024	Human genomic clon
423	19	82.6	18534	24	ABK84757	Human cDNA differe	C 496	19	82.6	43680	24	ABK62024	Human bradykinin r
424	19	82.6	18664	22	AAK65421	Human immune/haema	C 497	19	82.6	49744	24	ABK12807	Human tumour suppr
C 425	19	82.6	18664	22	AAK84438	Human immune/haema	C 498	19	82.6	50442	22	AAK73083	Human immune/haema
C 426	19	82.6	18820	22	ABA07938	Human ovarian and	C 499	19	82.6	50442	22	AAK87551	Human immune/haema
C 427	19	82.6	18820	22	AAL03764	Human reproductive	C 500	19	82.6	54548	21	AAZ45596	DNA sequence of th
C 428	19	82.6	19199	22	AAK70995	Human immune/haema	C 501	19	82.6	55008	22	AAK80495	Human immune/haema
429	19	82.6	19472	22	AAS26724	Human genomic DNA	C 502	19	82.6	57248	24	ABK83563	Human cDNA differe
C 430	19	82.6	19696	22	AAS40722	DNA encoding human	C 503	19	82.6	5837	24	ABK52612	Human Claspino geno
C 431	19	82.6	19696	22	AAL06639	Human reproductive	C 504	19	82.6	65608	24	ABL62910	Breast cancer rela
C 432	19	82.6	19815	22	AAS42084	Genomic sequence #	C 505	19	82.6	65608	24	ABL64414	Stomach cancer rel
C 433	19	82.6	19965	22	AAK73166	Human immune/haema	C 506	19	82.6	65608	24	ABL67668	Oesophagus cancer
C 434	19	82.6	19965	24	ABK69932	Human secreted pro	C 507	19	82.6	72928	20	AAZ18355	Human ASTHJ 5' ge
C 435	19	82.6	20420	22	AAK73165	Human immune/haema	C 508	19	82.6	72928	21	AAA80253	Human ASTHJ 5' ge
C 436	19	82.6	20420	24	ABK69933	Human secreted pro	C 509	19	82.6	78925	21	AAK89888	Human FN gene. Ho
C 437	19	82.6	20444	22	AAS34643	Human DNA for a no	C 510	19	82.6	86080	24	ABQ88164	Human osteoblast d
C 438	19	82.6	20444	22	AAL06734	Human reproductive	C 511	19	82.6	86080	24	ABQ88164	Human osteoblast d
C 439	19	82.6	20444	22	AAK66859	Human immune/haema	C 512	19	82.6	86080	24	ABK83561	Human cDNA differe
C 440	19	82.6	20444	22	AAI62640	Human breast or ov	C 513	19	82.6	86080	24	ABK83561	Human cDNA differe
441	19	82.6	20445	24	AAS19906	Reference sequence	C 514	19	82.6	103747	24	ABQ88139	Human osteoblast d
442	19	82.6	20835	22	AAK86765	Human immune/haema	C 515	19	82.6	107602	24	AAK99657	DNA of the PAC clo
443	19	82.6	20892	22	ABA15709	Human nervous syst	C 516	19	82.6	107602	24	AAK99657	DNA of the PAC clo
444	19	82.6	21371	22	AAL04330	Human reproductive	C 517	19	82.6	107612	24	ABL54503	Human PAC clone se
C 445	19	82.6	21371	22	AAL04330	Human reproductive	C 518	19	82.6	107612	24	ABL54503	Human PAC clone se
446	19	82.6	21441	22	AAI62661	Human reproductive	C 519	19	82.6	110000	22	AAK84800	Nucleotide sequenc
447	19	82.6	21441	22	AAI62661	Human breast or ov	C 520	19	82.6	114793	22	AAD08215	Human genome from

521	19	82.6	117574	24	AA45288	Human KCNB1 gene.	594	18	78.3	2598	24	ABL53964	Leukaemia-associat
522	19	82.6	117609	21	AA721435	Human receptor-rel	595	18	78.3	2724	22	AAK70661	Human immune/haema
523	19	82.6	149480	24	ABL61947	Colon adenocarcino	596	18	78.3	3441	22	ABL53963	Leukaemia-associat
524	19	82.6	149480	24	ABL61948	Colon adenocarcino	597	18	78.3	3858	24	ABK35905	CDNA sequence #296
525	19	82.6	149480	24	ABL68345	Kidney cancer rela	598	18	78.3	5646	22	ABL03136	Human reproductive
526	19	82.6	160271	22	AA85750	Bipolar affective	599	18	78.3	6298	22	ABAI5614	Human nervous syst
527	19	82.6	160271	22	AA85756	Human chromosome 1	600	18	78.3	6418	22	AAK80271	Human immune/haema
528	19	82.6	160271	22	AA804858	Human chromosome 1	601	18	78.3	6987	24	ABL53954	Leukaemia-associat
529	19	82.6	160271	22	AA804864	Human chromosome 1	602	18	78.3	6990	24	ABL53969	Leukaemia-associat
530	19	82.6	160271	22	AA806667	Human chromosome 1	603	18	78.3	8342	16	AAO75209	ALL-1 (acute lymph
531	19	82.6	160271	22	AA840997	160kb fragment of	604	18	78.3	8391	17	AAAT16333	MLL gene 8.3 kb fr
532	19	82.6	160271	22	AA823764	Human chromosome 1	605	18	78.3	8392	15	AAO53478	MLL gene 8.3 kb Ba
533	19	82.6	160271	22	AA851116	Nucleotide sequenc	606	18	78.3	8392	21	AAA99882	Human MLL gene 8.3
534	19	82.6	167343	24	ABL64403	Stomach cancer rel	607	18	78.3	8903	22	AAK81314	Human immune/haema
535	19	82.6	167343	24	ABL67239	Thyroid cancer rel	608	18	78.3	9910	22	ABA18525	Human nervous syst
536	19	82.6	172570	24	ABQ88207	Human osteoblast d	609	18	78.3	9968	22	AA832240	Human DNA repair a
537	19	82.6	201143	24	ABK83568	Human DNA differen	610	18	78.3	10646	22	AA842119	Genomic sequence #
538	19	82.6	220895	24	ABK84798	Human cDNA differe	611	18	78.3	11617	22	AAK75374	Human immune/haema
539	19	82.6	240825	22	AA824497	Human PG-3 gene.	612	18	78.3	11617	22	AAI62937	Human immune/haema
540	19	82.6	325791	22	AA843104	Human Oestrogen re	613	18	78.3	11618	22	AAI62937	Human genomic DNA
541	19	82.6	465237	24	ABQ87681	Human oestrogen re	614	18	78.3	12026	22	AAI07202	Human reproductive
542	19	82.6	465237	24	ABA90193	Human oestrogen re	615	18	78.3	11618	22	AAK87088	Human immune/haema
543	18	78.3	67	21	AA816875	Human secreted pro	616	18	78.3	11837	22	AAK33447	DNA encoding human
544	18	78.3	154	22	AAK69174	Human immune/haema	617	18	78.3	11837	22	AAK89070	Human digestive sy
545	18	78.3	154	22	AAK72592	Human immune/haema	618	18	78.3	11837	22	AAK33429	DNA encoding human
546	18	78.3	154	22	AAK87057	Human immune/haema	619	18	78.3	11977	22	AAK26752	Human genomic DNA
547	18	78.3	177	21	AA811637	Human secreted pro	620	18	78.3	15016	24	ABN97288	Human immune/haema
548	18	78.3	221	21	AA811576	Human secreted pro	621	18	78.3	15040	23	AAK83336	DNA encoding novel
549	18	78.3	221	21	AA811629	Human secreted pro	622	18	78.3	15413	22	AAK84002	Human immune/haema
550	18	78.3	222	21	AA820494	Human secreted pro	623	18	78.3	15714	22	AAK36855	Human cardiovascular
551	18	78.3	230	22	AA812556	Human secreted pro	624	18	78.3	16854	22	AAK29953	Human lung antigen
552	18	78.3	298	22	AA839880	Genomic sequence #	625	18	78.3	22609	22	AAK35781	Human musculooskele
553	18	78.3	298	22	AAK90251	Human digestive sy	626	18	78.3	22791	22	AAK69857	Human immune/haema
554	18	78.3	307	21	AA812365	Human secreted pro	627	18	78.3	27733	22	ABA19324	Human nervous syst
555	18	78.3	316	21	AA806081	Human secreted pro	628	18	78.3	28031	22	ABA15375	Human nervous syst
556	18	78.3	324	21	AA827575	Human secreted pro	629	18	78.3	28091	22	AAK77432	Human immune/haema
557	18	78.3	329	22	AA835078	Human musculooskele	630	18	78.3	28120	22	ABA15379	Human immune/haema
558	18	78.3	334	22	AA839680	Human cDNA encodin	631	18	78.3	28120	22	AAK77434	Human immune/haema
559	18	78.3	343	22	AA839950	Novel human diagno	632	18	78.3	32170	22	AAK28674	Genomic sequence #
560	18	78.3	344	21	AA804671	Human secreted pro	633	18	78.3	32172	22	AAI03473	Human reproductive
561	18	78.3	370	24	ABN62430	Human cancer relat	634	18	78.3	32191	22	AAI199472	Human excretory re
562	18	78.3	404	23	ABV13477	Human prostate exp	635	18	78.3	32191	22	AAI644117	Human bladder rela
563	18	78.3	415	22	ABAI5660	Human nervous syst	636	18	78.3	32193	22	AAI35782	Human musculooskele
564	18	78.3	420	23	ABV04308	Human prostate exp	637	18	78.3	32207	22	ABA19666	Human nervous syst
565	18	78.3	450	23	ABV434593	Human prostate exp	638	18	78.3	32220	22	AAK37568	Human musculooskele
566	18	78.3	450	23	ABV43449	Human prostate exp	639	18	78.3	35871	22	AAK84974	Human immune/haema
567	18	78.3	464	24	ABN63079	Human cancer relat	640	18	78.3	36485	22	AAK68958	Human immune/haema
568	18	78.3	471	24	ABN60790	Human cancer relat	641	18	78.3	36485	22	AAK74751	Human immune/haema
569	18	78.3	481	24	ABL67184	Thyroid cancer rel	642	18	78.3	36501	22	AAK64829	Human immune/haema
570	18	78.3	505	23	ABV59211	Human prostate exp	643	18	78.3	36741	22	AA803388	Human adenosine de
571	18	78.3	507	23	ABV56087	Human prostate exp	644	18	78.3	36741	24	ABQ88153	Human osteoblast d
572	18	78.3	522	22	AAH13056	Human cDNA clone (645	18	78.3	39567	22	AAK74053	Human immune/haema
573	18	78.3	589	22	AAK80167	Human immune/haema	646	18	78.3	44840	22	AAK71803	Human immune/haema
574	18	78.3	589	22	AAK80168	Human immune/haema	647	18	78.3	48045	22	AAK84730	Human immune/haema
575	18	78.3	589	23	ABK42206	Genomic sequence #	648	18	78.3	48045	22	AAK85984	Human immune/haema
576	18	78.3	589	23	ABK42207	Genomic sequence #	649	18	78.3	49634	24	ABL68647	Human osteoblast d
577	18	78.3	590	23	ABV54949	Human prostate exp	650	18	78.3	65854	22	AAK63282	Human immune/haema
578	18	78.3	614	20	AAV88921	EST clone HW591.	651	18	78.3	74586	24	AA816905	Genomic DNA encodi
579	18	78.3	624	22	ABAI3299	Human nervous syst	652	18	78.3	114793	22	AAO8215	Human genome from
580	18	78.3	646	22	AAH07587	Human cDNA clone (653	18	78.3	143899	24	AAI38336	Genomic sequence e
581	18	78.3	694	21	AA816599	N. meningitidis pa	654	18	78.3	154465	24	AAI38336	Human AKAP allelic
582	18	78.3	694	22	AAK71512	Human immune/haema	655	18	78.3	154465	24	AAI38336	Human AKAP allelic
583	18	78.3	700	22	AAH93132	Human inflammatory	656	18	78.3	158245	24	AAH28762	Human AKAP10 gene
584	18	78.3	749	22	AAI21412	Human breast cance	657	18	78.3	161425	22	AAH02340	Human AKAP10 gene
585	18	78.3	857	20	AAK20490	Human secreted pro	658	18	78.3	162025	22	AAH28758	Human AKAP allelic
586	18	78.3	890	22	ABA08695	Human secreted pro	659	18	78.3	162025	24	AAH28758	Human AKAP allelic
587	18	78.3	1007	22	ABAI15347	Human nervous syst	660	18	78.3	162450	21	AAI28763	Human AKAP allelic
588	18	78.3	1126	22	AAK90781	Human digestive sy	661	18	78.3	175737	24	ABK83571	Human cDNA differe
589	18	78.3	1133	22	AAK90783	Human digestive sy	662	18	78.3	198285	24	ABK84699	Human cDNA differe
590	18	78.3	1133	22	AAK90784	Human digestive sy	663	18	78.3	198285	24	ABK97319	Human cDNA differe
591	18	78.3	1485	21	AAK74370	Human secreted pro	664	18	78.3	201143	24	ABK83568	Human DNA differen
592	18	78.3	1730	22	ABA06547	Human cDNA SEQ ID	665	18	78.3	235033	19	AAV57926	Hereditary haemoch
593	18	78.3	2198	22	AAH18029	Human cDNA sequenc	666	18	78.3	237326	19	AAV57903	Hereditary haemoch

667	18	78.3	302250	24	ABL67703	Oesophagus cancer	740	17	73.9	266	24	ABL84721	Human ovarian canc
668	17	73.9	47	21	AAZ67562	Human map-related	741	17	73.9	269	22	ABA14427	Human nervous syst
669	17	73.9	51	22	AAI75713	Human silent SNP c	742	17	73.9	270	21	AAC23148	Human secreted pro
670	17	73.9	51	22	AAI75864	Human nonconservat	743	17	73.9	272	22	AAK85288	Human immune/haema
671	17	73.9	51	22	AAH89316	Human coding sequ	744	17	73.9	274	22	AAK82889	Human immune/haema
672	17	73.9	51	22	AAH89566	Human coding sequ	745	17	73.9	278	22	AAK82889	Human reproductive
673	17	73.9	83	22	AAI36934	Human musculoskele	746	17	73.9	281	21	AAL04186	Human secreted pro
674	17	73.9	83	22	AAK84808	Human immune/haema	747	17	73.9	289	21	AAC31043	Human secreted pro
675	17	73.9	83	22	AAK84809	Human immune/haema	748	17	73.9	300	20	AAK98324	Human cancer cell
676	17	73.9	86	22	AAK76473	Human immune/haema	749	17	73.9	300	21	AAC30183	Human secreted pro
677	17	73.9	87	22	AAK36541	Human cardiovascu	750	17	73.9	300	21	AAA00567	Human colon cancer
678	17	73.9	89	22	AAK85201	Human immune/haema	751	17	73.9	302	21	AAC23855	Human secreted pro
679	17	73.9	99	22	AAK83638	Human immune/haema	752	17	73.9	303	21	AAC00363	Human secreted pro
680	17	73.9	99	22	AAK83639	Human immune/haema	753	17	73.9	314	22	AAK72490	Human immune/haema
681	17	73.9	102	22	AAK87320	Human immune/haema	754	17	73.9	315	22	ABA19757	Human nervous syst
682	17	73.9	102	22	AAK67321	Human immune/haema	755	17	73.9	319	22	AAK79658	Human immune/haema
683	17	73.9	102	22	AAK67322	Human immune/haema	756	17	73.9	323	22	AAK79658	Human immune/haema
684	17	73.9	102	22	AAK83184	Human immune/haema	757	17	73.9	323	24	ABL83854	Human ovarian canc
685	17	73.9	102	22	AAK83187	Human immune/haema	758	17	73.9	324	22	AAK38626	Novel human diagno
686	17	73.9	102	22	AAK83201	Human immune/haema	759	17	73.9	325	22	AAK38626	Human breast canc
687	17	73.9	102	22	AAK83215	Human immune/haema	760	17	73.9	326	24	ABL85203	Human ovarian canc
688	17	73.9	102	22	AAK83216	Human immune/haema	761	17	73.9	327	22	ABL85203	Human immune/haema
689	17	73.9	103	22	AAK84802	Human immune/haema	762	17	73.9	328	22	AAK74195	Human immune/haema
690	17	73.9	106	22	ABA21361	Human nervous syst	763	17	73.9	328	22	AAK74195	Human immune/haema
691	17	73.9	106	22	ABA21364	Human nervous syst	764	17	73.9	328	24	ABN62283	Human cancer relat
692	17	73.9	107	22	AAI05621	Human reproductive	765	17	73.9	328	24	ABL80420	Human ovarian canc
693	17	73.9	107	22	AAK74126	Human immune/haema	766	17	73.9	331	22	AAI82792	Human polynucleoti
694	17	73.9	107	22	AAK74127	Human immune/haema	767	17	73.9	332	22	AAI89846	Human polynucleoti
695	17	73.9	107	22	AAK74128	Human immune/haema	768	17	73.9	334	22	AAI80060	Human polynucleoti
696	17	73.9	107	22	AAK79672	Human immune/haema	769	17	73.9	335	22	AAI80060	Human musculoskele
697	17	73.9	107	22	AAK83761	Human immune/haema	770	17	73.9	336	24	ABL84097	Human ovarian canc
698	17	73.9	107	22	AAK85307	Human immune/haema	771	17	73.9	348	22	ABL86240	Human polynucleoti
699	17	73.9	108	21	AAC26212	Human secreted pro	772	17	73.9	351	22	AAI83957	Human polynucleoti
700	17	73.9	114	22	ABA16309	Human nervous syst	773	17	73.9	351	22	AAI83957	Human ORFX polynuc
701	17	73.9	114	22	ABA16310	Human nervous syst	774	17	73.9	357	22	AAS40087	DNA encoding human
702	17	73.9	130	22	AAI04573	Human reproductive	775	17	73.9	357	22	AAI00662	Human reproductive
703	17	73.9	130	22	AAI05109	Human reproductive	776	17	73.9	359	24	ABN63013	Human cancer relat
704	17	73.9	130	23	ABL97496	Human testicular a	777	17	73.9	360	22	ABN63679	Human cancer relat
705	17	73.9	130	23	ABL98001	Human testicular a	778	17	73.9	362	22	AAI81586	Human polynucleoti
706	17	73.9	135	21	AAC13477	Human secreted pro	779	17	73.9	366	23	ABV00904	Human prostate exp
707	17	73.9	142	21	AAC20241	Human secreted pro	780	17	73.9	367	22	AAS39981	Genomic sequence #
708	17	73.9	147	22	AAK83526	Human immune/haema	781	17	73.9	367	22	AAS39982	Genomic sequence #
709	17	73.9	147	22	AAK85842	Human immune/haema	782	17	73.9	367	22	AAK90673	Human digestive sy
710	17	73.9	162	22	AAK65059	Human immune/haema	783	17	73.9	367	22	AAK90674	Human digestive sy
711	17	73.9	171	22	AAK65109	Human immune/haema	784	17	73.9	368	23	ABV08383	Human prostate exp
712	17	73.9	172	22	AAK32544	Human genomic DNA	785	17	73.9	369	22	AAK65052	Novel human polynu
713	17	73.9	175	22	AAK31645	Human immune/haema	786	17	73.9	371	22	AAI04928	Human reproductive
714	17	73.9	178	22	AAK78398	Human immune/haema	787	17	73.9	371	23	ABL97822	Human testicular a
715	17	73.9	179	22	AAK66061	Human immune/haema	788	17	73.9	372	14	AAQ60002	Human brain Expres
716	17	73.9	179	22	AAK66062	Human immune/haema	789	17	73.9	375	22	AAI86149	Human polynucleoti
717	17	73.9	179	22	AAK66065	Human immune/haema	790	17	73.9	378	22	AAK67442	Human polynucleoti
718	17	73.9	183	21	AAC25411	Human secreted pro	791	17	73.9	379	22	AAK65419	Novel human polynu
719	17	73.9	188	21	AAC15303	Human secreted pro	792	17	73.9	379	22	AAK65419	Novel human polynu
720	17	73.9	188	22	AAK30622	DNA encoding novel	793	17	73.9	379	23	AAK67015	Novel human polynu
721	17	73.9	188	22	AAK28168	Genomic sequence #	794	17	73.9	380	22	AAI84732	Human prostate exp
722	17	73.9	201	21	AAC26227	Human secreted pro	795	17	73.9	380	22	AAI91246	Human polynucleoti
723	17	73.9	209	21	AAC13197	Human secreted pro	796	17	73.9	383	22	AAK85975	Human immune/haema
724	17	73.9	213	22	AAK30318	DNA encoding novel	797	17	73.9	385	22	AAK66116	Novel human polynu
725	17	73.9	213	22	AAI01999	Human reproductive	798	17	73.9	387	23	ABV20595	Human prostate exp
726	17	73.9	214	21	AAC05925	Human secreted pro	799	17	73.9	387	23	ABV20823	Human prostate exp
727	17	73.9	216	22	AAK72299	Human immune/haema	800	17	73.9	387	23	ABV26435	Human prostate exp
728	17	73.9	216	22	AAK72300	Human immune/haema	801	17	73.9	387	23	ABV26670	Human prostate exp
729	17	73.9	221	21	AAC12462	Human secreted pro	802	17	73.9	388	24	ABL84947	Human ovarian canc
730	17	73.9	231	21	AAC29656	Human secreted pro	803	17	73.9	389	22	AAI89027	Human polynucleoti
731	17	73.9	233	22	AAI05834	Human reproductive	804	17	73.9	390	22	AAI89027	Novel human diagno
732	17	73.9	233	23	ABL98398	Human testicular a	805	17	73.9	391	24	AAS38763	Human colon tumour
733	17	73.9	243	22	AAK83640	Human immune/haema	806	17	73.9	392	22	AAI81540	Human polynucleoti
734	17	73.9	246	21	AAC14911	Human secreted pro	807	17	73.9	392	22	AAK58892	Human immune/haema
735	17	73.9	251	21	AAC26789	Human secreted pro	808	17	73.9	393	23	ABV01294	Human prostate exp
736	17	73.9	253	21	AAC21861	Human secreted pro	809	17	73.9	394	22	AAI83715	Human polynucleoti
737	17	73.9	259	22	AAI35889	Human musculoskele	810	17	73.9	395	22	AAI88167	Human polynucleoti
738	17	73.9	261	22	AAC04921	Human secreted pro	811	17	73.9	395	22	AAI88167	Human polynucleoti
739	17	73.9	265	23	ABV50154	Human prostate exp	812	17	73.9	395	24	ABL85373	Human ovarian canc

C 813	17	73.9	396	21	AAH30338	Human colon cancer	C 886	17	73.9	450	22	AAH10230	Human breast cancer
C 814	17	73.9	397	22	AAH193102	Human polynucleoti	887	17	73.9	451	22	ABA16121	Human nervous syst
C 815	17	73.9	397	23	ABV10463	Human prostate exp	888	17	73.9	451	22	AAK67925	Human immune/haema
C 816	17	73.9	397	24	ABK46028	cDNA encoding colo	889	17	73.9	451	22	AAK81748	Human immune/haema
C 817	17	73.9	399	22	AAI81227	Human polynucleoti	890	17	73.9	451	22	AAK86495	Human immune/haema
C 818	17	73.9	400	22	AAK55649	Human immune/haema	891	17	73.9	451	24	ABN64146	Human cancer relat
C 819	17	73.9	401	22	AAK26724	Human secreted pro	C 892	17	73.9	452	20	ABN66930	EST clone BK304
C 820	17	73.9	401	22	AAK96247	Human neurogulin g	893	17	73.9	452	24	ABN60246	Human cancer relat
C 821	17	73.9	401	22	AAK96363	Human neurogulin g	C 894	17	73.9	453	22	AAI87017	Human polynucleoti
C 822	17	73.9	401	22	AAK97740	Human neurogulin g	C 895	17	73.9	454	23	ABV31547	Human prostate exp
C 823	17	73.9	401	22	AAK97856	Human neurogulin g	C 896	17	73.9	454	23	ABV40516	Human prostate exp
C 824	17	73.9	401	22	AAI93768	Human polynucleoti	C 897	17	73.9	455	23	ABV04766	Human prostate exp
C 825	17	73.9	401	23	ABV38290	Human prostate exp	C 898	17	73.9	459	24	ABN64956	Human cancer relat
C 826	17	73.9	403	22	AAK78684	Human immune/haema	C 899	17	73.9	460	23	ABV35045	Human prostate exp
C 827	17	73.9	404	22	AAI13876	Human breast cancer	C 900	17	73.9	460	23	ABV43892	Human prostate exp
C 828	17	73.9	404	24	ABL82168	Human ovarian cancer	C 901	17	73.9	462	22	ABA13430	Human nervous syst
C 829	17	73.9	405	22	AAK96582	Human neurogulin g	C 902	17	73.9	462	22	AAK88726	Human digestive sy
C 830	17	73.9	405	22	AAK98075	Human neurogulin g	903	17	73.9	462	22	AAK31760	Human liver associ
C 831	17	73.9	405	22	AAH19810	Human breast cancer	904	17	73.9	462	24	ABN90115	Human liver associ
C 832	17	73.9	405	23	ABV17264	Human prostate exp	905	17	73.9	463	22	AAI92921	Human polynucleoti
C 833	17	73.9	405	24	ABN65098	Human cancer relat	C 906	17	73.9	465	22	AAK66120	Novel human polynu
C 834	17	73.9	406	22	AAI93108	Human polynucleoti	907	17	73.9	466	23	ABV54356	Human prostate exp
C 835	17	73.9	407	23	ABV10376	Human prostate exp	908	17	73.9	467	23	ABV05433	Human prostate exp
C 836	17	73.9	408	24	ABN62527	Human cancer relat	C 909	17	73.9	471	23	ABV50430	Human prostate exp
C 837	17	73.9	408	24	ABL69276	Prostate cancer re	910	17	73.9	471	23	ABV50430	Human prostate exp
C 838	17	73.9	411	22	AAI92812	Human polynucleoti	911	17	73.9	474	23	ABV35024	Human prostate exp
C 839	17	73.9	411	22	AAK58425	Human immune/haema	912	17	73.9	474	23	ABV43872	Human prostate exp
C 840	17	73.9	411	22	AAK72730	Human immune/haema	C 913	17	73.9	475	22	AAH06073	Human cdna clone (
C 841	17	73.9	411	22	AAK72731	Human immune/haema	C 914	17	73.9	475	22	AAH03691	Human prostate exp
C 842	17	73.9	413	23	ABV27839	Human prostate exp	915	17	73.9	479	21	AAH31036	Human colon cancer
C 843	17	73.9	418	22	AAI84692	Human polynucleoti	C 916	17	73.9	479	23	ABV20073	Human prostate exp
C 844	17	73.9	419	23	AAK83978	Human immune/haema	917	17	73.9	483	22	ABA07465	Human prostate exp
C 845	17	73.9	419	23	ABV13935	Human prostate exp	918	17	73.9	483	22	AAH00081	Human ovarian and
C 846	17	73.9	419	23	ABV31245	Human prostate exp	919	17	73.9	486	22	AAK98597	Human reproductive
C 847	17	73.9	420	14	AAQ59417	Human brain expres	920	17	73.9	486	22	AAK98603	Human ovarian cancer
C 848	17	73.9	420	22	AAK18266	Human breast cancer	921	17	73.9	488	22	AAH50757	Human tumour assoc
C 849	17	73.9	421	23	ABV16484	Human prostate exp	C 922	17	73.9	488	22	AAH13146	Human cdna clone (
C 850	17	73.9	423	23	ABV50907	Human prostate exp	923	17	73.9	490	23	ABV47336	Human prostate exp
C 851	17	73.9	424	20	AAK56588	Human R87078 DNA f	924	17	73.9	492	23	ABV18599	Human prostate exp
C 852	17	73.9	424	22	AAK77756	Human immune/haema	925	17	73.9	492	23	ABV57477	Human prostate exp
C 853	17	73.9	424	22	AAK77756	Human immune/haema	926	17	73.9	494	22	AAH14931	Human prostate exp
C 854	17	73.9	424	22	AAK80712	Human immune/haema	927	17	73.9	497	23	ABV47221	Human breast cancer
C 855	17	73.9	425	22	AAI92310	Human polynucleoti	928	17	73.9	499	24	ABN63949	Human prostate exp
C 856	17	73.9	425	22	AAK67972	Human immune/haema	929	17	73.9	499	24	ABN65076	Human cancer relat
C 857	17	73.9	425	22	AAK77758	Human immune/haema	C 930	17	73.9	500	22	AAK60873	Human immune/haema
C 858	17	73.9	426	24	ABL81527	Human ovarian cancer	931	17	73.9	501	24	ABN62125	Human cancer relat
C 859	17	73.9	428	22	AAH07285	Human reproductive	932	17	73.9	504	23	ABV46282	Human prostate exp
C 860	17	73.9	428	23	ABL98831	Human testicular a	C 933	17	73.9	506	22	AAH10348	Human cdna clone (
C 861	17	73.9	429	23	ABV13913	Human prostate exp	C 934	17	73.9	507	22	AAK65942	Human immune/haema
C 862	17	73.9	433	23	ABV31633	Human prostate exp	C 935	17	73.9	507	22	AAK65943	Human immune/haema
C 863	17	73.9	433	23	ABV40215	Human prostate exp	936	17	73.9	507	23	ABV59162	Human prostate exp
C 864	17	73.9	433	23	ABV40601	Human prostate exp	937	17	73.9	508	24	ABN64087	Human cancer relat
C 865	17	73.9	433	24	ABL82717	Human ovarian cancer	938	17	73.9	509	22	AAI87035	Human polynucleoti
C 866	17	73.9	434	22	AAH08822	Human breast cancer	939	17	73.9	509	23	ABV35880	Human prostate exp
C 867	17	73.9	434	24	ABN60782	Human cancer relat	940	17	73.9	509	23	ABV44485	Human prostate exp
C 868	17	73.9	436	21	AAK30648	Human secreted pro	941	17	73.9	509	24	ABN65466	Human cancer relat
C 869	17	73.9	439	23	ABV33986	Human prostate exp	942	17	73.9	511	23	ABV50613	Human prostate exp
C 870	17	73.9	439	23	ABV42853	Human prostate exp	943	17	73.9	512	22	AAH12079	Human breast cancer
C 871	17	73.9	440	22	AAI87406	Human polynucleoti	C 944	17	73.9	513	22	AAK78783	Human immune/haema
C 872	17	73.9	440	22	AAH04744	Human prostate exp	945	17	73.9	514	22	AAK78998	Human immune/haema
C 873	17	73.9	441	22	AAK74903	Human immune/haema	C 946	17	73.9	514	22	AAH09857	Human cdna clone (
C 874	17	73.9	442	21	AAK14949	Human secreted pro	947	17	73.9	514	23	ABN63007	Human cancer relat
C 875	17	73.9	442	24	ABL80544	Human ovarian cancer	C 948	17	73.9	518	24	ABV12860	Human prostate exp
C 876	17	73.9	443	22	AAI90641	Human polynucleoti	949	17	73.9	524	24	ABN61736	Human cancer relat
C 877	17	73.9	443	22	AAK70807	Human immune/haema	950	17	73.9	526	22	AAK78822	Human immune/haema
C 878	17	73.9	444	23	ABV01207	Human prostate exp	C 951	17	73.9	526	22	AAH12261	Human cdna clone (
C 879	17	73.9	444	23	ABL7427	Human prostate exp	952	17	73.9	527	24	ABN64882	Human cancer relat
C 880	17	73.9	445	24	ABL86841	Human ovarian cancer	C 953	17	73.9	530	22	AAH12591	Human cdna clone (
C 881	17	73.9	447	22	ABA16120	Human nervous syst	C 954	17	73.9	531	22	AAH09176	Human cdna clone (
C 882	17	73.9	447	22	ABA20765	Human nervous syst	955	17	73.9	531	24	ABN60671	Human cancer relat
C 883	17	73.9	447	22	AAK59455	Human immune/haema	C 956	17	73.9	533	24	ABN63875	Human cancer relat
C 884	17	73.9	448	22	AAH92630	Human inflammatory	C 957	17	73.9	537	23	ABV53454	Human prostate exp
C 885	17	73.9	449	23	ABV47059	Human prostate exp	C 958	17	73.9	539	22	AAH13209	Human cdna clone (

c 959 17 73.9 539 22 AAHL13377 Human CDNA clone (
 c 960 17 73.9 540 22 AAHL1668 Human CDNA clone (
 c 961 17 73.9 540 22 AAHL13348 Human CDNA clone (
 c 962 17 73.9 541 22 AAHL10011 Human CDNA clone (
 c 963 17 73.9 543 22 AAHL11477 Human CDNA clone (
 c 964 17 73.9 548 22 AAHL09840 Human CDNA clone (
 c 965 17 73.9 549 22 AAHL11757 Human CDNA clone (
 c 966 17 73.9 551 22 AAHL08023 Human breast cancer
 c 967 17 73.9 554 22 AAHL13592 Human CDNA clone (
 c 968 17 73.9 554 22 ABNG2717 Human cancer relat
 c 969 17 73.9 555 20 AAV90098 EST clone CW1682.
 c 970 17 73.9 557 23 ABV49831 Human prostate exp
 c 971 17 73.9 558 23 ABV52574 Human prostate exp
 c 972 17 73.9 567 22 AAK82860 Human immune/haema
 c 973 17 73.9 567 22 AAHL10209 Human CDNA clone (
 c 974 17 73.9 569 22 AAK83434 Human immune/haema
 c 975 17 73.9 569 22 AAK92551 Human CDNA 3'-end
 c 976 17 73.9 569 24 ABNG4487 Human cancer relat
 c 977 17 73.9 570 23 ABV59420 Human prostate exp
 c 978 17 73.9 572 23 ABV48382 Human prostate exp
 c 979 17 73.9 572 23 ABV48675 Human prostate exp
 c 980 17 73.9 573 23 ABV20085 Human prostate exp
 c 981 17 73.9 573 23 ABV20321 Human prostate exp
 c 982 17 73.9 573 23 ABV25915 Human prostate exp
 c 983 17 73.9 573 23 ABV26153 Human prostate exp
 c 984 17 73.9 574 23 ABV57915 Human prostate exp
 c 985 17 73.9 574 24 ABNG3280 Human cancer relat
 c 986 17 73.9 575 24 ABNG1271 Human cancer relat
 c 987 17 73.9 577 22 AAHL1883 Human CDNA clone (
 c 988 17 73.9 581 22 AAHL1274 Human CDNA clone (
 c 989 17 73.9 581 24 ABNG4519 Human cancer relat
 c 990 17 73.9 582 22 AAK75122 Human immune/haema
 c 991 17 73.9 582 23 ABV47242 Human prostate exp
 c 992 17 73.9 583 22 AAK75123 Human immune/haema
 c 993 17 73.9 585 22 AAS45098 cDNA encoding nove
 c 994 17 73.9 589 24 ABNG5211 Human cancer relat
 c 995 17 73.9 591 23 ABV50080 Human prostate exp
 c 996 17 73.9 592 22 ABA12000 Human nervous syst
 c 997 17 73.9 592 22 AAK54286 cDNA encoding nove
 c 998 17 73.9 597 22 AAK58693 Human immune/haema
 c 999 17 73.9 598 22 AAL16037 Human breast cancer
 c1000 17 73.9 598 23 ABV46839 Human prostate exp

ALIGNMENTS

RESULT 1
 AAA64507
 ID AAA64507 standard; DNA; 9048 BP.

XX AAA64507;

DT 02-JAN-2001 (first entry)

XX Nucleotide sequence comprising the human FEZ1 gene.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
 KW tumour proliferation; tubulin; microtubule; protein EPI-gamma;
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
 KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human
 PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
 PT cancer -

XX Claim 2; Fig 5A; 255pp; English..

XX The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour
 CC suppressor gene, located at chromosome location 8p22. Decreased or no
 CC expression of FEZ1 is detected in a variety of cancer cells. Expression
 CC of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts
 CC with tubulin, with microtubules, and with protein EPI-gamma.
 CC Post-translational phosphorylation and dephosphorylation modulates the
 CC effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are
 CC useful for inducing cells to proliferate. Compounds which modulate FEZ1
 CC association with tubulin are useful for alleviating tubulin hyper- or
 CC hypo- polymerisation disorders, such as those associated with aberrant
 CC initiation of mitosis, modulation of the initiation and rate of cell
 CC proliferation and cell growth, modulation of cell shape, cell rigidity,
 CC cell motility, rate and stage of cellular DNA replication, intracellular
 CC distribution of organelles, metastatic potential of cell and cellular
 CC transformation from a non-carcinogenic to carcinogenic phenotype. Compounds
 CC which modulate FEZ1 binding and phosphorylation are also useful for
 CC alleviating a disorder, such as tumorigenesis, tumour survival, growth
 CC and metastasis.

XX Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;

Query Match 100.0%; Score 23; DB 21; Length 9048;

Best Local Similarity 100.0%; Pred. No. 0.0066;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGTCGAGGTGT 23

Db 4451 CAGCCAGGCATGTCGAGGTGT 4473

RESULT 2

AAC15023/c

ID AAC15023 standard; cDNA; 204 BP.

XX AAC15023;

DT 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 19098.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EPI033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 19098; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 204 BP; 33 A; 50 C; 59 G; 57 T; 5 other;
 Query Match 95.7%; Score 22; DB 21; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGGCATGGTGGCAGGTG 22
 |||||
 DB 124 CAGCCAGGCATGGTGGCAGGTG 103
 RESULT 3
 ABV39095/c
 ID ABV39095 standard; cDNA; 389 BP.
 XX
 AC ABV39095;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 39086.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 7939; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 389 BP; 74 A; 99 C; 93 G; 123 T; 0 other;
 Query Match 95.7%; Score 22; DB 23; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCAGGCATGGTGGCAGGTG 22
 |||||
 DB 221 CAGCCAGGCATGGTGGCAGGTG 200
 RESULT 4
 ABV11210
 ID ABV11210 standard; cDNA; 440 BP.
 XX
 AC ABV11210;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 11201.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 1818-1819; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ Sequence 440 BP; 130 A; 100 C; 90 G; 119 T; 1 other;
Query Match 95.7%; Score 22; DB 23; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCCAGGCATGGTGGCAGGTG 22
DB 402 CAGCCAGGCATGGTGGCAGGTG 423

RESULT 5
ABV05712/c
ID ABV05712 standard; cDNA; 477 BP.
XX AC ABV05712;
XX 13-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 5703.
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX DR Claim 1; Page 954; 11750pp; English.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
XX PS Claim 1; Page 954; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ Sequence 477 BP; 93 A; 119 C; 111 G; 153 T; 1 other;
Query Match 95.7%; Score 22; DB 23; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCCAGGCATGGTGGCAGGTG 22
DB 193 CAGCCAGGCATGGTGGCAGGTG 172

RESULT 6
ABV32356
ID ABV32356 standard; cDNA; 478 BP.
XX AC ABV32356;
XX 16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 32347.
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX DR Claim 1; Page 6909; 11750pp; English.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
XX PS Claim 1; Page 6909; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ Sequence 478 BP; 141 A; 112 C; 102 G; 122 T; 1 other;
Query Match 95.7%; Score 22; DB 23; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22
 ID ABV41286
 Db 440 CAGCCAGGCATGGTGGCAGGTG 461

RESULT 7
 ABV41286
 ID ABV41286 standard; cDNA; 478 BP.
 XX
 AC ABV41286;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 41277.
 XX
 DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 8302; 11750pp; English.
 The invention relates to an isolated nucleic acid molecule (I) comprising
 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for:
 (a) assessing whether a patient is afflicted with prostate cancer;
 (b) monitoring the progression of prostate cancer in a patient;
 (c) assessing the efficacy of a test compound to inhibit prostate
 cancer in a patient;
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 in a patient;
 (e) selecting a composition for inhibiting prostate cancer in a patient;
 (f) assessing the prostate cell carcinogenic potential of a compound;
 (g) determining whether prostate cancer has metastasized in a patient;
 (h) assessing the aggressiveness or indolence of prostate cancer in a
 patient;
 (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 478 BP; 141 A; 112 C; 102 G; 122 T; 1 other;
 Query Match 95.7%; Score 22; DB 23; Length 478;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CAGCCAGGCATGGTGGCAGGTG 22
 ID ABV41286
 Db 440 CAGCCAGGCATGGTGGCAGGTG 461

RESULT 8
 ABV15013/c
 ID ABV15013 standard; cDNA; 495 BP.
 XX
 AC ABV15013;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 15004.
 XX
 DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 2518; 11750pp; English.
 The invention relates to an isolated nucleic acid molecule (I) comprising
 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for:
 (a) assessing whether a patient is afflicted with prostate cancer;
 (b) monitoring the progression of prostate cancer in a patient;
 (c) assessing the efficacy of a test compound to inhibit prostate
 cancer in a patient;
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 in a patient;
 (e) selecting a composition for inhibiting prostate cancer in a patient;
 (f) assessing the prostate cell carcinogenic potential of a compound;
 (g) determining whether prostate cancer has metastasized in a patient;
 (h) assessing the aggressiveness or indolence of prostate cancer in a
 patient;
 (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 495 BP; 97 A; 117 C; 109 G; 172 T; 0 other;
 Query Match 95.7%; Score 22; DB 23; Length 495;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CAGCCAGGCATGGTGGCAGGTG 22
 Db 177 CAGCCAGGCATGGTGGCAGGTG 156

RESULT 9
 ABV32243
 ID ABV32243 standard; cDNA; 506 BP.
 XX
 AC ABV32243;
 XX

```
DT 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 32234.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
KW
XX Homo sapiens.
OS
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 6890; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 506 BP; 158 A; 119 C; 112 G; 117 T; 0 other;
SQ
Query Match 95.7%; Score 22; DB 23; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGGTGGCAGGTG 22
|||||
DB 442 CAGCCAGGCATGGTGGCAGGTG 463

RESULT 10
ABV05844/c
ID ABV05844 standard; cDNA; 521 BP.
XX
XX ABV05844;
AC
XX
XX 13-SEP-2002 (first entry)
DT
XX Human prostate expression marker cDNA 5835.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
KW
XX Homo sapiens.
OS
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 6890; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 521 BP; 104 A; 118 C; 108 G; 158 T; 33 other;
SQ
Query Match 95.7%; Score 22; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGGTGGCAGGTG 22
|||||
DB 222 CAGCCAGGCATGGTGGCAGGTG 201

RESULT 11
ABV21254
ID ABV21254 standard; cDNA; 557 BP.
XX
XX ABV21254;
AC
XX
XX 13-SEP-2002 (first entry)
DT
XX Human prostate expression marker cDNA 21245.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
KW
XX Homo sapiens.
OS
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
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XX 20-FEB-2001; 2001WO-US05171.
PF
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
PR
XX 25-MAY-2000; 2000US-207454P.
PR
XX 09-JUN-2000; 2000US-211314P.
PR
XX 18-JUL-2000; 2000US-219007P.
PR
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3525; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;
XX
XX Query Match 95.7%; Score 22; DB 23; Length 557;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CAGCCAGGCATGGTGGCAGGTG 22
XX |||||
XX Db 410 CAGCCAGGCATGGTGGCAGGTG 431
XX
XX RESULT 12
XX ABV21288
XX ID ABV21288 standard; cDNA; 557 BP.
XX
XX AC ABV21288;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 21279.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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XX PA
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PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3531; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;
XX
XX Query Match 95.7%; Score 22; DB 23; Length 557;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CAGCCAGGCATGGTGGCAGGTG 22
XX |||||
XX Db 410 CAGCCAGGCATGGTGGCAGGTG 431
XX
XX RESULT 13
XX ABV21292
XX ID ABV21292 standard; cDNA; 557 BP.
XX
XX AC ABV21292;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 21283.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX PA
XX
```


CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;

Query Match 95.7%; Score 22; DB 23; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22
|||||
Db 410 CAGCCAGGCATGGTGGCAGGTG 431

Search completed: June 16, 2003, 20:03:08.
Job time : 26.0604 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 0.900335 Seconds
(without alignments)
7834.381 Million cell updates/sec

Title: US-09-513-888C-1_COPY_4451_4473

Perfect score: 23

Sequence: 1 cagccaggcatgtgcaggtgt 23

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents_NA:**

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- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:**
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:**
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:**
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:**
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	91.3	59065	4	US-09-813-817-3
2	21	91.3	59065	4	US-09-878-197-3
3	21	91.3	70000	4	US-09-851-896-3
C 4	21	91.3	81001	4	US-09-750-580-1
C 5	21	91.3	84495	4	US-09-797-906-3
C 6	20	87.0	2950	5	PCT-US93-08386-7
C 7	20	87.0	2968	5	PCT-US93-08386-1
8	19	82.6	443	4	US-09-385-982-28
9	19	82.6	3807	4	US-08-482-918-43
10	19	82.6	3807	4	US-09-224-681-43
11	19	82.6	3807	4	US-08-336-728A-43
12	19	82.6	5864	4	US-08-482-918-47
13	19	82.6	5864	4	US-09-224-681-47
14	19	82.6	5864	4	US-08-336-728A-47
15	19	82.6	5917	4	US-09-780-175-17
C 16	19	82.6	6235	4	US-09-305-384-5
17	19	82.6	6679	4	US-09-305-384-1
18	19	82.6	10684	3	US-08-618-100B-3
19	19	82.6	12571	4	US-09-810-347-3
20	19	82.6	62804	4	US-09-800-960-3
C 21	19	82.6	72928	3	US-09-009-913-1
22	19	82.6	112132	4	US-09-741-150-3
23	18	78.3	2598	4	US-09-026-033-18
24	18	78.3	3441	4	US-09-026-033-17
25	18	78.3	6987	4	US-09-026-033-3
26	18	78.3	6990	4	US-09-026-033-23
27	18	78.3	8342	3	US-08-545-860D-63

101	17	73.9	99500	4	US-09-798-096-10	Sequence 10, Appl	174	16	69.6	40352	3	US-08-846-111D-15	Sequence 15, Appl
C 102	17	73.9	99500	4	US-09-798-096-10	Sequence 10, Appl	175	16	69.6	40352	4	US-09-443-077-15	Sequence 15, Appl
C 103	17	73.9	112132	4	US-09-741-150-3	Sequence 3, Appl	176	16	69.6	43950	4	US-09-735-934A-3	Sequence 3, Appl
C 104	16	69.6	20	4	US-09-780-175-26	Sequence 26, Appl	177	16	69.6	45716	4	US-08-965-048-5	Sequence 5, Appl
C 105	16	69.6	434	2	US-08-332-766A-10	Sequence 10, Appl	178	16	69.6	45989	4	US-08-965-048-6	Sequence 6, Appl
C 106	16	69.6	620	4	US-09-385-982-245	Sequence 245, App	179	16	69.6	50000	4	US-09-146-053-3	Sequence 3, Appl
C 107	16	69.6	1001	4	US-09-641-638-113	Sequence 113, App	180	16	69.6	56516	2	US-08-996-306-1	Sequence 1, Appl
C 108	16	69.6	1001	4	US-09-641-638-131	Sequence 131, App	181	16	69.6	56516	4	US-09-338-907-1	Sequence 1, Appl
C 109	16	69.6	1811	1	US-08-848-252-1	Sequence 1, Appl	182	16	69.6	56516	4	US-09-218-207-1	Sequence 1, Appl
C 110	16	69.6	3366	4	US-09-345-650-2	Sequence 2, Appl	183	16	69.6	56520	4	US-09-338-907-179	Sequence 179, App
C 111	16	69.6	3586	4	US-08-847-296B-3	Sequence 3, Appl	184	16	69.6	56520	4	US-09-218-207-179	Sequence 179, App
C 112	16	69.6	3877	2	US-08-599-895-1	Sequence 1, Appl	185	16	69.6	70000	4	US-09-851-896-3	Sequence 3, Appl
C 113	16	69.6	3877	3	US-09-211-230-1	Sequence 1, Appl	186	16	69.6	72604	4	US-09-268-992-7	Sequence 7, Appl
C 114	16	69.6	3877	3	US-09-322-676-1	Sequence 1, Appl	187	16	69.6	72604	4	US-09-857-474-7	Sequence 7, Appl
C 115	16	69.6	3877	4	US-09-466-036A-1	Sequence 1, Appl	188	16	69.6	84435	4	US-09-757-906-3	Sequence 3, Appl
C 116	16	69.6	4342	4	US-09-338-907-107	Sequence 107, App	189	16	69.6	152331	3	US-09-128-155-16	Sequence 16, Appl
C 117	16	69.6	4342	4	US-09-218-207-107	Sequence 107, App	190	16	69.6	168575	4	US-09-426-290-1	Sequence 1, Appl
C 118	16	69.6	4582	4	US-09-338-907-118	Sequence 118, App	191	16	69.6	169998	4	US-09-676-610B-24	Sequence 24, Appl
C 119	16	69.6	4582	4	US-09-218-207-118	Sequence 118, App	192	16	69.6	176373	3	US-09-128-155-17	Sequence 17, Appl
C 120	16	69.6	4686	4	US-09-338-907-117	Sequence 117, App	193	15	65.2	34	1	US-08-644-664B-20	Sequence 20, Appl
C 121	16	69.6	4686	4	US-09-218-207-117	Sequence 117, App	194	15	65.2	34	2	US-08-761-277A-20	Sequence 20, Appl
C 122	16	69.6	4875	4	US-09-338-907-114	Sequence 114, App	195	15	65.2	239	2	US-08-687-080-93	Sequence 93, Appl
C 123	16	69.6	4875	4	US-09-218-207-114	Sequence 114, App	196	15	65.2	330	4	US-09-078-294-24	Sequence 24, Appl
C 124	16	69.6	4958	4	US-09-338-907-116	Sequence 116, App	197	15	65.2	364	4	US-09-222-575-167	Sequence 167, App
C 125	16	69.6	4958	4	US-09-218-207-116	Sequence 116, App	198	15	65.2	470	2	US-08-967-101-77	Sequence 77, Appl
C 126	16	69.6	4986	4	US-09-338-907-121	Sequence 121, App	199	15	65.2	470	2	US-08-592-541-77	Sequence 77, Appl
C 127	16	69.6	4986	4	US-09-218-207-121	Sequence 121, App	200	15	65.2	470	3	US-09-124-698-77	Sequence 77, Appl
C 128	16	69.6	5020	4	US-09-338-907-120	Sequence 120, App	201	15	65.2	470	4	US-09-127-480-77	Sequence 77, Appl
C 129	16	69.6	5020	4	US-09-218-207-120	Sequence 120, App	202	15	65.2	470	4	US-08-496-841C-77	Sequence 77, Appl
C 130	16	69.6	5044	4	US-09-338-907-115	Sequence 115, App	203	15	65.2	470	4	US-09-124-523-77	Sequence 77, Appl
C 131	16	69.6	5044	4	US-09-218-207-115	Sequence 115, App	204	15	65.2	483	2	US-08-475-844-14	Sequence 14, Appl
C 132	16	69.6	5057	4	US-09-338-907-123	Sequence 123, App	205	15	65.2	483	5	PCT-US95-08429-14	Sequence 14, Appl
C 133	16	69.6	5057	4	US-09-218-207-123	Sequence 123, App	206	15	65.2	500	2	US-08-967-101-57	Sequence 57, Appl
C 134	16	69.6	5100	4	US-09-338-907-122	Sequence 122, App	207	15	65.2	500	2	US-08-967-101-90	Sequence 90, Appl
C 135	16	69.6	5100	4	US-09-218-207-122	Sequence 122, App	208	15	65.2	500	2	US-08-592-541-57	Sequence 57, Appl
C 136	16	69.6	5148	4	US-09-338-907-112	Sequence 112, App	209	15	65.2	500	2	US-08-592-541-90	Sequence 90, Appl
C 137	16	69.6	5148	4	US-09-218-207-112	Sequence 112, App	210	15	65.2	500	3	US-09-124-698-57	Sequence 57, Appl
C 138	16	69.6	5227	2	US-08-996-306-3	Sequence 3, Appl	211	15	65.2	500	3	US-09-124-698-90	Sequence 90, Appl
C 139	16	69.6	5234	4	US-09-338-907-113	Sequence 113, App	212	15	65.2	500	4	US-09-127-480-57	Sequence 57, Appl
C 140	16	69.6	5234	4	US-09-218-207-113	Sequence 113, App	213	15	65.2	500	4	US-09-127-480-90	Sequence 90, Appl
C 141	16	69.6	5245	4	US-09-338-907-3	Sequence 3, Appl	214	15	65.2	500	4	US-08-496-841C-57	Sequence 57, Appl
C 142	16	69.6	5245	4	US-09-218-207-3	Sequence 3, Appl	215	15	65.2	500	4	US-08-496-841C-90	Sequence 90, Appl
C 143	16	69.6	5250	4	US-09-338-907-69	Sequence 69, Appl	216	15	65.2	500	4	US-09-124-523-57	Sequence 57, Appl
C 144	16	69.6	5250	4	US-09-218-207-69	Sequence 69, Appl	217	15	65.2	500	4	US-09-124-523-90	Sequence 90, Appl
C 145	16	69.6	5290	4	US-09-338-907-119	Sequence 119, App	218	15	65.2	565	4	US-09-328-111-267	Sequence 267, App
C 146	16	69.6	5290	4	US-09-218-207-119	Sequence 119, App	219	15	65.2	615	4	US-09-385-982-528	Sequence 528, App
C 147	16	69.6	5326	4	US-09-338-907-124	Sequence 124, App	220	15	65.2	668	4	US-09-347-114A-93	Sequence 93, Appl
C 148	16	69.6	5326	4	US-09-218-207-124	Sequence 124, App	221	15	65.2	1000	4	US-09-018-584A-30	Sequence 30, Appl
C 149	16	69.6	6232	4	US-08-456-200B-11	Sequence 11, Appl	222	15	65.2	1000	4	US-09-018-584A-31	Sequence 31, Appl
C 150	16	69.6	6330	4	US-09-880-427-2	Sequence 2, Appl	223	15	65.2	1320	1	US-08-599-252-84	Sequence 84, Appl
C 151	16	69.6	6330	4	US-09-306-538B-2	Sequence 2, Appl	224	15	65.2	1320	1	US-08-436-074-57	Sequence 57, Appl
C 152	16	69.6	6769	1	US-08-480-784-20	Sequence 20, Appl	225	15	65.2	1320	5	PCT-US96-06352-84	Sequence 84, Appl
C 153	16	69.6	6769	1	US-08-483-553-20	Sequence 20, Appl	226	15	65.2	1320	5	PCT-US96-06583-84	Sequence 84, Appl
C 154	16	69.6	6769	1	US-08-487-002-20	Sequence 20, Appl	227	15	65.2	1630	4	US-09-175-928-17	Sequence 17, Appl
C 155	16	69.6	6769	1	US-08-483-554B-20	Sequence 20, Appl	228	15	65.2	1763	4	US-09-449-437A-3	Sequence 3, Appl
C 156	16	69.6	6769	1	US-08-488-011B-20	Sequence 20, Appl	229	15	65.2	2133	3	US-08-808-032-1	Sequence 1, Appl
C 157	16	69.6	6769	4	US-08-850-727-20	Sequence 20, Appl	230	15	65.2	2309	4	US-09-449-437A-5	Sequence 5, Appl
C 158	16	69.6	6769	5	PCT-US95-10202-20	Sequence 20, Appl	231	15	65.2	2309	4	US-09-195-106-1	Sequence 1, Appl
C 159	16	69.6	6769	5	PCT-US95-10203-20	Sequence 20, Appl	232	15	65.2	2713	2	US-08-916-901-6	Sequence 6, Appl
C 160	16	69.6	6769	5	PCT-US95-10220-20	Sequence 20, Appl	233	15	65.2	2713	2	US-09-154-602-6	Sequence 6, Appl
C 161	16	69.6	8353	3	US-08-611-587-1	Sequence 1, Appl	234	15	65.2	2854	2	US-08-724-394A-17	Sequence 17, Appl
C 162	16	69.6	10079	2	US-08-476-866-20	Sequence 20, Appl	235	15	65.2	3336	4	US-09-026-033-1	Sequence 1, Appl
C 163	16	69.6	14581	4	US-08-520-373D-4	Sequence 4, Appl	236	15	65.2	3336	4	US-08-026-033-2	Sequence 2, Appl
C 164	16	69.6	15602	4	US-09-844-634-17	Sequence 17, Appl	237	15	65.2	3373	1	US-08-273-411-2	Sequence 2, Appl
C 165	16	69.6	17327	1	US-07-906-871-15	Sequence 15, Appl	238	15	65.2	3507	2	US-08-832-883-67	Sequence 67, Appl
C 166	16	69.6	22481	4	US-08-367-841A-43	Sequence 43, Appl	239	15	65.2	3507	2	US-08-832-877-67	Sequence 67, Appl
C 167	16	69.6	2481	5	PCT-US95-07201-43	Sequence 43, Appl	240	15	65.2	3621	2	US-09-019-201A-1	Sequence 1, Appl
C 168	16	69.6	2484	4	US-09-875-223-2	Sequence 2, Appl	241	15	65.2	4157	2	US-08-162-146-2	Sequence 2, Appl
C 169	16	69.6	28001	4	US-09-819-993-3	Sequence 3, Appl	242	15	65.2	4157	2	US-09-314-127-2	Sequence 2, Appl
C 170	16	69.6	28629	4	US-09-729-995-3	Sequence 3, Appl	243	15	65.2	4326	2	US-08-852-807-12	Sequence 12, Appl
C 171	16	69.6	32042	4	US-09-245-281-44	Sequence 44, Appl	244	15	65.2	8174	1	US-07-914-281-5	Sequence 5, Appl
C 172	16	69.6	36651	4	US-09-738-894A-3	Sequence 3, Appl	245	15	65.2	8174	1	US-08-393-246-5	Sequence 5, Appl
C 173	16	69.6	38844	4	US-09-734-675-3	Sequence 3, Appl	246	15	65.2	8174	1	US-08-525-058A-5	Sequence 5, Appl

c 247	15	65.2	8174	2	US-08-696-731-5	Sequence 5, Appli	320	14	60.9	2561	4	US-09-270-542-101	Sequence 101, App
c 248	15	65.2	8174	4	US-09-042-531-5	Sequence 5, Appli	321	14	60.9	2561	4	US-09-270-542-119	Sequence 119, App
c 249	15	65.2	8174	5	PCT-US91-00899-3	Sequence 3, Appli	322	14	60.9	2886	2	US-08-687-080-55	Sequence 55, Appl
c 250	15	65.2	8453	4	US-09-167-681-45	Sequence 45, Appl	323	14	60.9	3035	1	US-08-726-725-2	Sequence 2, Appli
c 251	15	65.2	8835	3	US-08-884-324-10	Sequence 10, Appl	324	14	60.9	3061	2	US-08-692-787-47	Sequence 47, Appl
c 252	15	65.2	9734	4	US-09-347-114A-80	Sequence 80, Appl	325	14	60.9	3061	4	US-09-097-199-47	Sequence 47, Appl
c 253	15	65.2	12394	4	US-09-488-856A-10	Sequence 10, Appl	326	14	60.9	3715	4	US-09-085-199B-44	Sequence 44, Appl
c 254	15	65.2	12597	4	US-09-705-299-12	Sequence 12, Appl	327	14	60.9	3715	2	US-08-381-691-16	Sequence 16, Appl
c 255	15	65.2	13674	2	US-08-852-807-1	Sequence 1, Appli	328	14	60.9	4015	4	US-08-810-009-4	Sequence 4, Appli
c 256	15	65.2	15652	4	US-09-422-936-60	Sequence 60, Appl	329	14	60.9	4042	4	US-08-406-030A-17	Sequence 17, Appl
c 257	15	65.2	16389	4	US-09-741-154-3	Sequence 3, Appli	330	14	60.9	4084	3	US-08-866-340-1	Sequence 1, Appli
c 258	15	65.2	17041	1	US-08-076-011-1	Sequence 1, Appli	331	14	60.9	4338	4	US-09-360-237-4	Sequence 4, Appli
c 259	15	65.2	20137	4	US-09-262-773-206	Sequence 206, App	332	14	60.9	4460	4	US-09-103-875-A	Sequence 4, Appli
c 260	15	65.2	20138	4	US-09-262-773-9	Sequence 9, Appli	333	14	60.9	4576	1	US-08-832-883-49	Sequence 49, Appl
c 261	15	65.2	20674	4	US-09-641-638-651	Sequence 651, App	334	14	60.9	4576	2	US-08-832-877-49	Sequence 49, Appl
c 262	15	65.2	23071	4	US-09-262-773-210	Sequence 210, App	335	14	60.9	4586	1	US-08-832-883-53	Sequence 53, Appl
c 263	15	65.2	29598	4	US-08-341-587-6	Sequence 6, Appli	336	14	60.9	4586	2	US-08-832-877-53	Sequence 53, Appl
c 264	15	65.2	35100	1	US-08-306-691B-19	Sequence 19, Appl	337	14	60.9	4773	3	US-08-884-324-9	Sequence 9, Appli
c 265	15	65.2	35100	5	PCT-US93-06251-19	Sequence 19, Appl	338	14	60.9	5109	4	US-08-930-055A-2	Sequence 2, Appli
c 266	15	65.2	36651	4	US-09-738-894A-3	Sequence 3, Appli	339	14	60.9	6678	3	US-08-816-617A-1	Sequence 1, Appli
c 267	15	65.2	36741	4	US-09-301-665-3	Sequence 3, Appli	340	14	60.9	8396	4	US-09-328-174A-1	Sequence 1, Appli
c 268	15	65.2	38564	4	US-09-734-673-3	Sequence 3, Appli	341	14	60.9	8409	4	US-09-167-681-37	Sequence 37, Appl
c 269	15	65.2	40000	4	US-09-780-049-18	Sequence 18, Appl	342	14	60.9	11454	3	US-08-884-324-13	Sequence 13, Appl
c 270	15	65.2	44453	4	US-09-146-053-5	Sequence 5, Appli	343	14	60.9	12597	4	US-09-705-299-12	Sequence 12, Appl
c 271	15	65.2	56516	2	US-08-996-306-1	Sequence 1, Appli	344	14	60.9	13104	4	US-08-256-799-4	Sequence 4, Appli
c 272	15	65.2	56516	4	US-09-338-907-1	Sequence 1, Appli	345	14	60.9	13104	4	US-08-462-437-4	Sequence 4, Appli
c 273	15	65.2	56516	4	US-09-218-207-1	Sequence 1, Appli	346	14	60.9	16063	4	US-09-801-052-3	Sequence 3, Appli
c 274	15	65.2	56520	4	US-09-338-907-179	Sequence 179, App	347	14	60.9	17327	1	US-07-906-871-15	Sequence 15, Appl
c 275	15	65.2	56520	4	US-09-218-207-179	Sequence 179, App	348	14	60.9	17410	1	US-07-841-646-3	Sequence 3, Appli
c 276	15	65.2	59065	4	US-09-813-817-3	Sequence 3, Appli	349	14	60.9	17410	1	US-08-147-023-3	Sequence 3, Appli
c 277	15	65.2	59065	4	US-09-978-197-3	Sequence 3, Appli	350	14	60.9	17410	2	US-08-447-570-3	Sequence 3, Appli
c 278	15	65.2	80246	4	US-09-078-294-4	Sequence 4, Appli	351	14	60.9	17410	2	US-08-449-700-3	Sequence 3, Appli
c 279	15	65.2	80595	4	US-09-078-294-3	Sequence 3, Appli	352	14	60.9	17410	2	US-08-449-699A-3	Sequence 3, Appli
c 280	15	65.2	81001	4	US-09-750-580-1	Sequence 1, Appli	353	14	60.9	17415	3	US-08-486-343A-1	Sequence 1, Appli
c 281	15	65.2	87350	3	US-08-781-891-79	Sequence 79, Appl	354	14	60.9	17415	5	PCT-US95-07343-1	Sequence 1, Appli
c 282	15	65.2	87350	4	US-09-791-211-3	Sequence 3, Appli	355	14	60.9	17425	4	US-09-511-625B-5	Sequence 5, Appli
c 283	15	65.2	98844	4	US-09-791-211-10	Sequence 10, Appl	356	14	60.9	26664	4	US-09-564-805-28	Sequence 28, Appl
c 284	15	65.2	111282	4	US-09-754-250-3	Sequence 3, Appli	357	14	60.9	29629	4	US-09-729-995-3	Sequence 3, Appli
c 285	15	65.2	111282	4	US-09-754-250-3	Sequence 3, Appli	358	14	60.9	48974	4	US-08-920-422-17	Sequence 17, Appl
c 286	15	65.2	12331	3	US-09-128-155-16	Sequence 16, Appl	359	14	60.9	53526	3	US-08-658-136-2	Sequence 2, Appli
c 287	15	65.2	162450	4	US-09-345-882-1	Sequence 1, Appli	360	14	60.9	53577	4	US-08-658-136-1	Sequence 1, Appli
c 288	15	65.2	168575	4	US-09-426-290-1	Sequence 1, Appli	361	14	60.9	55827	4	US-09-813-133A-3	Sequence 3, Appli
c 289	15	65.2	176373	3	US-09-128-155-17	Sequence 17, Appl	362	14	60.9	80246	4	US-09-078-294-4	Sequence 4, Appli
c 290	15	65.2	246240	2	US-08-724-394A-20	Sequence 20, Appl	363	14	60.9	80595	4	US-09-078-294-3	Sequence 3, Appli
c 291	15	65.2	246240	2	US-08-724-394A-21	Sequence 21, Appl	364	13	56.5	20	1	US-08-384-490-8	Sequence 8, Appli
c 292	15	65.2	246240	2	US-08-724-394A-22	Sequence 22, Appl	365	13	56.5	20	1	US-08-459-383-8	Sequence 8, Appli
c 293	14	60.9	39	4	US-08-849-764C-8	Sequence 8, Appli	366	13	56.5	38	1	US-08-424-424B-5	Sequence 5, Appli
c 294	14	60.9	39	4	US-08-262-087-8	Sequence 8, Appli	367	13	56.5	48	1	US-08-468-709B-7	Sequence 7, Appli
c 295	14	60.9	265	2	US-08-463-261B-5	Sequence 5, Appli	368	13	56.5	48	2	US-08-241-664B-7	Sequence 7, Appli
c 296	14	60.9	295	4	US-08-849-701-1	Sequence 1, Appli	369	13	56.5	190	4	US-09-723-473-1	Sequence 1, Appli
c 297	14	60.9	312	4	US-09-172-108-21	Sequence 21, Appl	370	13	56.5	190	4	US-09-517-933-1	Sequence 1, Appli
c 298	14	60.9	312	4	US-09-172-108-7	Sequence 7, Appli	371	13	56.5	190	4	US-09-723-424A-1	Sequence 1, Appli
c 299	14	60.9	317	4	US-09-172-111-6	Sequence 6, Appli	372	13	56.5	282	1	US-08-121-063-6	Sequence 6, Appli
c 300	14	60.9	350	4	US-08-732-139A-10	Sequence 10, Appl	373	13	56.5	282	1	US-08-121-063-3	Sequence 3, Appli
c 301	14	60.9	602	4	US-09-018-584A-14	Sequence 14, Appl	374	13	56.5	363	4	US-09-657-453A-26	Sequence 26, Appl
c 302	14	60.9	626	4	US-09-385-982-254	Sequence 254, App	375	13	56.5	372	4	US-09-018-584A-13	Sequence 13, Appl
c 303	14	60.9	652	4	US-08-998-416-121	Sequence 121, App	376	13	56.5	388	1	US-08-121-063-1	Sequence 1, Appli
c 304	14	60.9	652	4	US-08-998-416-1121	Sequence 1121, App	377	13	56.5	439	1	US-08-121-063-5	Sequence 5, Appli
c 305	14	60.9	720	4	US-08-998-416-901	Sequence 901, App	378	13	56.5	468	3	US-08-665-259-33	Sequence 33, Appl
c 306	14	60.9	819	4	US-09-605-785-571	Sequence 571, App	379	13	56.5	468	3	US-08-665-259-33	Sequence 33, Appl
c 307	14	60.9	850	4	US-09-288-143-26	Sequence 26, Appl	380	13	56.5	505	1	US-08-121-063-4	Sequence 4, Appli
c 308	14	60.9	990	4	US-09-641-638-277	Sequence 277, App	381	13	56.5	515	1	US-08-375-170-21	Sequence 21, Appl
c 309	14	60.9	1000	4	US-09-018-584A-34	Sequence 34, Appl	382	13	56.5	515	1	US-08-367-968-21	Sequence 21, Appl
c 310	14	60.9	1002	4	US-09-641-638-587	Sequence 587, App	383	13	56.5	515	1	US-08-665-484-21	Sequence 21, Appl
c 311	14	60.9	1110	2	US-08-719-758-1	Sequence 1, Appli	384	13	56.5	561	4	US-09-404-879A-50	Sequence 50, Appl
c 312	14	60.9	1110	4	US-09-119-827-1	Sequence 1, Appli	385	13	56.5	569	4	US-09-449-285A-18	Sequence 18, Appl
c 313	14	60.9	1110	4	US-09-511-625B-43	Sequence 43, Appl	386	13	56.5	582	4	US-09-385-982-98	Sequence 98, Appl
c 314	14	60.9	1145	4	US-09-078-294-17	Sequence 17, Appl	387	13	56.5	601	4	US-09-814-951A-12	Sequence 12, Appl
c 315	14	60.9	1243	4	US-09-103-875-16	Sequence 16, Appl	388	13	56.5	700	4	US-08-998-416-1131	Sequence 1131, Ap
c 316	14	60.9	1820	4	US-09-732-199A-3	Sequence 3, Appli	389	13	56.5	727	1	US-08-367-968-27	Sequence 27, Appl
c 317	14	60.9	1838	4	US-09-227-357-32	Sequence 32, Appl	390	13	56.5	926	4	US-08-665-484-27	Sequence 27, Appl
c 318	14	60.9	2336	1	US-08-247-946A-1	Sequence 1, Appli	391	13	56.5	926	4	US-08-938-669A-4	Sequence 4, Appli
c 319	14	60.9	2336	5	PCT-US95-06420-1	Sequence 1, Appli	392	13	56.5	926	4		

393	13	56.5	937	4	US-09-484-970B-136	Sequence 136, App	466	13	56.5	17949	4	US-09-087-465-3	Sequence 3, Appli
394	13	56.5	996	1	US-07-975-526-2	Sequence 2, Appli	467	13	56.5	19011	1	US-08-310-356-36	Sequence 36, Appl
395	13	56.5	996	4	US-07-974-409C-424	Sequence 424, App	468	13	56.5	19357	5	PCT-US92-06300-1	Sequence 1, Appli
396	13	56.5	996	5	PCT-US95-15353-38	Sequence 38, Appl	469	13	56.5	24417	2	US-08-846-762-1	Sequence 1, Appli
397	13	56.5	996	5	PCT-US95-15353-40	Sequence 40, Appl	470	13	56.5	28720	4	US-09-341-587-7	Sequence 7, Appli
398	13	56.5	1000	4	US-09-018-584A-33	Sequence 33, Appl	471	13	56.5	35060	3	US-08-814-095-7	Sequence 7, Appli
399	13	56.5	1001	4	US-09-641-638-458	Sequence 458, App	472	13	56.5	40000	4	US-09-780-049-18	Sequence 18, Appl
400	13	56.5	1096	4	US-09-000-127-2	Sequence 2, Appli	473	13	56.5	44453	4	US-09-146-053-5	Sequence 5, Appli
401	13	56.5	1101	4	US-09-134-001C-2665	Sequence 2665, Ap	474	13	56.5	48974	4	US-08-920-422-17	Sequence 17, Appl
402	13	56.5	1224	1	US-08-127-278-3	Sequence 3, Appli	475	13	56.5	50000	4	US-09-146-053-3	Sequence 3, Appli
403	13	56.5	1224	1	US-08-555-860-3	Sequence 3, Appli	476	13	56.5	50000	4	US-09-146-053-4	Sequence 4, Appli
404	13	56.5	1279	1	US-08-146-010A-4	Sequence 4, Appli	477	13	56.5	169998	4	US-09-676-610B-24	Sequence 24, Appl
405	13	56.5	1279	1	US-08-674-168-9	Sequence 9, Appli	478	13	56.5	18	2	US-08-117-952-375	Sequence 375, App
406	13	56.5	1328	1	US-08-592-126-94	Sequence 94, Appl	479	13	56.5	19	3	US-09-135-021-58	Sequence 58, Appl
407	13	56.5	1357	4	US-09-668-680-3	Sequence 3, Appli	480	13	56.5	19	4	US-09-135-020-60	Sequence 60, Appl
408	13	56.5	1445	4	US-09-814-951A-1	Sequence 1, Appli	481	13	56.5	19	4	US-09-135-010A-60	Sequence 60, Appl
409	13	56.5	1701	4	US-08-936-165A-137	Sequence 137, App	482	13	56.5	19	4	US-09-444-871-60	Sequence 60, Appl
410	13	56.5	1761	4	US-08-481-190-1	Sequence 1, Appli	483	13	56.5	19	4	US-09-597-735-60	Sequence 60, Appl
411	13	56.5	1761	5	PCT-US93-00869-1	Sequence 1, Appli	484	13	56.5	19	4	US-09-444-295-60	Sequence 60, Appl
412	13	56.5	1772	1	US-08-362-706A-1	Sequence 1, Appli	485	13	56.5	19	4	US-09-597-732-60	Sequence 60, Appl
413	13	56.5	1772	4	US-09-549-808-1	Sequence 1, Appli	486	13	56.5	20	4	US-09-210-748A-4	Sequence 4, Appli
414	13	56.5	1974	3	US-08-762-500-78	Sequence 78, Appl	487	13	56.5	21	4	US-09-177-650-33	Sequence 33, Appl
415	13	56.5	2055	3	US-08-872-855-3	Sequence 3, Appli	488	13	56.5	32	4	US-08-482-073-18	Sequence 18, Appl
416	13	56.5	2071	4	US-09-816-088-1	Sequence 1, Appli	489	13	56.5	33	2	US-08-411-607A-9	Sequence 9, Appli
417	13	56.5	2096	5	PCT-US94-08119-9	Sequence 9, Appli	490	13	56.5	39	4	US-09-428-589-3	Sequence 3, Appli
418	13	56.5	2096	5	PCT-US94-08120-9	Sequence 9, Appli	491	13	56.5	40	2	US-08-411-607A-7	Sequence 7, Appli
419	13	56.5	2096	5	PCT-US94-12913A-9	Sequence 9, Appli	492	13	56.5	41	2	US-08-822-830B-9	Sequence 9, Appli
420	13	56.5	2099	1	US-08-094-533B-9	Sequence 9, Appli	493	13	56.5	41	2	US-08-950-660-9	Sequence 9, Appli
421	13	56.5	2099	1	US-08-276-860A-9	Sequence 9, Appli	494	13	56.5	41	4	US-09-026-033-22	Sequence 22, Appl
422	13	56.5	2099	1	US-08-444-393-9	Sequence 9, Appli	495	13	56.5	243	4	US-08-905-223-63	Sequence 63, Appl
423	13	56.5	2099	1	US-08-799-913-9	Sequence 9, Appli	496	13	56.5	276	2	US-08-481-658B-62	Sequence 62, Appl
424	13	56.5	2099	2	US-08-711-893-9	Sequence 9, Appli	497	13	56.5	276	2	US-08-477-504A-62	Sequence 62, Appl
425	13	56.5	2099	2	US-09-150-200-9	Sequence 9, Appli	498	13	56.5	276	2	US-08-486-756A-62	Sequence 62, Appl
426	13	56.5	2099	3	US-09-150-201-9	Sequence 9, Appli	499	13	56.5	276	2	US-08-485-862B-62	Sequence 62, Appl
427	13	56.5	2099	4	US-09-452-370-9	Sequence 9, Appli	500	13	56.5	276	3	US-08-787-739-62	Sequence 62, Appl
428	13	56.5	2099	4	US-09-461-649-9	Sequence 9, Appli	501	13	56.5	276	3	US-08-487-077A-62	Sequence 62, Appl
429	13	56.5	2145	3	US-09-078-862-1	Sequence 1, Appli	502	13	56.5	276	3	US-08-485-863A-62	Sequence 62, Appl
430	13	56.5	2254	1	US-08-153-848-27	Sequence 27, Appl	503	13	56.5	276	4	US-08-485-049D-62	Sequence 62, Appl
431	13	56.5	2254	3	US-09-239-843A-27	Sequence 27, Appl	504	13	56.5	276	4	US-09-178-115-62	Sequence 62, Appl
432	13	56.5	2254	4	US-09-088-337B-27	Sequence 27, Appl	505	13	56.5	276	4	US-09-177-776-62	Sequence 62, Appl
433	13	56.5	2254	5	PCT-US93-11153-27	Sequence 27, Appl	506	13	56.5	344	3	US-08-925-230-3	Sequence 3, Appli
434	13	56.5	2507	4	US-09-605-785-332	Sequence 332, App	507	13	56.5	344	3	US-08-925-230-4	Sequence 4, Appli
435	13	56.5	2507	4	US-09-439-313-332	Sequence 332, App	508	13	56.5	388	2	US-08-967-101-68	Sequence 68, Appl
436	13	56.5	2507	4	US-09-352-616A-332	Sequence 332, App	509	13	56.5	388	2	US-08-592-541-68	Sequence 68, Appl
437	13	56.5	2507	4	US-09-232-149A-332	Sequence 332, App	510	13	56.5	388	3	US-09-124-698-68	Sequence 68, Appl
438	13	56.5	2520	4	US-08-931-608A-2	Sequence 2, Appli	511	13	56.5	388	4	US-09-127-480-68	Sequence 68, Appl
439	13	56.5	2800	3	US-08-872-855-1	Sequence 1, Appli	512	13	56.5	388	4	US-08-496-841C-68	Sequence 68, Appl
440	13	56.5	3011	1	US-07-821-716-1	Sequence 1, Appli	513	13	56.5	388	4	US-09-124-523-68	Sequence 68, Appl
441	13	56.5	3119	4	US-09-199-637A-173	Sequence 173, App	514	13	56.5	484	4	US-09-325-932A-11	Sequence 11, Appl
442	13	56.5	3487	4	US-08-931-608A-1	Sequence 1, Appli	515	13	56.5	489	2	US-08-967-101-27	Sequence 27, Appl
443	13	56.5	3518	4	US-09-412-210-2	Sequence 2, Appli	516	13	56.5	489	2	US-08-592-541-27	Sequence 27, Appl
444	13	56.5	3609	4	US-09-705-299-11	Sequence 11, Appl	517	13	56.5	489	3	US-09-124-698-27	Sequence 27, Appl
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447	13	56.5	4129	2	US-08-370-319C-12	Sequence 12, Appl	520	13	56.5	489	4	US-09-124-523-27	Sequence 27, Appl
448	13	56.5	4129	2	US-09-224-834-12	Sequence 12, Appl	521	13	56.5	500	4	US-09-370-838-128	Sequence 128, App
449	13	56.5	5191	1	US-08-340-428B-1	Sequence 1, Appli	522	13	56.5	516	2	US-08-967-101-55	Sequence 55, Appl
450	13	56.5	5191	5	PCT-US93-07306-1	Sequence 1, Appli	523	13	56.5	516	2	US-08-592-541-55	Sequence 55, Appl
451	13	56.5	5375	3	US-08-757-223-7	Sequence 7, Appli	524	13	56.5	516	3	US-09-124-698-55	Sequence 55, Appl
452	13	56.5	6803	3	US-08-665-259-19	Sequence 19, App	525	13	56.5	516	4	US-09-127-480-55	Sequence 55, Appl
453	13	56.5	7301	4	US-08-762-500-19	Sequence 19, App	526	13	56.5	516	4	US-08-496-841C-55	Sequence 55, Appl
454	13	56.5	7301	4	US-09-816-088-3	Sequence 3, Appli	527	13	56.5	516	4	US-09-124-523-55	Sequence 55, Appl
455	13	56.5	8396	4	US-09-328-174A-1	Sequence 1, Appli	528	13	56.5	516	1	US-08-468-709B-3	Sequence 3, Appli
456	13	56.5	8409	4	US-09-167-681-37	Sequence 37, Appl	529	13	56.5	525	2	US-08-241-664B-3	Sequence 3, Appli
457	13	56.5	9301	4	US-09-449-218D-18	Sequence 18, Appl	530	13	56.5	525	5	PCT-US93-03936-3	Sequence 3, Appli
458	13	56.5	9704	4	US-09-814-951A-3	Sequence 3, Appli	531	13	56.5	526	1	US-08-686-878A-35	Sequence 35, Appl
459	13	56.5	11531	1	US-08-068-945A-1	Sequence 1, Appli	532	13	56.5	526	4	US-09-175-928-35	Sequence 35, Appl
460	13	56.5	11531	1	US-08-442-806-1	Sequence 1, Appli	533	13	56.5	526	4	US-08-991-789A-15	Sequence 15, Appl
461	13	56.5	11601	2	US-08-222-617A-3	Sequence 3, Appli	534	13	56.5	526	4	US-09-062-451-15	Sequence 15, Appl
462	13	56.5	11601	2	US-08-334-240-3	Sequence 4, Appl	535	13	56.5	526	4	US-09-598-326-15	Sequence 15, Appl
463	13	56.5	11673	4	US-09-078-294-7	Sequence 7, Appli	536	13	56.5	576	2	US-09-385-982-440	Sequence 440, App
464	13	56.5	11811	4	US-09-453-702B-71	Sequence 71, Appl	537	13	56.5	576	2	US-08-334-545-1	Sequence 1, Appli
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540	12	52.2	611	4	US-09-328-111-517	Sequence 517, App	C 613	12	52.2	1319	3	US-08-458-731-17	Sequence 17, Appl
541	12	52.2	618	4	US-09-328-111-215	Sequence 215, App	C 614	12	52.2	1319	3	US-08-149-223A-17	Sequence 17, Appl
C 542	12	52.2	635	1	US-08-455-633A-35	Sequence 35, Appl	C 615	12	52.2	1360	4	US-09-820-001-1	Sequence 1, Appl
C 543	12	52.2	635	1	US-08-416-336-5	Sequence 5, Appl	C 616	12	52.2	1363	1	US-08-776-088-21	Sequence 21, Appl
C 544	12	52.2	635	2	US-08-456-460C-35	Sequence 35, Appl	C 617	12	52.2	1363	5	PCT-US95-09145A-21	Sequence 21, Appl
C 545	12	52.2	635	5	PCT-US94-0535A-35	Sequence 35, Appl	C 618	12	52.2	1371	3	US-08-884-324-11	Sequence 11, Appl
546	12	52.2	649	4	US-09-040-984-59	Sequence 59, App	C 619	12	52.2	1383	3	US-09-400-742-7	Sequence 7, Appl
547	12	52.2	649	4	US-09-123-912-59	Sequence 59, App	C 620	12	52.2	1383	3	US-08-618-651A-7	Sequence 7, Appl
548	12	52.2	649	4	US-09-643-597-59	Sequence 59, App	C 621	12	52.2	1383	3	US-09-215-252-6	Sequence 6, Appl
C 549	12	52.2	654	4	US-09-288-143-37	Sequence 37, App	C 622	12	52.2	1400	1	US-07-930-686-9	Sequence 9, Appl
C 550	12	52.2	668	4	US-09-129-030-31	Sequence 31, App	C 623	12	52.2	1400	2	US-08-460-998-9	Sequence 9, Appl
551	12	52.2	697	4	US-09-450-072-14	Sequence 14, App	C 624	12	52.2	1400	2	US-08-481-658B-43	Sequence 43, Appl
552	12	52.2	697	4	US-09-351-348-14	Sequence 14, App	C 625	12	52.2	1400	2	US-08-477-504A-43	Sequence 43, Appl
C 553	12	52.2	734	4	US-08-896-164-79	Sequence 79, App	C 626	12	52.2	1400	2	US-08-486-756A-43	Sequence 43, Appl
C 554	12	52.2	737	4	US-08-469-260A-22	Sequence 22, App	C 627	12	52.2	1400	2	US-08-485-862B-43	Sequence 43, Appl
C 555	12	52.2	780	4	US-09-385-982-32	Sequence 32, App	C 628	12	52.2	1400	3	US-08-787-739-43	Sequence 43, Appl
C 556	12	52.2	789	4	US-09-280-116-114	Sequence 114, App	C 629	12	52.2	1400	3	US-08-487-077A-43	Sequence 43, Appl
557	12	52.2	813	4	US-09-288-143-30	Sequence 30, App	C 630	12	52.2	1400	3	US-08-485-863A-43	Sequence 43, Appl
C 558	12	52.2	823	2	US-08-967-101-11	Sequence 11, App	C 631	12	52.2	1400	3	US-08-485-049D-43	Sequence 43, Appl
C 559	12	52.2	823	2	US-08-967-101-159	Sequence 159, App	C 632	12	52.2	1400	4	US-09-178-115-43	Sequence 43, Appl
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C 561	12	52.2	823	2	US-08-592-541-159	Sequence 159, App	C 634	12	52.2	1419	4	US-08-943-731-214	Sequence 214, App
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C 564	12	52.2	823	3	US-09-124-698-159	Sequence 159, App	C 637	12	52.2	1442	2	US-08-340-426D-120	Sequence 120, App
C 565	12	52.2	823	4	US-09-127-480-11	Sequence 11, App	C 638	12	52.2	1442	2	US-08-450-673C-120	Sequence 120, App
C 566	12	52.2	823	4	US-09-127-480-159	Sequence 159, App	C 639	12	52.2	1479	1	US-08-476-008-68	Sequence 68, Appl
C 567	12	52.2	823	4	US-08-496-841C-11	Sequence 11, App	C 640	12	52.2	1479	1	US-08-306-063-68	Sequence 68, Appl
C 568	12	52.2	823	4	US-08-496-841C-159	Sequence 159, App	C 641	12	52.2	1479	1	US-08-833-485-68	Sequence 68, Appl
C 569	12	52.2	823	4	US-09-124-523-11	Sequence 11, App	C 642	12	52.2	1479	4	US-09-137-440-68	Sequence 68, Appl
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571	12	52.2	834	2	US-08-967-101-113	Sequence 113, App	C 644	12	52.2	1482	4	US-08-884-235-13	Sequence 13, Appl
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573	12	52.2	834	3	US-09-124-698-113	Sequence 113, App	C 646	12	52.2	1489	2	US-08-886-640-4	Sequence 4, Appl
574	12	52.2	834	4	US-09-127-480-113	Sequence 113, App	C 647	12	52.2	1489	4	US-08-884-235-12	Sequence 12, Appl
575	12	52.2	834	4	US-08-496-841C-113	Sequence 113, App	C 648	12	52.2	1493	3	US-08-820-170A-9	Sequence 9, Appl
C 576	12	52.2	834	4	US-08-832-877-52	Sequence 52, App	C 649	12	52.2	1493	3	US-09-055-699-9	Sequence 9, Appl
C 577	12	52.2	837	1	US-08-832-883-56	Sequence 56, App	C 650	12	52.2	1493	4	US-09-273-565-9	Sequence 9, Appl
C 578	12	52.2	837	1	US-08-832-877-56	Sequence 56, App	C 651	12	52.2	1493	4	US-09-565-538-9	Sequence 9, Appl
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580	12	52.2	849	4	US-08-953-326-5	Sequence 5, Appl	C 653	12	52.2	1501	2	US-08-886-640-6	Sequence 6, Appl
C 581	12	52.2	889	1	US-08-832-883-52	Sequence 52, App	C 654	12	52.2	1501	4	US-08-884-235-14	Sequence 14, Appl
C 582	12	52.2	889	2	US-08-832-877-52	Sequence 52, App	C 655	12	52.2	1553	4	US-09-364-230-31	Sequence 31, Appl
583	12	52.2	923	4	US-09-336-643A-15	Sequence 15, App	C 656	12	52.2	1596	1	US-08-531-601-2	Sequence 2, Appl
584	12	52.2	951	4	US-09-605-785-570	Sequence 570, App	C 657	12	52.2	1596	2	US-08-859-032-2	Sequence 2, Appl
C 585	12	52.2	1000	2	US-08-747-121-20	Sequence 20, App	C 658	12	52.2	1600	3	US-08-602-791-1	Sequence 1, Appl
586	12	52.2	1001	4	US-09-641-638-175	Sequence 175, App	C 659	12	52.2	1600	3	US-09-522-217-7	Sequence 7, Appl
587	12	52.2	1001	4	US-09-641-638-400	Sequence 400, App	C 660	12	52.2	1620	3	US-08-925-230-2	Sequence 2, Appl
C 588	12	52.2	1001	4	US-09-641-638-514	Sequence 514, App	C 661	12	52.2	1631	1	US-08-583-318-4	Sequence 4, Appl
C 589	12	52.2	1039	4	US-09-011-197-2	Sequence 2, App	C 662	12	52.2	1631	1	US-08-886-640-1	Sequence 1, Appl
590	12	52.2	1045	2	US-09-014-969-6	Sequence 6, Appl	C 663	12	52.2	1659	2	US-08-886-640-2	Sequence 2, Appl
C 591	12	52.2	1062	2	US-08-466-103A-13	Sequence 13, App	C 664	12	52.2	1659	2	US-08-884-235-1	Sequence 1, Appl
C 592	12	52.2	1079	1	US-08-454-196-16	Sequence 16, App	C 665	12	52.2	1659	4	US-08-884-235-2	Sequence 2, Appl
C 593	12	52.2	1079	3	US-09-064-033-16	Sequence 16, App	C 666	12	52.2	1674	6	5194375-1	Patent No. 5194375
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C 595	12	52.2	1080	2	US-08-722-050-1	Sequence 1, App	C 668	12	52.2	1701	2	US-08-429-964-2	Sequence 2, Appl
C 596	12	52.2	1129	4	US-09-383-586-10	Sequence 10, App	C 669	12	52.2	1701	3	US-07-935-087-2	Sequence 2, Appl
C 597	12	52.2	1259	4	US-08-672-814D-12	Sequence 12, App	C 670	12	52.2	1701	5	PCT-US93-08062-2	Sequence 2, Appl
C 598	12	52.2	1259	4	US-09-333-696-12	Sequence 12, App	C 671	12	52.2	1735	3	US-09-440-936-3	Sequence 3, Appl
599	12	52.2	1277	1	US-08-176-427B-1	Sequence 1, App	C 672	12	52.2	1743	3	US-09-221-235-9	Sequence 9, Appl
600	12	52.2	1277	2	US-08-356-060A-1	Sequence 1, App	C 673	12	52.2	1743	3	US-09-221-928-9	Sequence 9, Appl
C 601	12	52.2	1277	4	US-08-460-900C-1	Sequence 1, App	C 674	12	52.2	1743	3	US-09-221-527-9	Sequence 9, Appl
602	12	52.2	1277	4	US-08-674-509B-1	Sequence 1, App	C 675	12	52.2	1743	3	US-09-221-236-9	Sequence 9, Appl
C 603	12	52.2	1277	4	US-08-954-698-1	Sequence 1, App	C 676	12	52.2	1743	3	US-09-221-416-9	Sequence 9, Appl
604	12	52.2	1277	4	US-08-957-874-1	Sequence 1, App	C 677	12	52.2	1743	4	US-09-221-245-9	Sequence 9, Appl
C 605	12	52.2	1277	4	US-09-325-256-5	Sequence 5, App	C 678	12	52.2	1743	4	US-09-163-115-9	Sequence 9, Appl
C 606	12	52.2	1290	4	US-09-289-349-9	Sequence 9, App	C 679	12	52.2	1743	4	US-09-221-528-9	Sequence 9, Appl
607	12	52.2	1295	4	US-09-254-465A-8	Sequence 8, App	C 680	12	52.2	1743	4	US-09-593-553-9	Sequence 9, Appl
C 608	12	52.2	1306	3	US-08-948-705-7	Sequence 7, App	C 681	12	52.2	1743	4	US-09-221-237-9	Sequence 9, Appl
C 609	12	52.2	1319	2	US-08-484-993B-17	Sequence 17, App	C 682	12	52.2	1746	4	US-09-422-936-58	Sequence 58, Appl
C 610	12	52.2	1319	2	US-08-484-158B-17	Sequence 17, App	C 683	12	52.2	1749	4	US-09-450-072-56	Sequence 56, Appl
C 611	12	52.2	1319	2	US-08-484-596A-17	Sequence 17, App	C 684	12	52.2	1749	4	US-09-450-072-57	Sequence 57, Appl

685	12	52.2	1749	4	US-09-450-072-58	Sequence 58, Appl	758	12	52.2	2765	4	US-08-706-344C-27	Sequence 27, Appl
686	12	52.2	1749	4	US-09-351-348-56	Sequence 56, Appl	759	12	52.2	2765	4	US-08-706-344C-29	Sequence 29, Appl
687	12	52.2	1749	4	US-09-351-348-57	Sequence 57, Appl	760	12	52.2	2765	4	US-08-706-344C-31	Sequence 31, Appl
688	12	52.2	1749	4	US-09-351-348-58	Sequence 58, Appl	761	12	52.2	2772	3	US-09-280-420-1	Sequence 1, Appl
689	12	52.2	1750	3	US-08-670-964-3	Sequence 3, Appl	762	12	52.2	2788	4	US-09-221-017B-644	Sequence 644, App
690	12	52.2	1762	3	US-08-670-964-1	Sequence 1, Appl	763	12	52.2	2791	2	US-08-967-101-1	Sequence 1, Appl
691	12	52.2	1816	2	US-08-951-148-2	Sequence 2, Appl	764	12	52.2	2791	2	US-08-967-101-133	Sequence 133, App
692	12	52.2	1816	2	US-08-165-234-2	Sequence 2, Appl	765	12	52.2	2791	2	US-08-592-541-1	Sequence 1, Appl
693	12	52.2	1816	3	US-09-274-570-2	Sequence 2, Appl	766	12	52.2	2791	2	US-08-592-541-133	Sequence 133, App
694	12	52.2	1821	4	US-09-522-217-96	Sequence 96, Appl	767	12	52.2	2791	3	US-09-124-698-1	Sequence 1, Appl
695	12	52.2	1855	4	US-08-810-009-1	Sequence 1, Appl	768	12	52.2	2791	3	US-09-124-698-133	Sequence 133, App
696	12	52.2	1896	1	US-08-605-541B-11	Sequence 11, Appl	769	12	52.2	2791	4	US-09-127-480-1	Sequence 1, Appl
697	12	52.2	1914	2	US-08-670-479-24	Sequence 24, Appl	770	12	52.2	2791	4	US-09-127-480-133	Sequence 133, App
698	12	52.2	1937	1	US-08-370-193A-10	Sequence 10, Appl	771	12	52.2	2791	4	US-08-496-841C-1	Sequence 1, Appl
699	12	52.2	1967	4	US-09-398-395A-23	Sequence 23, Appl	772	12	52.2	2791	4	US-09-124-523-1	Sequence 1, Appl
700	12	52.2	1968	2	US-08-937-540-3	Sequence 3, Appl	773	12	52.2	2791	4	US-09-124-523-133	Sequence 133, App
701	12	52.2	1997	2	US-08-667-809B-3	Sequence 3, Appl	774	12	52.2	2792	4	US-08-496-841C-133	Sequence 133, App
702	12	52.2	1999	4	US-09-167-109-4	Sequence 4, Appl	775	12	52.2	2808	3	US-08-870-126-7	Sequence 7, Appl
703	12	52.2	2002	2	US-08-747-121-1	Sequence 1, Appl	776	12	52.2	2808	4	US-09-445-247-7	Sequence 7, Appl
704	12	52.2	2002	4	US-08-819-993-1	Sequence 1, Appl	777	12	52.2	2821	4	US-09-484-970B-44	Sequence 44, Appl
705	12	52.2	2004	2	US-08-651-814B-1	Sequence 1, Appl	778	12	52.2	2857	4	US-08-981-392-4	Sequence 4, Appl
706	12	52.2	2004	3	US-09-188-930-230	Sequence 230, App	779	12	52.2	2883	4	US-09-422-936-44	Sequence 44, Appl
707	12	52.2	2099	4	US-08-938-669A-5	Sequence 5, Appl	780	12	52.2	2895	4	US-09-422-936-52	Sequence 52, Appl
708	12	52.2	2127	1	US-08-832-883-54	Sequence 54, Appl	781	12	52.2	2896	2	US-08-709-923-1	Sequence 1, Appl
709	12	52.2	2127	2	US-08-832-877-54	Sequence 54, Appl	782	12	52.2	2900	3	US-09-038-832-1	Sequence 1, Appl
710	12	52.2	2132	4	US-08-552-322-1	Sequence 1, Appl	783	12	52.2	2933	2	US-09-262-773-209	Sequence 209, App
711	12	52.2	2162	3	US-08-948-705-5	Sequence 5, Appl	784	12	52.2	2935	4	US-09-480-921B-27	Sequence 27, Appl
712	12	52.2	2192	1	US-08-035-392-1	Sequence 1, Appl	785	12	52.2	3018	2	US-08-860-150-6	Sequence 6, Appl
713	12	52.2	2192	1	US-08-504-511A-1	Sequence 1, Appl	786	12	52.2	3018	3	US-09-338-132-6	Sequence 2, Appl
714	12	52.2	2205	1	US-08-035-392-3	Sequence 3, Appl	787	12	52.2	3031	1	US-08-785-241-2	Sequence 2, Appl
715	12	52.2	2205	1	US-08-504-511A-3	Sequence 3, Appl	788	12	52.2	3064	3	US-09-600-776-5	Sequence 5, Appl
716	12	52.2	2236	3	US-08-948-705-4	Sequence 4, Appl	789	12	52.2	3086	3	US-08-888-077B-3	Sequence 3, Appl
717	12	52.2	2260	2	US-08-788-750-1	Sequence 1, Appl	790	12	52.2	3087	2	US-08-967-101-5	Sequence 5, Appl
718	12	52.2	2274	3	US-09-440-936-1	Sequence 1, Appl	791	12	52.2	3087	2	US-08-592-541-5	Sequence 5, Appl
719	12	52.2	2289	3	US-08-948-705-8	Sequence 8, Appl	792	12	52.2	3087	3	US-09-124-698-5	Sequence 5, Appl
720	12	52.2	2311	3	US-08-712-709-6	Sequence 6, Appl	793	12	52.2	3087	4	US-09-127-480-5	Sequence 5, Appl
721	12	52.2	2311	3	US-09-111-444-6	Sequence 6, Appl	794	12	52.2	3087	4	US-08-496-841C-5	Sequence 5, Appl
722	12	52.2	2311	4	US-09-541-228-6	Sequence 6, Appl	795	12	52.2	3087	4	US-09-124-523-5	Sequence 5, Appl
723	12	52.2	2361	4	US-09-011-197-1	Sequence 1, Appl	796	12	52.2	3115	4	US-09-221-017B-849	Sequence 849, App
724	12	52.2	2370	4	US-09-031-295-1	Sequence 1, Appl	797	12	52.2	3158	2	US-08-464-517-36	Sequence 36, Appl
725	12	52.2	2377	4	US-09-479-195-1	Sequence 1, Appl	798	12	52.2	3158	2	US-08-246-361A-36	Sequence 36, Appl
726	12	52.2	2387	4	US-09-634-957-1	Sequence 1, Appl	799	12	52.2	3158	3	US-08-463-772-36	Sequence 36, Appl
727	12	52.2	2387	4	US-09-723-153-1	Sequence 1, Appl	800	12	52.2	3214	1	US-08-484-105-17	Sequence 17, Appl
728	12	52.2	2387	4	US-08-723-429-1	Sequence 1, Appl	801	12	52.2	3214	1	US-08-484-106-17	Sequence 17, Appl
729	12	52.2	2403	1	US-08-454-720A-41	Sequence 41, Appl	802	12	52.2	3216	2	US-08-828-007-1	Sequence 1, Appl
730	12	52.2	2454	3	US-09-221-235-7	Sequence 7, Appl	803	12	52.2	3223	4	US-07-980-528-1	Sequence 1, Appl
731	12	52.2	2454	3	US-09-221-235-7	Sequence 7, Appl	804	12	52.2	3224	4	US-08-965-729A-2	Sequence 2, Appl
732	12	52.2	2454	3	US-09-221-236-7	Sequence 7, Appl	805	12	52.2	3288	1	US-08-208-008C-3	Sequence 3, Appl
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734	12	52.2	2454	3	US-09-221-416-7	Sequence 7, Appl	807	12	52.2	3321	4	US-08-855-146-3	Sequence 3, Appl
735	12	52.2	2454	4	US-09-221-245-7	Sequence 7, Appl	808	12	52.2	3386	4	US-09-041-886-1	Sequence 1, Appl
736	12	52.2	2454	4	US-08-163-115-7	Sequence 7, Appl	809	12	52.2	3748	2	US-08-958-240-1	Sequence 1, Appl
737	12	52.2	2454	4	US-09-221-528-7	Sequence 7, Appl	810	12	52.2	3789	1	US-08-454-455-5	Sequence 5, Appl
738	12	52.2	2454	4	US-09-593-553-7	Sequence 7, Appl	811	12	52.2	3825	1	US-08-737-597-1	Sequence 1, Appl
739	12	52.2	2454	4	US-09-221-237-7	Sequence 7, Appl	812	12	52.2	3825	3	US-08-823-110-2	Sequence 2, Appl
740	12	52.2	2484	4	US-09-276-531-46	Sequence 46, Appl	813	12	52.2	3833	3	US-08-823-110-2	Sequence 2, Appl
741	12	52.2	2522	3	US-09-062-416-13	Sequence 13, Appl	814	12	52.2	3833	2	US-08-604-298-2	Sequence 2, Appl
742	12	52.2	2535	4	US-08-422-936-46	Sequence 46, Appl	815	12	52.2	3870	2	US-08-853-659A-26	Sequence 26, Appl
743	12	52.2	2556	3	US-08-699-103B-9	Sequence 9, Appl	816	12	52.2	4072	4	US-09-272-496-7	Sequence 7, Appl
744	12	52.2	2556	4	US-09-229-059-9	Sequence 9, Appl	817	12	52.2	4104	1	US-07-998-003A-94	Sequence 94, Appl
745	12	52.2	2559	2	US-09-070-060-2	Sequence 2, Appl	818	12	52.2	4104	1	US-08-453-274B-94	Sequence 94, Appl
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748	12	52.2	2692	4	US-08-981-392-11	Sequence 11, Appl	821	12	52.2	4104	2	US-08-453-702A-94	Sequence 94, Appl
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751	12	52.2	2731	3	US-08-699-103B-11	Sequence 11, Appl	824	12	52.2	4104	5	PCT-US95-08071-94	Sequence 94, Appl
752	12	52.2	2731	4	US-09-229-059-11	Sequence 11, Appl	825	12	52.2	4296	4	US-09-060-410-3	Sequence 3, Appl
753	12	52.2	2764	3	US-08-923-454A-9	Sequence 9, Appl	826	12	52.2	4326	2	US-08-852-807-12	Sequence 12, Appl
754	12	52.2	2764	3	US-08-832-867-2	Sequence 2, Appl	827	12	52.2	4508	5	PCT-US93-06251-34	Sequence 34, Appl
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756	12	52.2	2765	4	US-08-706-344C-1	Sequence 1, Appl	829	12	52.2	4606	4	US-09-221-017B-282	Sequence 282, App
757	12	52.2	2765	4	US-08-706-344C-3	Sequence 3, Appl	830	12	52.2	4635	2	US-08-404-531B-27	Sequence 27, Appl

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C 854	12	52.2	5615	4	US-09-302-769-47	Sequence 47, Appl	C 927	12	52.2	45546	4	US-09-146-053-6	Sequence 6, Appl
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C 859	12	52.2	6405	4	US-09-281-481A-18	Sequence 18, Appl	C 932	12	52.2	87563	4	US-09-453-702B-57	Sequence 57, Appl
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C 861	12	52.2	7152	4	US-09-167-681-29	Sequence 29, Appl	C 934	12	52.2	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C 862	12	52.2	7505	4	US-09-078-294-13	Sequence 13, Appl	C 935	12	52.2	4411529	4	US-09-103-840A-2	Sequence 2, Appl
C 863	12	52.2	7676	1	US-08-451-777A-7	Sequence 7, Appl	C 936	12	52.2	4411529	4	US-09-103-840A-13	Sequence 13, Appl
C 864	12	52.2	7676	2	US-08-451-777A-7	Sequence 7, Appl	C 937	12	52.2	4411529	4	US-09-103-840A-13	Sequence 13, Appl
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C 866	12	52.2	7676	5	PCT-US93-06743-7	Sequence 7, Appl	C 939	12	52.2	4718	20	US-08-246-855A-15	Sequence 15, Appl
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C 877	12	52.2	8878	1	US-08-206-176-3	Sequence 3, Appl	C 950	12	52.2	4718	29	US-08-814-567A-10	Sequence 10, Appl
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C 881	12	52.2	8967	2	US-08-853-659A-67	Sequence 67, Appl	C 954	12	52.2	4718	29	US-09-734-036-5	Sequence 5, Appl
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C 884	12	52.2	9365	4	US-09-370-285-8	Sequence 8, Appl	C 957	12	52.2	4718	34	US-08-465-687A-5	Sequence 5, Appl
C 885	12	52.2	9493	2	US-08-639-857-23	Sequence 23, Appl	C 958	12	52.2	4718	34	US-08-471-496-7	Sequence 7, Appl
C 886	12	52.2	9493	4	US-08-469-260A-163	Sequence 163, Appl	C 959	12	52.2	4718	34	US-08-894-840-7	Sequence 7, Appl
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C 889	12	52.2	10898	2	US-08-481-658B-5	Sequence 5, Appl	C 962	12	52.2	4718	35	US-09-522-217-68	Sequence 68, Appl
C 890	12	52.2	10898	2	US-08-477-504A-5	Sequence 5, Appl	C 963	12	52.2	4718	35	US-09-648-667-3	Sequence 3, Appl
C 891	12	52.2	10898	2	US-08-486-756A-5	Sequence 5, Appl	C 964	12	52.2	4718	36	US-08-816-757-3	Sequence 3, Appl
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C 896	12	52.2	10898	4	US-08-485-049D-5	Sequence 5, Appl	C 969	12	52.2	4718	40	US-09-823-177-1	Sequence 1, Appl
C 897	12	52.2	10898	4	US-09-178-115-5	Sequence 5, Appl	C 970	12	52.2	4718	42	US-08-596-387B-38	Sequence 38, Appl
C 898	12	52.2	10898	4	US-09-177-776-5	Sequence 5, Appl	C 971	12	52.2	4718	42	US-09-067-615-38	Sequence 38, Appl
C 899	12	52.2	11531	1	US-08-068-945A-1	Sequence 1, Appl	C 972	12	52.2	4718	42	US-09-453-702B-155	Sequence 155, Appl
C 900	12	52.2	11531	1	US-08-442-806-1	Sequence 1, Appl	C 973	12	52.2	4718	42	PCT-US95-09816A-38	Sequence 38, Appl
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C 902	12	52.2	13187	4	US-09-422-936-61	Sequence 61, Appl	C 975	12	52.2	4718	70	US-08-901-710-7	Sequence 7, Appl
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c 995 11 47.8 280 4 US-09-060-756-488 Sequence 488, App
c 996 11 47.8 292 2 US-08-481-558B-56 Sequence 56, Appl
c 997 11 47.8 292 2 US-08-481-558B-59 Sequence 59, Appl
c 998 11 47.8 292 2 US-08-477-504A-56 Sequence 56, Appl
c 999 11 47.8 292 2 US-08-477-504A-59 Sequence 56, Appl
c1000 11 47.8 292 2 US-08-486-756A-56 Sequence 56, Appl
```

ALIGNMENTS

```
RESULT 1
US-09-813-817-3
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813.817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match 91.3%; Score 21; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGTTGGCAGGTG 22
|||||
Db 53714 AGCCAGGCATGTTGGCAGGTG 53734

RESULT 2
US-09-978-197-3
; Sequence 3, Application US/09978197
; Patent No. 6403353
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178DIV
; CURRENT APPLICATION NUMBER: US/09/978.197
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/813.817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-978-197-3

Query Match 91.3%; Score 21; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGTTGGCAGGTG 22
|||||
Db 53714 AGCCAGGCATGTTGGCAGGTG 53734

RESULT 3
US-09-851-896-3
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: R1S-0220
; CURRENT APPLICATION NUMBER: US/09/851.896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match 91.3%; Score 21; DB 4; Length 70000;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGTTGGCAGGTG 22
|||||
Db 24102 AGCCAGGCATGTTGGCAGGTG 24122

RESULT 4
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US2 CIP
; CURRENT APPLICATION NUMBER: US/09/750.580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599.362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
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PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 10945..12946
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc feature
LOCATION: 15969..17969
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu

NAME/KEY: primer bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match 91.3%; Score 21; DB 4; Length 81001;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGCAGGTG 22
Db 37881 AGCCAGGCATGGTGCAGGTG 37861

RESULT 5
US-09-797-906-3/c
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianche YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 91.3%; Score 21; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCGATGGTGGCAGGTG 22
Db 16317 AGCCAGGCGATGGTGGCAGGTG 16297

RESULT 6
PCT-US93-08386-7/c
; Sequence 7, Application PC/TUS9308386
; GENERAL INFORMATION:
; APPLICANT: Bernardo Nadal-Ginard
; TITLE OF INVENTION: MYOCYTE-SPECIFIC
; TITLE OF INVENTION: TRANSCRIPTION
; TITLE OF INVENTION: ENHANCING FACTOR 2
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: .00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2950

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-08386-7

Query Match 87.0%; Score 20; DB 5; Length 2950;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCGATGGTGGCAGG 20
Db 202 CAGCCAGGCGATGGTGGCAGG 183

RESULT 7
PCT-US93-08386-1/c
; Sequence 1, Application PC/TUS9308386
; GENERAL INFORMATION:
; APPLICANT: Bernardo Nadal-Ginard
; TITLE OF INVENTION: MYOCYTE-SPECIFIC
; TITLE OF INVENTION: TRANSCRIPTION
; TITLE OF INVENTION: ENHANCING FACTOR 2
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: .00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2968
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-08386-1

Query Match 87.0%; Score 20; DB 5; Length 2968;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCGATGGTGGCAGG 20
Db 202 CAGCCAGGCGATGGTGGCAGG 183

RESULT 8
US-09-385-982-28
; Sequence 28, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.

;; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;; FILE REFERENCE: CCDNA-260XX
;; CURRENT APPLICATION NUMBER: US/09/385,982
;; CURRENT FILING DATE: 1999-08-30
;; EARLIER APPLICATION NUMBER: 09/328,111
;; EARLIER FILING DATE: 1999-06-08
;; EARLIER APPLICATION NUMBER: 60/117,393
;; EARLIER FILING DATE: 1999-01-27
;; EARLIER APPLICATION NUMBER: 60/098,639
;; EARLIER FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 544
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 28
;; LENGTH: 443
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(443)
;; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-28

Query Match 82.6%; Score 19; DB 4; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGCGCATGGTGGCAGG 20
|||||
Db 242 AGCCAGCGCATGGTGGCAGG 260

RESULT 9
US-08-482-918-43
; Sequence 43, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
;; LOCATION: ..3307, 3513..3595)
;; FEATURE:
;; NAME/KEY: mat_peptide
;; LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
;; LOCATION: ..3307, 3513..3595)
US-08-482-918-43

Query Match 82.6%; Score 19; DB 4; Length 3807;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGCGCATGGTGGCAGG 20
|||||
Db 2412 AGCCAGCGCATGGTGGCAGG 2430

RESULT 10
US-09-224-681-43
; Sequence 43, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.

```

; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3513..3595)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3513..3595)
; US-09-224-681-43
Query Match 82.6%; Score 19; DB 4; Length 3807;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AGCCAGGCATGGTGGCAGG 20
Db 2412 AGCCAGGCATGGTGGCAGG 2430

RESULT 11
US-08-336-728A-43
; Sequence 43, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
;
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3512..3597)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3512..3597)
; US-08-336-728A-43
Query Match 82.6%; Score 19; DB 4; Length 3807;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 AGCCAGGCATGGTGGCAGG 20
Db 2412 AGCCAGGCATGGTGGCAGG 2430

RESULT 12
US-08-482-918-47
; Sequence 47, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5964 base pairs
;
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5964 base pairs
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PRIOR APPLICATION DATA: 07/422,383
APPLICATION NUMBER: 16-OCT-1989
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 47:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
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LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677
LOCATION: 5677..5713)
FEATURE:
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US-09-224-681-47
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Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3191 AGCCAGGCATGTTGGCAGG 3209
RESULT 14
US-08-336-728A-47
Sequence 47, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
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; LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,
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; LOCATION: 5677..5713)
; FEATURE:
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; LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932
; LOCATION: ..4088, 4314..4397, 4778..4887, 5208..5275, 5677
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; US-08-336-728A-47

Query Match      82.6%; Score 19; DB 4; Length 5864;
Best Local Similarity 100.0%; Pred. No. 0.087;
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RESULT 15
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; Patent No. 6440738
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
; FILE REFERENCE: RTS-0164
; CURRENT APPLICATION NUMBER: US/09/780,175
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 17
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; ORGANISM: Homo sapiens
; FEATURE:
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US-09-780-175-17

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Sequence: 1 cagccaggcatggtgcaggtgt 23

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Searched: 1029858 seqs, 724030393 residues

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and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	21	91.3	278	9	US-09-764-868-1310
C 5	21	91.3	278	9	US-09-764-868-1311
C 6	21	91.3	300	9	US-09-796-692-8688
C 7	21	91.3	300	9	US-10-040-862-8688
C 8	21	91.3	383	12	US-10-033-528-1863
C 9	21	91.3	401	9	US-09-946-807-876
C 10	21	91.3	401	9	US-09-946-807-877
C 11	21	91.3	401	9	US-09-946-807-878
C 12	21	91.3	401	9	US-09-946-807-879
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C 16	21	91.3	401	10	US-09-795-668-879
C 17	21	91.3	401	10	US-09-795-668-876
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c 244	18	78.3	237326	9	US-10-301-844-2	Sequence 2, Appli	317	17	73.9	461	US-09-918-995-28860	Sequence 28860, A
c 245	18	78.3	302250	10	US-09-962-832-154	Sequence 154, App	318	17	73.9	462	US-10-073-961-90	Sequence 90, Appl
c 246	18	78.3	397658	10	US-09-813-320-3	Sequence 3, Appli	319	17	73.9	462	US-09-764-887-90	Sequence 10286, A
c 247	17	73.9	83	10	US-09-764-877-3299	Sequence 3299, Ap	320	17	73.9	463	US-09-918-995-10286	Sequence 10286, A
c 248	17	73.9	87	10	US-10-091-504-2041	Sequence 2041, Ap	321	17	73.9	471	US-09-867-701-296	Sequence 296, App
c 249	17	73.9	87	10	US-09-764-869-2041	Sequence 809, Ap	322	17	73.9	472	US-09-918-995-15068	Sequence 15068, A
c 250	17	73.9	107	9	US-09-764-891-8309	Sequence 8309, Ap	323	17	73.9	474	US-09-918-995-1926	Sequence 192, App
c 251	17	73.9	130	9	US-09-764-891-7261	Sequence 7261, Ap	324	17	73.9	476	US-10-198-846-6926	Sequence 132, App
c 252	17	73.9	130	9	US-09-764-891-7797	Sequence 7797, Ap	325	17	73.9	478	US-09-918-995-36512	Sequence 36512, A
c 253	17	73.9	155	7	US-08-781-986A-1509	Sequence 1509, Ap	326	17	73.9	480	US-09-728-444-820	Sequence 820, App
c 254	17	73.9	188	9	US-09-764-904-74	Sequence 74, Appl	327	17	73.9	482	US-09-918-995-19739	Sequence 19739, A
c 255	17	73.9	188	9	US-10-091-548-74	Sequence 74, Appl	328	17	73.9	483	US-09-918-995-11118	Sequence 11118, A
c 256	17	73.9	188	9	US-10-074-095-602	Sequence 602, App	329	17	73.9	483	US-09-764-891-82	Sequence 82, Appl
c 257	17	73.9	188	10	US-09-764-860-602	Sequence 602, App	c 330	17	73.9	487	US-10-060-036-820	Sequence 820, App
c 258	17	73.9	213	9	US-09-764-891-2000	Sequence 2000, Ap	331	17	73.9	491	US-09-783-590-10242	Sequence 10242, A
c 259	17	73.9	222	9	US-09-918-995-29702	Sequence 29702, A	c 332	17	73.9	494	US-09-918-995-14808	Sequence 14808, A
c 260	17	73.9	233	9	US-09-764-891-8522	Sequence 8522, Ap	c 333	17	73.9	504	US-09-783-590-405	Sequence 405, App
c 261	17	73.9	259	10	US-09-764-877-2254	Sequence 2254, Ap	334	17	73.9	508	US-09-796-692-5235	Sequence 5235, Ap
c 262	17	73.9	266	10	US-09-867-701-7659	Sequence 7659, Ap	c 335	17	73.9	508	US-10-040-862-5235	Sequence 5235, Ap
c 263	17	73.9	278	9	US-09-764-891-6874	Sequence 6874, Ap	c 336	17	73.9	550	US-09-918-995-15924	Sequence 15924, A
c 264	17	73.9	291	9	US-09-918-995-7570	Sequence 7570, Ap	c 337	17	73.9	569	US-10-198-846-8551	Sequence 8551, Ap
c 265	17	73.9	299	12	US-10-068-067-12	Sequence 12, Appl	c 338	17	73.9	584	US-09-796-692-9560	Sequence 9560, Ap
c 266	17	73.9	323	10	US-09-867-701-6832	Sequence 6832, Ap	c 339	17	73.9	584	US-10-040-862-9560	Sequence 9560, Ap
c 267	17	73.9	324	9	US-09-803-719-1684	Sequence 1684, Ap	c 340	17	73.9	604	US-10-271-887-22	Sequence 22, Appl
c 268	17	73.9	326	10	US-09-867-701-8181	Sequence 8181, Ap	c 341	17	73.9	646	US-09-871-161-314	Sequence 314, App
c 269	17	73.9	328	10	US-09-867-701-3398	Sequence 3398, Ap	c 342	17	73.9	689	US-09-776-724A-65	Sequence 65, Appl
c 270	17	73.9	335	10	US-09-764-877-2742	Sequence 2742, Ap	c 343	17	73.9	693	US-09-764-877-3235	Sequence 3235, Ap
c 271	17	73.9	336	10	US-09-867-701-7075	Sequence 7075, Ap	c 344	17	73.9	728	US-09-986-480-87	Sequence 87, Appl
c 272	17	73.9	339	9	US-09-918-995-17954	Sequence 17954, A	c 345	17	73.9	761	US-09-764-891-6039	Sequence 6039, Ap
c 273	17	73.9	352	10	US-09-998-598-1659	Sequence 1699, Ap	c 346	17	73.9	811	US-09-907-969-55	Sequence 55, Appl
c 274	17	73.9	357	9	US-10-031-572-28	Sequence 28, Appl	c 347	17	73.9	811	US-09-884-441-55	Sequence 55, Appl
c 275	17	73.9	357	9	US-09-918-995-18791	Sequence 18791, A	c 348	17	73.9	825	US-10-091-504-1980	Sequence 1980, Ap
c 276	17	73.9	357	9	US-09-764-891-6663	Sequence 6663, App	c 349	17	73.9	825	US-09-764-869-1980	Sequence 1980, Ap
c 277	17	73.9	362	9	US-09-918-995-18953	Sequence 18953, A	c 350	17	73.9	828	US-10-198-846-5092	Sequence 5092, Ap
c 278	17	73.9	367	9	US-09-764-872-878	Sequence 878, App	c 351	17	73.9	853	US-09-764-872-814	Sequence 814, App
c 279	17	73.9	367	9	US-09-764-872-879	Sequence 879, App	c 352	17	73.9	853	US-09-764-891-9105	Sequence 9105, Ap
c 280	17	73.9	369	9	US-09-918-995-16631	Sequence 16631, A	c 353	17	73.9	853	US-10-198-846-6104	Sequence 6104, Ap
c 281	17	73.9	371	9	US-09-764-891-7616	Sequence 7616, Ap	c 354	17	73.9	859	US-10-023-282-18	Sequence 18, Appl
c 282	17	73.9	373	9	US-09-918-995-37769	Sequence 37769, A	c 355	17	73.9	879	US-09-764-853-13	Sequence 13, Appl
c 283	17	73.9	388	9	US-10-046-935-843	Sequence 843, App	c 356	17	73.9	911	US-09-776-724A-77	Sequence 77, Appl
c 284	17	73.9	388	9	US-09-878-178-843	Sequence 843, App	c 357	17	73.9	923	US-10-119-926-80	Sequence 80, Appl
c 285	17	73.9	388	9	US-10-146-502-843	Sequence 843, App	c 358	17	73.9	926	US-10-198-846-11389	Sequence 11389, A
c 286	17	73.9	388	10	US-09-867-701-7925	Sequence 7925, Ap	c 359	17	73.9	954	US-10-198-846-3411	Sequence 3411, Ap
c 287	17	73.9	390	9	US-09-803-719-1821	Sequence 1821, Ap	c 360	17	73.9	978	US-09-776-724A-33	Sequence 33, Appl
c 288	17	73.9	395	10	US-10-198-846-12628	Sequence 12628, A	c 361	17	73.9	1020	US-09-822-830A-297	Sequence 297, App
c 289	17	73.9	395	10	US-09-867-701-8351	Sequence 8351, Ap	c 362	17	73.9	1022	US-09-764-891-5693	Sequence 5693, Ap
c 290	17	73.9	397	10	US-09-920-300A-1579	Sequence 1579, Ap	c 363	17	73.9	1091	US-10-198-846-13908	Sequence 13908, A
c 291	17	73.9	397	12	US-10-033-528-1579	Sequence 1579, Ap	c 364	17	73.9	1195	US-09-822-830A-285	Sequence 285, App
c 292	17	73.9	401	9	US-09-946-807-1046	Sequence 1046, Ap	c 365	17	73.9	1241	US-10-198-846-7146	Sequence 7146, Ap
c 293	17	73.9	401	9	US-09-946-807-1162	Sequence 1162, Ap	c 366	17	73.9	1300	US-09-764-872-817	Sequence 817, App
c 294	17	73.9	401	10	US-09-795-668-1046	Sequence 1046, Ap	c 367	17	73.9	1300	US-09-764-891-9108	Sequence 9108, Ap
c 295	17	73.9	401	10	US-09-795-668-1162	Sequence 1162, Ap	c 368	17	73.9	1364	US-09-822-830A-363	Sequence 363, App
c 296	17	73.9	401	10	US-09-795-686-1046	Sequence 1046, Ap	c 369	17	73.9	1453	US-10-072-349-253	Sequence 253, App
c 297	17	73.9	401	10	US-09-795-686-1162	Sequence 1162, Ap	c 370	17	73.9	1453	US-09-764-855-253	Sequence 253, App
c 298	17	73.9	404	10	US-09-867-701-5146	Sequence 5146, Ap	c 371	17	73.9	1457	US-09-989-920-93	Sequence 93, Appl
c 299	17	73.9	405	9	US-09-946-807-1381	Sequence 1381, Ap	c 372	17	73.9	1496	US-09-822-830A-130	Sequence 130, App
c 300	17	73.9	405	10	US-09-795-668-1381	Sequence 1381, Ap	c 373	17	73.9	1560	US-10-068-067-20	Sequence 20, Appl
c 301	17	73.9	405	10	US-09-795-686-1381	Sequence 1381, Ap	c 374	17	73.9	1785	US-10-198-846-10306	Sequence 10306, A
c 302	17	73.9	408	10	US-09-969-708-142	Sequence 142, App	c 375	17	73.9	1812	US-10-198-846-12998	Sequence 12998, A
c 303	17	73.9	410	9	US-09-918-995-3686	Sequence 3686, Ap	c 376	17	73.9	1815	US-09-822-846-60	Sequence 60, Appl
c 304	17	73.9	426	10	US-09-867-701-4505	Sequence 4505, Ap	c 377	17	73.9	1821	US-10-023-282-43	Sequence 43, Appl
c 305	17	73.9	427	9	US-09-918-995-33743	Sequence 33743, A	c 378	17	73.9	1866	US-09-822-849A-468	Sequence 468, App
c 306	17	73.9	428	9	US-09-764-891-9973	Sequence 9973, Ap	c 379	17	73.9	1916	US-09-833-381-905	Sequence 905, App
c 307	17	73.9	433	10	US-09-867-701-5715	Sequence 5715, Ap	c 380	17	73.9	1938	US-09-764-891-8557	Sequence 8557, Ap
c 308	17	73.9	441	9	US-09-918-995-26270	Sequence 26270, A	c 381	17	73.9	1938	US-09-764-891-8558	Sequence 8558, Ap
c 309	17	73.9	442	10	US-09-867-701-3522	Sequence 3522, Ap	c 382	17	73.9	2105	US-09-939-823-15	Sequence 15, Appl
c 310	17	73.9	445	9	US-09-918-995-15101	Sequence 15101, A	c 383	17	73.9	2113	US-09-938-803-22	Sequence 22, Appl
c 311	17	73.9	445	10	US-09-867-701-9819	Sequence 9819, Ap	c 384	17	73.9	2125	US-09-802-807-6	Sequence 6, Appl

C 823	17	73.9	2895	12	US-10-068-067-11	Sequence 11, Appl	17	73.9	3719	9	US-10-147-500-49	Sequence 49, Appl
C 824	17	73.9	2969	10	US-09-764-877-3578	Sequence 3578, Ap	17	73.9	3719	9	US-10-147-502-49	Sequence 49, Appl
C 825	17	73.9	3064	9	US-10-092-154-1289	Sequence 1289, Ap	17	73.9	3719	9	US-10-147-515-49	Sequence 49, Appl
C 826	17	73.9	3064	10	US-09-764-847-1289	Sequence 1289, Ap	17	73.9	3719	9	US-10-147-517-49	Sequence 49, Appl
C 827	17	73.9	3162	10	US-09-764-877-2937	Sequence 2937, Ap	17	73.9	3719	9	US-10-147-519-49	Sequence 49, Appl
C 828	17	73.9	3192	9	US-09-764-891-7590	Sequence 7590, Ap	17	73.9	3719	9	US-10-147-526-49	Sequence 49, Appl
C 829	17	73.9	3276	9	US-09-764-891-7591	Sequence 7591, Ap	17	73.9	3719	9	US-10-147-527-49	Sequence 49, Appl
C 830	17	73.9	3276	9	US-09-764-868-266	Sequence 266, Ap	17	73.9	3719	9	US-10-152-395-49	Sequence 49, Appl
C 831	17	73.9	3314	10	US-09-954-456-1171	Sequence 1171, Ap	17	73.9	3719	9	US-10-157-782-49	Sequence 49, Appl
C 832	17	73.9	3422	9	US-09-764-891-6046	Sequence 6046, Ap	17	73.9	3719	9	US-10-121-040-49	Sequence 49, Appl
C 833	17	73.9	3422	9	US-09-764-891-6048	Sequence 6048, Ap	17	73.9	3719	9	US-10-121-056-49	Sequence 49, Appl
C 834	17	73.9	3422	9	US-10-091-438-271	Sequence 271, App	17	73.9	3719	9	US-10-121-061-49	Sequence 49, Appl
C 835	17	73.9	3422	9	US-10-091-438-273	Sequence 273, App	17	73.9	3719	9	US-10-123-235-49	Sequence 49, Appl
C 836	17	73.9	3623	9	US-09-764-891-8854	Sequence 8854, Ap	17	73.9	3719	9	US-10-124-818-49	Sequence 49, Appl
C 837	17	73.9	3695	9	US-10-097-340-337	Sequence 337, App	17	73.9	3719	9	US-10-125-926A-49	Sequence 49, Appl
C 838	17	73.9	3719	9	US-10-028-072-49	Sequence 49, Appl	17	73.9	3719	9	US-10-125-930A-49	Sequence 49, Appl
C 839	17	73.9	3719	9	US-10-121-049-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-831A-49	Sequence 49, Appl
C 840	17	73.9	3719	9	US-10-123-904-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-837A-49	Sequence 49, Appl
C 841	17	73.9	3719	9	US-10-140-470-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-838B-49	Sequence 49, Appl
C 842	17	73.9	3719	9	US-10-175-746-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-842A-49	Sequence 49, Appl
C 843	17	73.9	3719	9	US-10-176-918-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-843A-49	Sequence 49, Appl
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C 845	17	73.9	3719	9	US-10-137-855-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-846A-49	Sequence 49, Appl
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C 848	17	73.9	3719	9	US-10-143-114-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-850A-49	Sequence 49, Appl
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C 851	17	73.9	3719	9	US-10-123-262-49	Sequence 49, Appl	17	73.9	3719	9	US-10-128-686A-49	Sequence 49, Appl
C 852	17	73.9	3719	9	US-10-142-423-49	Sequence 49, Appl	17	73.9	3719	9	US-10-128-690A-49	Sequence 49, Appl
C 853	17	73.9	3719	9	US-10-121-050-49	Sequence 49, Appl	17	73.9	3719	9	US-10-128-691A-49	Sequence 49, Appl
C 854	17	73.9	3719	9	US-10-141-755-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-819A-49	Sequence 49, Appl
C 855	17	73.9	3719	9	US-10-143-032-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-829A-49	Sequence 49, Appl
C 856	17	73.9	3719	9	US-10-123-108-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-836A-49	Sequence 49, Appl
C 857	17	73.9	3719	9	US-10-123-236-49	Sequence 49, Appl	17	73.9	3719	9	US-10-137-868-49	Sequence 49, Appl
C 858	17	73.9	3719	9	US-10-123-261-49	Sequence 49, Appl	17	73.9	3719	9	US-10-146-729-49	Sequence 49, Appl
C 859	17	73.9	3719	9	US-10-140-921-49	Sequence 49, Appl	17	73.9	3719	9	US-10-146-791-49	Sequence 49, Appl
C 860	17	73.9	3719	9	US-10-140-928-49	Sequence 49, Appl	17	73.9	3719	9	US-10-147-484-49	Sequence 49, Appl
C 861	17	73.9	3719	9	US-10-121-045-49	Sequence 49, Appl	17	73.9	3719	9	US-10-147-492-49	Sequence 49, Appl
C 862	17	73.9	3719	9	US-10-123-292-49	Sequence 49, Appl	17	73.9	3719	9	US-10-147-508-49	Sequence 49, Appl
C 863	17	73.9	3719	9	US-10-123-903-49	Sequence 49, Appl	17	73.9	3719	9	US-10-147-512-49	Sequence 49, Appl
C 864	17	73.9	3719	9	US-10-124-819-49	Sequence 49, Appl	17	73.9	3719	9	US-10-158-782-49	Sequence 49, Appl
C 865	17	73.9	3719	9	US-10-124-825-49	Sequence 49, Appl	17	73.9	3719	9	US-10-175-735-49	Sequence 49, Appl
C 866	17	73.9	3719	9	US-10-140-925-49	Sequence 49, Appl	17	73.9	3719	9	US-10-123-905-49	Sequence 49, Appl
C 867	17	73.9	3719	9	US-10-160-498-49	Sequence 49, Appl	17	73.9	3719	9	US-10-123-907-49	Sequence 49, Appl
C 868	17	73.9	3719	9	US-10-121-041-49	Sequence 49, Appl	17	73.9	3719	9	US-10-124-815-49	Sequence 49, Appl
C 869	17	73.9	3719	9	US-10-121-043-49	Sequence 49, Appl	17	73.9	3719	9	US-10-125-921A-49	Sequence 49, Appl
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C 880	17	73.9	3719	9	US-10-125-924-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-834A-49	Sequence 49, Appl
C 881	17	73.9	3719	9	US-10-127-825A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-127-836A-49	Sequence 49, Appl
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C 887	17	73.9	3719	9	US-10-131-813A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-128-694A-49	Sequence 49, Appl
C 888	17	73.9	3719	9	US-10-131-818A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-825A-49	Sequence 49, Appl
C 889	17	73.9	3719	9	US-10-131-823A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-825A-49	Sequence 49, Appl
C 890	17	73.9	3719	9	US-10-131-824A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-230-417-49	Sequence 49, Appl
C 891	17	73.9	3719	9	US-10-131-830A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-121-051-49	Sequence 49, Appl
C 892	17	73.9	3719	9	US-10-131-837A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-815A-49	Sequence 49, Appl
C 893	17	73.9	3719	9	US-10-137-872A-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-817A-49	Sequence 49, Appl
C 894	17	73.9	3719	9	US-10-140-860-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-821A-49	Sequence 49, Appl
C 895	17	73.9	3719	9	US-10-142-417-49	Sequence 49, Appl	17	73.9	3719	9	US-10-131-822A-49	Sequence 49, Appl
	17	73.9	3719	9			17	73.9	3719	9	US-10-131-828A-49	Sequence 49, Appl

```
c 969      17 73.9 3719 9 US-10-131-835A-49
c 970      17 73.9 3719 9 US-10-137-864A-49
c 971      17 73.9 3719 9 US-10-137-869A-49
c 972      17 73.9 3719 9 US-10-147-523-49
c 973      17 73.9 3719 9 US-10-158-785-49
c 974      17 73.9 3719 9 US-10-121-042-49
c 975      17 73.9 3719 9 US-10-123-912-49
c 976      17 73.9 3719 9 US-10-132-007-49
c 977      17 73.9 3719 9 US-10-194-359-49
c 978      17 73.9 3978 9 US-10-198-846-9888
c 979      17 73.9 4039 9 US-10-079-854-225
c 980      17 73.9 4039 10 US-09-764-878-225
c 981      17 73.9 4082 9 US-09-764-891-8663
c 982      17 73.9 4132 9 US-10-198-846-13133
c 983      17 73.9 4206 9 US-10-091-504-1884
c 984      17 73.9 4206 10 US-09-764-869-1884
c 985      17 73.9 4374 9 US-10-028-072-125
c 986      17 73.9 4374 9 US-10-121-049-125
c 987      17 73.9 4374 9 US-10-123-904-125
c 988      17 73.9 4374 9 US-10-140-470-125
c 989      17 73.9 4374 9 US-10-175-746-125
c 990      17 73.9 4374 9 US-10-176-921-125
c 991      17 73.9 4374 9 US-10-176-921-125
c 992      17 73.9 4374 9 US-10-137-865-125
c 993      17 73.9 4374 9 US-10-140-474-125
c 994      17 73.9 4374 9 US-10-142-431-125
c 995      17 73.9 4374 9 US-10-143-114-125
c 996      17 73.9 4374 9 US-10-140-002-125
c 997      17 73.9 4374 9 US-10-142-419-125
c 998      17 73.9 4374 9 US-10-123-262-125
c 999      17 73.9 4374 9 US-10-142-423-125
c 1000     17 73.9 4374 9 US-10-121-050-125
```

ALIGNMENTS

```
RESULT 1
US-09-777-921A-68/c
; Sequence 68, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-921A-68
```

```
Query Match          95.7%; Score 22; DB 10; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 CAGCCAGGCATGGTGGCAGGTG 22
Db      552 CAGCCAGGCATGGTGGCAGGTG 531
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RESULT 2

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US-09-777-921A-69/c
; Sequence 69, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
```

```
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (301)...(301)
; OTHER INFORMATION: T may be either present or absent
US-09-777-921A-69
```

```
Query Match          95.7%; Score 22; DB 10; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 CAGCCAGGCATGGTGGCAGGTG 22
Db      136 CAGCCAGGCATGGTGGCAGGTG 115
```

RESULT 3

```
US-09-777-921A-3/c
; Sequence 3, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 69327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(69327)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-921A-3
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Query Match          95.7%; Score 22; DB 10; Length 69327;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 CAGCCAGGCATGGTGGCAGGTG 22
Db      20327 CAGCCAGGCATGGTGGCAGGTG 20306
```

RESULT 4

```
US-09-764-868-1310/c
; Sequence 1310, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1310
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; LENGTH: 278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1310

Query Match          91.3%; Score 21; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2  AGCCAGGCGATGGTGCAGGTG 22
    |||||
Db  176 AGCCAGGCGATGGTGCAGGTG 156

RESULT 5
US-09-764-868-1311/c
; Sequence 1311, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1311
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1311

Query Match          91.3%; Score 21; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2  AGCCAGGCGATGGTGCAGGTG 22
    |||||
Db  176 AGCCAGGCGATGGTGCAGGTG 156

RESULT 6
US-09-796-692-8688/c
; Sequence 8688, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Aigate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8688
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (48)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (57)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (70)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (88)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (89)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (97)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (120)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (127)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (129)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (163)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (202)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (203)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (213)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (229)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (235)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (274)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (287)
; OTHER INFORMATION: n=A,T,C or G
; US-09-796-692-8688

Query Match          91.3%; Score 21; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 ACCCAGCATGGTGGCAGGTG 22
Db 34 ACCCAGCATGGTGGCAGGTG 14

RESULT 7

US-10-040-862-8688/c
; Sequence 8688, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Alsate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8688
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (48)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (57)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (70)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (88)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (89)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (97)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (120)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (127)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (129)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (163)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (202)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (203)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (213)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (229)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (235)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (274)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (287)
; OTHER INFORMATION: n=A,T,C or G
; US-10-040-862-8688

Query Match 91.3%; Score 21; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ACCCAGCATGGTGGCAGGTG 22
Db 34 ACCCAGCATGGTGGCAGGTG 14

RESULT 8

US-10-033-528-1863
; Sequence 1863, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547C1
 CURRENT APPLICATION NUMBER: US/10/033.528
 CURRENT FILING DATE: 2001-12-26
 NUMBER OF SEQ ID NOS: 1896
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1863
 LENGTH: 383
 TYPE: DNA
 ORGANISM: Homo sapiens
 NAME/KEY: misc feature
 LOCATION: 1, 35, 37, 375
 OTHER INFORMATION: n = A,T,C or G
 US-10-033-528-1863

Query Match 91.3%; Score 21; DB 12; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
 Db 215 AGCCAGGCATGGTGGCAGGTG 235

RESULT 9

US-09-946-807-876
 Sequence 876, Application US/09946807
 Patent No. US20020165144A1
 GENERAL INFORMATION:
 APPLICANT: Stefansson, Hreinn
 APPLICANT: Steinthorsdottir, Valgerdur
 APPLICANT: Gulcher, Jeffrey R.
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
 FILE REFERENCE: 2345.2004-001
 CURRENT APPLICATION NUMBER: US/09/946.807
 CURRENT FILING DATE: 2001-09-05
 PRIOR APPLICATION NUMBER: US/09/795.668
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: US 09/515,716
 PRIOR FILING DATE: 2000-02-28
 NUMBER OF SEQ ID NOS: 1531
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 876
 LENGTH: 401
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-946-807-876

Query Match 91.3%; Score 21; DB 9; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
 Db 340 AGCCAGGCATGGTGGCAGGTG 360

RESULT 10

US-09-946-807-877
 Sequence 877, Application US/09946807
 Patent No. US20020165144A1
 GENERAL INFORMATION:
 APPLICANT: Stefansson, Hreinn
 APPLICANT: Steinthorsdottir, Valgerdur
 APPLICANT: Gulcher, Jeffrey R.
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
 FILE REFERENCE: 2345.2004-001
 CURRENT APPLICATION NUMBER: US/09/946.807
 CURRENT FILING DATE: 2001-09-05
 PRIOR APPLICATION NUMBER: US/09/795.668
 PRIOR FILING DATE: 2001-02-28
 NUMBER OF SEQ ID NOS: 1531
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 879
 LENGTH: 401
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-946-807-879

NUMBER OF SEQ ID NOS: 1531
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 877
 LENGTH: 401
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-946-807-877

Query Match 91.3%; Score 21; DB 9; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
 Db 29 AGCCAGGCATGGTGGCAGGTG 49

RESULT 11

US-09-946-807-878
 Sequence 878, Application US/09946807
 Patent No. US20020165144A1
 GENERAL INFORMATION:
 APPLICANT: Stefansson, Hreinn
 APPLICANT: Steinthorsdottir, Valgerdur
 APPLICANT: Gulcher, Jeffrey R.
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
 FILE REFERENCE: 2345.2004-001
 CURRENT APPLICATION NUMBER: US/09/946.807
 CURRENT FILING DATE: 2001-09-05
 PRIOR APPLICATION NUMBER: US/09/795.668
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: US 09/515,716
 PRIOR FILING DATE: 2000-02-28
 NUMBER OF SEQ ID NOS: 1531
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 878
 LENGTH: 401
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-946-807-878

Query Match 91.3%; Score 21; DB 9; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
 Db 27 AGCCAGGCATGGTGGCAGGTG 47

RESULT 12

US-09-946-807-879
 Sequence 879, Application US/09946807
 Patent No. US20020165144A1
 GENERAL INFORMATION:
 APPLICANT: Stefansson, Hreinn
 APPLICANT: Steinthorsdottir, Valgerdur
 APPLICANT: Gulcher, Jeffrey R.
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
 FILE REFERENCE: 2345.2004-001
 CURRENT APPLICATION NUMBER: US/09/946.807
 CURRENT FILING DATE: 2001-09-05
 PRIOR APPLICATION NUMBER: US/09/795.668
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: US 09/515,716
 PRIOR FILING DATE: 2000-02-28
 NUMBER OF SEQ ID NOS: 1531
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 879
 LENGTH: 401
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-946-807-879

```
Query Match          91.3%; Score 21; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
21 AGCCAGGCATGGTGGCAGGTG 41
Db

RESULT 13

US-09-795-668-876
; Sequence 876, Application US/09795668
; Patent No. US20020045577A1

: GENERAL INFORMATION:

APPLICANT: Stefansson Hreinn

APPLICANT: STEINTHORSDOTTIR VALGERDUR

APPLICANT: Gulcher Jeffrey R

APPLICANT: GUICHER, JEFFREY R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE

; TITLE OF INVENTION: HUMAN SCHEDULING
: FILE REFERENCE: 3345 3004 - 001

FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: USC/08/785 558

; CURRENT APPLICATION NUMBER: US/08/000000

; CURRENT FILING DATE: 2001-02-28

;
PRIOR APPLICATION NUMBER: 00000000

; PRIOR FILING DATE: 2000-02-

; NUMBER OF SEQ ID NOS: 1531

; SOFTWARE: Fa

; SEQ ID NO 876

; LENGTH: 40

; TYPE: DNA

; ORGANISM: Homo

Query Match 91.3%; Score 21; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
340 AGCCAGGCATGGTGGCAGGTG 360
Db

RESULT 14

US-09-795-668-877
; Sequence 877, Application US/09795668
; Patent No. US2002004557A1

GENERAL INFORMATION:

: APPLICANT: Stefansson, Hreinn

APPLICANT: Steinthorsdottir. Valgerdur

APPLICANT: Gulcher, Jeffrey R.

APPLICANT: GUICHET, JELLEY K.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE

FILE REFERENCE: 2345 2004-001

FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: IIS/09/795 668

; CURRENT APPLICATION NUMBER: US/0
 : CURRENT FILING DATE: 2001-03-28

;; CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 3000 00

; PRIOR FILING DATE: 2000-02

; NUMBER OF SEQ ID NOS: 1531

; SOFTWARE: Fa

; SEQ ID NO 877

; LENGTH: 40

; TYPE: DNA

; ORGANISM: Hom

Query Match 91.3%; Score 21; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
Db 29 AGCCAGGCATGGTGGCAGGTG 49

RESULT 15'

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 26.1364 Seconds
(without alignments)
14252.028 Million cell updates/sec

Title: US-09-513-888C-1_COPY_4451_4473
Perfect score: 23
Sequence: 1 cagccagcagtcgtggtgagcgtgt 23

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

- 1: em_estba:*
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- 3: em_estin:*
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- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	22	95.7	217 9	A1174766
2	22	95.7	237 9	AA372667
3	22	95.7	361 17	AQ102785
4	22	95.7	375 13	EG960515
5	22	95.7	538 12	BF084762
6	22	95.7	587 17	AQ714377

AG034167	Pan trogl	674	17	AG034167	95.7	22	7	95.7
AG096453	Pan trogl	679	17	AG096453	95.7	22	8	95.7
BG617547	602615028	723	12	BG617547	95.7	22	9	95.7
BF676568	602084486	766	12	BF676568	95.7	22	10	95.7
AA089829	chn1495.s	11	21	AA089829	91.3	21	11	91.3
N84649	J0399F Huma	12	21	N84649	91.3	21	12	91.3
T28260	EST34105 Hu	13	21	T28260	91.3	21	13	91.3
A1925839	w052h09.x	14	21	A1925839	91.3	21	14	91.3
BE179910	IL3-HT061	15	21	BE179910	91.3	21	15	91.3
N63388	Yz35g09.s1	16	21	N63388	91.3	21	16	91.3
BF929825	QV3-NT021	17	21	BF929825	91.3	21	17	91.3
AA772370	ai44b02.s	18	21	AA772370	91.3	21	18	91.3
A1886056	w08h04.x	19	21	A1886056	91.3	21	19	91.3
AQ274955	RPCI-1-16	20	21	AQ274955	91.3	21	20	91.3
AA582350	nm53c04.s	21	21	AA582350	91.3	21	21	91.3
B76199	RPCI11-13P1	22	21	B76199	91.3	21	22	91.3
BI495422	df118a06	23	21	BI495422	91.3	21	23	91.3
BI495423	df118a06	24	21	BI495423	91.3	21	24	91.3
CI8993	CI8993 Huma	25	21	CI8993	91.3	21	25	91.3
A1872513	w09b04.x	26	21	A1872513	91.3	21	26	91.3
H60185	Yr38e03.s1	27	21	H60185	91.3	21	27	91.3
BG011328	RC3-GN027	28	21	BG011328	91.3	21	28	91.3
AQ633140	RPCI-11-4	29	21	AQ633140	91.3	21	29	91.3
AQ275813	CITBI-E1-	30	21	AQ275813	91.3	21	30	91.3
BF813663	IL5-CI014	31	21	BF813663	91.3	21	31	91.3
AQ280901	CITBI-E1-	32	21	AQ280901	91.3	21	32	91.3
BE180440	RC3-HT062	33	21	BE180440	91.3	21	33	91.3
BE706669	PM0-HT033	34	21	BE706669	91.3	21	34	91.3
AQ347987	RPCI11-11	35	21	AQ347987	91.3	21	35	91.3
F09946	HSC38E072.n	36	21	F09946	91.3	21	36	91.3
A1423625	tf61c11.x	37	21	A1423625	91.3	21	37	91.3
BI050545	PM2-GN001	38	21	BI050545	91.3	21	38	91.3
R67701	Y124f04.r1	39	21	R67701	91.3	21	39	91.3
AA347908	EST54285	40	21	AA347908	91.3	21	40	91.3
AA650244	ns93f08.s	41	21	AA650244	91.3	21	41	91.3
B54136	CIT-HSP-201	42	21	B54136	91.3	21	42	91.3
AQ309845	CIT-HSP-2	43	21	AQ309845	91.3	21	43	91.3
EG980452	CM3-CN009	44	21	EG980452	91.3	21	44	91.3
AA581895	nm32a01.s	45	21	AA581895	91.3	21	45	91.3
R64046	Y122b04.r1	46	21	R64046	91.3	21	46	91.3
AQ333353	HS 5001.A	47	21	AQ333353	91.3	21	47	91.3
R83710	Yq14f12.r1	48	21	R83710	91.3	21	48	91.3
AQ810680	HS_5421.A	49	21	AQ810680	91.3	21	49	91.3
BQ440984	AGENCOURT	50	21	BQ440984	91.3	21	50	91.3
AQ075234	CIT-HSP-2	51	21	AQ075234	91.3	21	51	91.3
Z23155	ph218/1LM.O	52	21	Z23155	91.3	21	52	91.3
B58538	CIT-HSP-201	53	21	B58538	91.3	21	53	91.3
BF873285	CM0-ET012	54	21	BF873285	91.3	21	54	91.3
BF809550	QV0-CI019	55	21	BF809550	91.3	21	55	91.3
AW974839	EST386944	56	21	AW974839	91.3	21	56	91.3
AQ166077	HS 3071.A	57	21	AQ166077	91.3	21	57	91.3
AA452440	zx39e08.f	58	21	AA452440	91.3	21	58	91.3
AQ020880	RPCI11-58	59	21	AQ020880	91.3	21	59	91.3
AA602971	ns97d03.s	60	21	AA602971	91.3	21	60	91.3
AQ167549	HS_3071.B	61	21	AQ167549	91.3	21	61	91.3
BG011109	IL5-GN023	62	21	BG011109	91.3	21	62	91.3
H57265	Yr08b09.r1	63	21	H57265	91.3	21	63	91.3
AQ123388	HS 3079.B	64	21	AQ123388	91.3	21	64	91.3
AQ108498	CIT-HSP-2	65	21	AQ108498	91.3	21	65	91.3
BE830383	RC6-ET008	66	21	BE830383	91.3	21	66	91.3
AQ005348	CIT-HSP-2	67	21	AQ005348	91.3	21	67	91.3
BM014948	603640886	68	21	BM014948	91.3	21	68	91.3
AQ197424	CIT-HSP-2	69	21	AQ197424	91.3	21	69	91.3
BF935129	MR4-NT014	70	21	BF935129	91.3	21	70	91.3
AQ812736	HS 5252.A	71	21	AQ812736	91.3	21	71	91.3
AW768784	hl53c02.x	72	21	AW768784	91.3	21	72	91.3
BI018136	CM1-WF024	73	21	BI018136	91.3	21	73	91.3
AA747037	nx70f06.s	74	21	AA747037	91.3	21	74	91.3
AV761504	AV761504	75	21	AV761504	91.3	21	75	91.3
A1312596	qp77a04.x	76	21	A1312596	91.3	21	76	91.3
AQ228128	HS_2014.B	77	21	AQ228128	91.3	21	77	91.3
AQ412534	RPCI-11-1	78	21	AQ412534	91.3	21	78	91.3
		79	21		91.3	21	79	91.3

C 80	21	91.3	428	10	AV709052	AV709052 AV709052	153	21	91.3	567	17	AQ635013	AQ635013	RPCI-11-4
C 81	21	91.3	429	9	AA678499	AA678499 ah06f12.s	154	21	91.3	568	17	AQ417152	AQ417152	RPCI-11-2
C 82	21	91.3	430	12	BF819892	BF819892 ME1-RT002	155	21	91.3	569	17	AQ601577	AQ601577	HS 2105 B
C 83	21	91.3	433	17	AQ592472	AQ592472 HS 5455 A	156	21	91.3	570	14	BM994846	BM994846	UI-H-DHO-
C 84	21	91.3	434	17	AQ723808	AQ723808 HS 5370 A	157	21	91.3	571	14	BM994846	BM994846	UI-H-DHO-
C 85	21	91.3	437	9	AA583518	AA583518 nf24g12.s	158	21	91.3	572	9	AI760700	AI760700	HS 2053 A
C 86	21	91.3	437	17	AQ379751	AQ379751 RPCI11-13	159	21	91.3	573	17	AQ534115	AQ534115	RPCI-11-3
C 87	21	91.3	441	14	H72109	H72109 y502f01.s1	160	21	91.3	579	17	AQ569782	AQ569782	HS 5334 B
C 88	21	91.3	443	10	BE677702	BE677702 7d90f07.x	161	21	91.3	583	17	AQ779286	AQ779286	HS 3185 A
C 89	21	91.3	445	12	BF772474	BF772474 IL5-IT002	162	21	91.3	585	17	AQ712589	AQ712589	HS 2134 A
C 90	21	91.3	445	17	AQ428107	AQ428107 CITBI-EL-	163	21	91.3	606	13	BI765292	BI765292	603050395
C 91	21	91.3	448	17	AQ228914	AQ228914 HS 2013 B	164	21	91.3	610	17	AQ349950	AQ349950	RPCI11-11
C 92	21	91.3	450	10	AW276769	AW276769 xp65g07.x	165	21	91.3	611	10	AV709937	AV709937	AV709937
C 93	21	91.3	451	17	AQ466677	AQ466677 HS 5161 B	166	21	91.3	620	17	AQ534862	AQ534862	RPCI-11-3
C 94	21	91.3	452	14	N33374	N33374 y40c10.s1	167	21	91.3	621	17	AQ390071	AQ390071	RPCI11-15
C 95	21	91.3	453	14	R56101	R56101 y94a06.s1	168	21	91.3	622	10	AW963196	AW963196	EST375269
C 96	21	91.3	453	17	AQ020765	AQ020765 CIT-HSP-2	169	21	91.3	629	14	BQ000257	BQ000257	UI-H-D10-
C 97	21	91.3	453	17	AQ0708713	AQ0708713 HS 5370 A	170	21	91.3	637	13	BG927341	BG927341	HNC66-1-D
C 98	21	91.3	454	10	BE148910	BE148910 CM0-HT024	171	21	91.3	643	17	AQ279940	AQ279940	CITBI-EL-
C 99	21	91.3	456	17	AQ087064	AQ087064 HS 3248 A	172	21	91.3	655	17	AG152442	AG152442	Pan trogl
C 100	21	91.3	461	14	H71868	H71868 yf82c03.s1	173	21	91.3	655	17	AQ480046	AQ480046	RPCI-11-2
C 101	21	91.3	461	14	R44961	R44961 y933c08.s1	174	21	91.3	657	17	AG178656	AG178656	Pan trogl
C 102	21	91.3	462	14	BM697126	BM697126 UI-E-DWO-	175	21	91.3	658	17	AG183574	AG183574	Pan trogl
C 103	21	91.3	464	17	AQ404481	AQ404481 HS 5069 B	176	21	91.3	659	10	AV707441	AV707441	AV707441
C 104	21	91.3	466	17	AQ144744	AQ144744 HS 3092 A	177	21	91.3	661	12	BG566535	BG566535	602585562
C 105	21	91.3	468	10	AW029269	AW029269 wx08b12.x	178	21	91.3	663	17	AG119366	AG119366	Pan trogl
C 106	21	91.3	468	14	N57791	N57791 yv56b08.s1	179	21	91.3	663	17	AQ527989	AQ527989	RPCI-11-3
C 107	21	91.3	469	17	B82499	B82499 RPCI11-16F9	180	21	91.3	667	17	AQ482571	AQ482571	RPCI-11-2
C 108	21	91.3	470	14	N57770	N57770 yv56e08.s1	181	21	91.3	668	10	AV701541	AV701541	AV701541
C 109	21	91.3	471	10	AW904850	AW904850 RC5-NN106	182	21	91.3	669	17	AG148600	AG148600	Pan trogl
C 110	21	91.3	471	10	BE145294	BE145294 CM3-HT019	183	21	91.3	669	17	AG151884	AG151884	Pan trogl
C 111	21	91.3	472	17	AQ142184	AQ142184 HS 3179 B	184	21	91.3	670	17	AQ414253	AQ414253	RPCI-11-1
C 112	21	91.3	473	17	AQ693237	AQ693237 HS 5429 B	185	21	91.3	671	17	AG168614	AG168614	Pan trogl
C 113	21	91.3	475	17	AQ231773	AQ231773 HS 2026 A	186	21	91.3	672	17	AQ386522	AQ386522	RPCI11-14
C 114	21	91.3	479	9	AL921765	AL921765 wo29h11.x	187	21	91.3	673	17	AG101374	AG101374	Pan trogl
C 115	21	91.3	482	17	AQ377523	AQ377523 RPCI11-16	188	21	91.3	674	12	BF817005	BF817005	MR2-C1012
C 116	21	91.3	484	17	AQ314669	AQ314669 RPCI11-10	189	21	91.3	679	10	AW975969	AW975969	EST388078
C 117	21	91.3	484	17	AQ428466	AQ428466 CITBI-EL-	190	21	91.3	681	17	AG088220	AG088220	Pan trogl
C 118	21	91.3	485	17	AQ282171	AQ282171 RPCI11-79	191	21	91.3	684	17	AG115638	AG115638	Pan trogl
C 119	21	91.3	487	17	AZ694787	AZ694787 UP 390-17	192	21	91.3	685	17	AG056681	AG056681	Pan trogl
C 120	21	91.3	488	17	AQ351270	AQ351270 RPCI11-11	193	21	91.3	690	17	B68459	B68459	CIT-HSP-205
C 121	21	91.3	489	17	AQ178561	AQ178561 HS 2242 B	194	21	91.3	694	14	BM969614	BM969614	UI-CF-D01
C 122	21	91.3	490	12	BF903967	BF903967 MR1-MT028	195	21	91.3	695	9	AL037383	AL037383	DKF2P5641
C 123	21	91.3	492	14	BM792592	BM792592 K-EST0072	196	21	91.3	697	14	BM989475	BM989475	UI-H-DHO-
C 124	21	91.3	492	14	BM792592	BM792592 K-EST0072	197	21	91.3	697	17	AG101761	AG101761	Pan trogl
C 125	21	91.3	493	17	AQ001060	AQ001060 CIT-HSP-2	198	21	91.3	705	17	AG168762	AG168762	Pan trogl
C 126	21	91.3	494	17	AQ674646	AQ674646 HS 5474 B	199	21	91.3	710	14	BM989661	BM989661	UI-H-DHO-
C 127	21	91.3	495	12	AQ485341	AQ485341 RPCI-11-2	200	21	91.3	711	17	AG178705	AG178705	Pan trogl
C 128	21	91.3	496	12	BF951417	BF951417 PM0-NN117	201	21	91.3	713	9	AI114653	AI114653	HAI248 Hu
C 129	21	91.3	501	9	AA722505	AA722505 zh31g08.s	202	21	91.3	715	17	AG182904	AG182904	Pan trogl
C 130	21	91.3	503	17	AQ555044	AQ555044 RPCI-11-4	203	21	91.3	719	17	AG175181	AG175181	CITBI-EL-
C 131	21	91.3	504	17	AQ171244	AQ171244 HS 3073 B	204	21	91.3	724	17	AQ392119	AQ392119	CITBI-EL-
C 132	21	91.3	506	17	AZ694837	AZ694837 UP 389-6N	205	21	91.3	731	17	AG175563	AG175563	Pan trogl
C 133	21	91.3	506	17	B42283	B42283 HS 1055-B1-	206	21	91.3	732	17	AZ520661	AZ520661	RPCI-11-7
C 134	21	91.3	508	17	AQ340535	AQ340535 HS 2256 B	207	21	91.3	743	17	AQ391552	AQ391552	CITBI-EL-
C 135	21	91.3	510	17	AZ694838	AZ694838 UP 392-2H	208	21	91.3	755	17	AQ0888318	AQ0888318	HS 3184 A
C 136	21	91.3	511	17	AQ674545	AQ674545 HS 5476 B	209	21	91.3	765	12	BG571409	BG571409	602592685
C 137	21	91.3	514	17	AQ483553	AQ483553 RPCI-11-2	210	21	91.3	768	17	AG089754	AG089754	Pan trogl
C 138	21	91.3	515	14	BM850925	BM850925 K-EST0131	211	21	91.3	771	17	AG112726	AG112726	Pan trogl
C 139	21	91.3	517	17	AQ684457	AQ684457 HS 5506 B	212	21	91.3	775	17	AG393755	AG393755	CITBI-EL-
C 140	21	91.3	519	17	AQ556254	AQ556254 HS 5223 B	213	21	91.3	779	13	BM555512	BM555512	AGENCOURT
C 141	21	91.3	526	9	AL707966	AL707966 DKF2P686G	214	21	91.3	813	17	AG175362	AG175362	Pan trogl
C 142	21	91.3	527	17	AQ804461	AQ804461 HS 3078 A	215	21	91.3	835	17	AQ897779	AQ897779	HS 3144 A
C 143	21	91.3	532	12	BF155049	BF155049 QV2-BT081	216	21	91.3	843	14	BQ215569	BQ215569	AGENCOURT
C 144	21	91.3	534	10	BE147668	BE147668 RC3-HT023	217	21	91.3	870	12	BF695231	BF695231	602080457
C 145	21	91.3	536	17	AQ772371	AQ772371 HS 5493 B	218	21	91.3	872	14	BQ894318	BQ894318	AGENCOURT
C 146	21	91.3	537	17	AQ678329	AQ678329 HS 5529 B	219	21	91.3	905	12	BF970546	BF970546	602274036
C 147	21	91.3	540	9	AL712660	AL712660 DKF2P686M	220	21	91.3	920	12	BG121028	BG121028	602527474
C 148	21	91.3	545	14	N78122	N78122 yv73b05.r1	221	21	91.3	933	12	BG566706	BG566706	602585769
C 149	21	91.3	552	17	AQ754231	AQ754231 HS 5326 B	222	21	91.3	962	14	BQ941784	BQ941784	AGENCOURT
C 150	21	91.3	559	9	AL703693	AL703693 DKF2P686C	223	21	91.3	965	14	BQ719185	BQ719185	AGENCOURT
C 151	21	91.3	561	17	AQ699466	AQ699466 HS 5558 B	224	21	91.3	997	12	BF679103	BF679103	602153366
C 152	21	91.3	563	9	AL712057	AL712057 DKF2P686I	225	21	91.3	1010	12	BG679564	BG679564	6026227607

C 226	21	91.3	1145	14	BM928279	AGENCOURT	299	19	82.6	219	10	BE241474
C 227	21	91.3	1210	12	BF678472	602085924	300	19	82.6	223	14	FI6569
C 228	20	87.0	238	17	B41230	HS-1053-A2-	C 301	19	82.6	223	17	AQ509074
C 229	20	87.0	290	9	AA330610	EST34548	C 302	19	82.6	224	9	AL729254
C 230	20	87.0	307	17	AQ490922	RPCI-11-2	303	19	82.6	224	9	AL596991
C 231	20	87.0	341	10	AW844439	RC2-CN005	C 304	19	82.6	226	9	AA748089
C 232	20	87.0	357	17	AQ275520	RPCI-5-10	C 305	19	82.6	226	14	C05720
C 233	20	87.0	358	10	AV658912	AV658912	C 306	19	82.6	228	12	AQ280060
C 234	20	87.0	363	17	AW844508	RC2-CN005	C 307	19	82.6	231	12	BF295338
C 235	20	87.0	367	17	B50288	CIT-HSP-282	C 308	19	82.6	231	14	W06010
C 236	20	87.0	376	17	AQ132635	HS 3048 B	C 309	19	82.6	234	9	AI363977
C 237	20	87.0	409	12	BG897426	HOA13-1-C	C 310	19	82.6	235	9	AA176505
C 238	20	87.0	417	17	AQ061707	CIT-HSP-2	C 311	19	82.6	235	14	AA176505
C 239	20	87.0	421	17	B63582	RC11-1-D13	C 312	19	82.6	239	13	BI037888
C 240	20	87.0	421	17	AQ606178	HS 5396 A	C 313	19	82.6	239	13	BG984500
C 241	20	87.0	423	17	AQ315539	RPCI11-97	C 314	19	82.6	244	13	BF869535
C 242	20	87.0	436	17	AQ817641	HS 5265 B	C 315	19	82.6	248	12	AA369743
C 243	20	87.0	439	12	EG111039	602284720	C 316	19	82.6	252	12	BF945553
C 244	20	87.0	443	17	AZ521031	RPCI-11-1	C 317	19	82.6	253	17	AQ417185
C 245	20	87.0	443	17	AQ238984	RPCI11-68	C 318	19	82.6	257	10	AW779204
C 246	20	87.0	452	10	AW859924	QV1-CT036	C 319	19	82.6	267	17	AQ323494
C 247	20	87.0	454	9	A1879130	au55a05.Y	C 320	19	82.6	268	9	AA302400
C 248	20	87.0	454	17	AQ041802	CIT-HSP-2	C 321	19	82.6	269	17	AQ487705
C 249	20	87.0	465	17	AQ342906	RPCI11-12	C 322	19	82.6	270	17	AQ508046
C 250	20	87.0	465	17	AQ353535	CITBI-EI-	C 323	19	82.6	272	17	AQ628712
C 251	20	87.0	476	17	AQ053073	RPCI11-50	C 324	19	82.6	273	9	AA516305
C 252	20	87.0	483	14	BM709802	UT-E-CK1-	C 325	19	82.6	274	12	BF948836
C 253	20	87.0	489	17	AQ695677	HS 2159 A	C 326	19	82.6	277	9	AA654627
C 254	20	87.0	503	17	AQ203561	HS 3103 B	C 327	19	82.6	277	12	BF914340
C 255	20	87.0	535	17	AZ372553	IN0124A01	C 328	19	82.6	279	17	AQ540913
C 256	20	87.0	554	17	AQ281871	RPCI11-76	C 329	19	82.6	280	9	AA508506
C 257	20	87.0	565	17	AQ348354	RPCI11-13	C 330	19	82.6	280	14	FI7196
C 258	20	87.0	566	17	AQ526465	HS 5309 B	C 331	19	82.6	281	9	AI453660
C 259	20	87.0	583	17	AQ197980	RPCI11-48	C 332	19	82.6	281	10	BE159380
C 260	20	87.0	586	17	AQ490786	RPCI-11-2	C 333	19	82.6	283	12	BF931795
C 261	20	87.0	587	17	AQ541733	RPCI-11-3	C 334	19	82.6	284	9	AA713720
C 262	20	87.0	661	17	AG156547	Pan trogl	C 335	19	82.6	287	9	AA643451
C 263	20	87.0	682	17	AG066350	Pan trogl	C 336	19	82.6	287	17	AQ101021
C 264	20	87.0	715	12	BE874842	601488786	C 337	19	82.6	289	12	BF772427
C 265	20	87.0	728	17	AG110850	Pan trogl	C 338	19	82.6	291	17	AQ711291
C 266	20	87.0	729	17	AG110065	Pan trogl	C 339	19	82.6	292	10	AW873951
C 267	20	87.0	747	17	AG141278	Pan trogl	C 340	19	82.6	292	14	T07019
C 268	20	87.0	753	14	BQ707143	AGENCOURT	C 341	19	82.6	293	17	AQ096010
C 269	20	87.0	775	12	BG570538	602591217	C 342	19	82.6	294	17	BE245198
C 270	20	87.0	823	17	AQ746445	HS 2278 A	C 343	19	82.6	296	9	AA995189
C 271	20	87.0	844	17	AQ888222	HS 3081 A	C 344	19	82.6	296	17	AQ592980
C 272	20	87.0	861	17	AQ741554	HS 5567 B	C 345	19	82.6	300	9	AA668148
C 273	19	82.6	57	12	BF542036	602069193	C 346	19	82.6	300	9	AI434750
C 274	19	82.6	103	10	BE165639	CM1-HT048	C 347	19	82.6	303	9	AA718906
C 275	19	82.6	121	10	AW083839	XC35H05.X	C 348	19	82.6	304	9	AA355177
C 276	19	82.6	124	10	AW885941	RC4-OT007	C 349	19	82.6	304	9	AA573543
C 277	19	82.6	135	13	BI059889	IL3-UT011	C 350	19	82.6	305	12	BF830366
C 278	19	82.6	149	13	BG982074	MR3-CN014	C 351	19	82.6	305	12	BF912307
C 279	19	82.6	152	10	AW793990	MR1-UM000	C 352	19	82.6	309	10	AW079301
C 280	19	82.6	152	17	AQ262347	CITBI-EI-	C 353	19	82.6	310	9	AA090387
C 281	19	82.6	160	17	B42150	HS-1055-A2-	C 354	19	82.6	313	14	BQ311827
C 282	19	82.6	163	17	AQ283089	RPCI11-79	C 355	19	82.6	315	17	B75820
C 283	19	82.6	166	13	BG996768	CM0-HT129	C 356	19	82.6	317	9	AA643441
C 284	19	82.6	168	10	AW873788	hq48a10.X	C 357	19	82.6	323	9	AI926102
C 285	19	82.6	171	12	BF927273	CM1-NT024	C 358	19	82.6	330	12	BG154184
C 286	19	82.6	180	14	H65170	yu64905.X1	C 359	19	82.6	331	9	AI190960
C 287	19	82.6	182	9	AA721616	ny87a06.S	C 360	19	82.6	336	12	BF871261
C 288	19	82.6	184	9	AA885578	oj31a12.S	C 361	19	82.6	336	17	AQ066842
C 289	19	82.6	187	9	AA908328	og75d01.S	C 362	19	82.6	336	17	AQ067768
C 290	19	82.6	187	9	AA093195	110234.S8	C 363	19	82.6	336	17	AQ507181
C 291	19	82.6	194	14	F25733	HSPD12316.H	C 364	19	82.6	337	9	AI453155
C 292	19	82.6	196	13	BG978412	RC4-CI019	C 365	19	82.6	337	9	AA508882
C 293	19	82.6	198	17	AQ075272	CIT-HSP-2	C 366	19	82.6	338	13	BI496293
C 294	19	82.6	200	10	AW277235	xg80c03.X	C 367	19	82.6	338	14	F37291
C 295	19	82.6	208	14	T05426	EST03315.Fe	C 368	19	82.6	340	17	AQ478365
C 296	19	82.6	213	9	AA714477	nm06g03.S	C 369	19	82.6	342	9	AA484022
C 297	19	82.6	213	12	BF904023	MR1-NT028	C 370	19	82.6	343	12	BF986334
C 298	19	82.6	215	9	AA366961	EST77975	C 371	19	82.6	346	13	BG982460

BE241474 TCAAP1D00
FI6569 HSPD01067 H
AQ509074 RPCI-11-2
AL729254 nx55a12.s
AL596991 DKPZP313M
AA748089 nx68h02.s
C05720 C05720 Huma
AQ280060 CITBI-EI-
BF929538 QV3-NT021
W06010 zc91e02.s1
AI363977 qn35a03.x
AA176505 zp33f05.s
N43790 yy42d11.r1
BI037888 CM4-NT029
BG984500 CM0-CN015
BF869535 IL3-ET011
AA369743 EST81222
BF945553 PM3-NN108
AQ417185 RPCI-11-2
AW779204 h050e07.X
AQ323494 RPCI11-10
AA302400 EST15536
AQ487705 RPCI-11-2
AQ508046 RPCI-11-2
AQ628712 RPCI-11-4
AA516305 ng68h01.s
BF948836 MR3-NN021
AA654627 nt59h01.s
BF914340 IL3-UT011
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AA643451 nv31f05.r
AQ101021 HS 3061.A
BF772427 IL5-IT002
AQ771291 HS 2106.A
AW873951 hq50g04.X
T07019 EST04908 Fe
AQ96010 HS 3035.A
BE245198 TCAAP1D28
AA995189 ou90c04.s
AQ592980 HS 5430.B
AA668148 ab76f04.s
AI434750 t340d03.x
AA718906 zh22f11.s
AA355177 EST63622
AA573543 nf41b08.s
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BF912307 MR4-UT005
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AQ066842 HS 2227.B
AQ067768 HS-2239.B
AQ507181 RPCI-11-3
AI453155 tj35c02.x
AA508882 ng86f06.s
BI496293 df124b09.
F37291 HSPD35517 H
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AA484022 ne77a06.s
BF986334 RCI-NT014
BG982460 MR4-CN011

C 372	19	82.6	348	9	AA491862	AA491862 ne72a09.s	C 445	19	82.6	415	14	C06141	C06141 C06141 Huma
C 373	19	82.6	349	10	AW874331	AW874331 hq45e12.x	446	19	82.6	415	17	B63136	B63136 CIT978SK-A-
C 374	19	82.6	349	12	BF942169	BF942169 nae8a03.	447	19	82.6	416	17	AAQ669064	AAQ669064 HS 5414.A
C 375	19	82.6	349	12	BF942169	BF942169 nae8a03.	448	19	82.6	416	9	AAQ307292	AAQ307292 EST178209
C 376	19	82.6	351	17	AAQ151158	AAQ151158 HS 2186.A	449	19	82.6	418	17	BH614821	BH614821 UP 535-10
C 377	19	82.6	352	9	AA491650	AA491650 ne80f07.s	C 450	19	82.6	418	17	AAQ556945	AAQ556945 HS 5328.A
C 378	19	82.6	352	17	AAQ389958	AAQ389958 RPT111-15	C 451	19	82.6	419	10	AAW403829	AAW403829 UT-HF-BKO
C 379	19	82.6	352	17	AAQ007136	AAQ007136 CIT-HSP-2	C 452	19	82.6	419	10	BE155302	BE155302 PM1-HT035
C 380	19	82.6	356	17	AAQ003519	AAQ003519 HS 3178.A	C 453	19	82.6	419	17	AAQ36584	AAQ36584 CIT-HSP-2
C 381	19	82.6	357	9	AI338350	AI338350 qq96g12.x	C 454	19	82.6	420	9	AI717989	AI717989 aeg3a02.x
C 382	19	82.6	359	17	AAQ085420	AAQ085420 HS 2270.B	C 455	19	82.6	420	9	AA653154	AA653154 aeg4c005.s
C 383	19	82.6	360	13	BI712069	BI712069 i601c02.x	C 456	19	82.6	421	10	AW975904	AW975904 EST388013
C 384	19	82.6	360	17	AAQ682145	AAQ682145 HS 5503.B	C 457	19	82.6	421	14	HS9066	HS9066 y33b02.s1
C 385	19	82.6	360	17	AZ515814	AZ515814 RPT11-11	C 458	19	82.6	422	9	AL601258	AL601258 DKFZP313K
C 386	19	82.6	361	17	AAQ471450	AAQ471450 CITBI-EI-	C 459	19	82.6	423	9	AA226047	AA226047 nc09e01.s
C 387	19	82.6	361	17	AAQ36459	AAQ36459 RPT11-11-S	C 460	19	82.6	423	13	BM506690	BM506690 in24a11.x
C 388	19	82.6	361	17	AAQ116881	AAQ116881 HS 2175.B	C 461	19	82.6	423	14	R82650	R82650 yj20d04.s1
C 389	19	82.6	362	13	BI496292	BI496292 dfi24b09.	C 462	19	82.6	425	9	AI491867	AI491867 t001f10.x
C 390	19	82.6	363	12	BF917688	BF917688 IL3-UT011	C 463	19	82.6	427	17	AAQ060020	AAQ060020 CIT-HSP-2
C 391	19	82.6	364	9	AA508103	AA508103 ng93d10.s	C 464	19	82.6	428	9	AA648979	AA648979 ns41f01.s
C 392	19	82.6	365	9	AA834683	AA834683 cd99a05.s	C 465	19	82.6	430	9	AA488746	AA488746 aeg5h05.x
C 393	19	82.6	365	14	T06598	T06598 EST04487.Fe	C 466	19	82.6	432	17	AAQ057431	AAQ057431 CIT-HSP-2
C 394	19	82.6	365	17	AAQ03530	AAQ03530 HS 3178.A	C 467	19	82.6	432	17	AAQ25898	AAQ25898 HS 2011.B
C 395	19	82.6	366	17	AAQ388598	AAQ388598 RPT11-15	C 468	19	82.6	433	9	AA302979	AA302979 EST113212
C 396	19	82.6	367	9	AI521525	AI521525 t064b10.x	C 469	19	82.6	433	17	AAQ234523	AAQ234523 HS 2052.B
C 397	19	82.6	367	17	AAQ146635	AAQ146635 HS 2233.B	C 470	19	82.6	433	17	B92880	B92880 CIT-HSP-216
C 398	19	82.6	369	14	W93917	W93917 zd97g02.r1	C 471	19	82.6	434	9	AI929627	AI929627 au61g01.y
C 399	19	82.6	369	17	AAQ49605	AAQ49605 RPT11-11	C 472	19	82.6	434	9	AI929627	AI929627 au61g01.y
C 400	19	82.6	370	9	AI282511	AI282511 qv04e04.x	C 473	19	82.6	435	9	AA228877	AA228877 nc16g03.r
C 401	19	82.6	370	14	F25593	F25593 HSPD12698.H	C 474	19	82.6	435	14	N69462	N69462 zal8a08.s1
C 402	19	82.6	373	9	AA468271	AA468271 nc76a08.x	C 475	19	82.6	436	9	AA259174	AA259174 nc17a08.x
C 403	19	82.6	373	17	AAQ152907	AAQ152907 HS 3045.B	C 476	19	82.6	436	14	R98406	R98406 yq65b12.s1
C 404	19	82.6	374	12	BF817826	BF817826 MR2-C1012	C 477	19	82.6	437	13	BM72501	BM72501 i942901.y
C 405	19	82.6	376	17	AAQ284447	AAQ284447 RPT11-90	C 478	19	82.6	437	17	AAQ59739	AAQ59739 HS 2257.A
C 406	19	82.6	377	9	AA719073	AA719073 zh33a05.s	C 479	19	82.6	439	9	AA604751	AA604751 nc04e04.s
C 407	19	82.6	377	17	AA547053	AA547053 CITBI-EI-	C 480	19	82.6	439	17	AAQ36180	AAQ36180 RPT11-11-S
C 408	19	82.6	378	14	N52480	N52480 yv51b10.s1	C 481	19	82.6	440	9	AA767297	AA767297 nz81c06.s
C 409	19	82.6	378	14	T62539	T62539 yC04d04.s1	C 482	19	82.6	440	13	BM127350	BM127350 i988b10.x
C 410	19	82.6	380	10	BE155299	BE155299 PM1-HT035	C 483	19	82.6	441	17	AAQ798736	AAQ798736 HS 3032.A
C 411	19	82.6	380	12	BF840062	BF840062 IL0-HT106	C 484	19	82.6	441	17	AAQ557783	AAQ557783 HS 2083.A
C 412	19	82.6	380	17	AAQ119439	AAQ119439 HS 2165.B	C 485	19	82.6	442	12	BF871533	BF871533 IL5-ET011
C 413	19	82.6	383	9	AA877992	AA877992 oh95h04.s	C 486	19	82.6	442	12	BF871533	BF871533 IL5-ET011
C 414	19	82.6	385	14	T90080	T90080 yd39b07.s1	C 487	19	82.6	443	17	AAQ207564	AAQ207564 HS 2243.B
C 415	19	82.6	386	13	EG939818	EG939818 C-63305.x	C 488	19	82.6	443	17	AAQ233796	AAQ233796 HS 2046.B
C 416	19	82.6	386	13	EG939828	EG939828 C-63b11.x	C 489	19	82.6	444	17	AAQ222139	AAQ222139 HS 2193.A
C 417	19	82.6	386	13	EG939834	EG939834 C-63c11.x	C 490	19	82.6	445	17	AAQ112607	AAQ112607 CIT-HSP-2
C 418	19	82.6	387	9	AI537368	AI537368 tp07g09.x	C 491	19	82.6	446	17	AAQ183180	AAQ183180 HS 3132.A
C 419	19	82.6	388	10	AAW338506	AAW338506 xw71g01.x	C 492	19	82.6	448	17	AAQ35361	AAQ35361 CIT-HSP-2
C 420	19	82.6	388	14	BQ268842	BQ268842 ik21c02.x	C 493	19	82.6	448	17	AAQ280660	AAQ280660 CITBI-EI-
C 421	19	82.6	389	17	AAQ263739	AAQ263739 CITBI-EI-	C 494	19	82.6	449	13	BI714784	BI714784 ic31h04.x
C 422	19	82.6	391	9	AA311522	AA311522 EST182266	C 495	19	82.6	450	9	AA705333	AA705333 zj97f12.s
C 423	19	82.6	392	17	AAQ380122	AAQ380122 RPT11-13	C 496	19	82.6	450	13	BM264564	BM264564 i936h10.x
C 424	19	82.6	395	9	AA663786	AA663786 ae72f07.s	C 497	19	82.6	450	13	BM310600	BM310600 i950b09.x
C 425	19	82.6	397	10	AAW020150	AAW020150 df05a09.y	C 498	19	82.6	450	17	AAQ381517	AAQ381517 RPT11-16
C 426	19	82.6	397	12	BG896311	BG896311 HOA29-1-C	C 499	19	82.6	452	17	AAQ595781	AAQ595781 HS 2131.B
C 427	19	82.6	400	10	AAW028403	AAW028403 wv88f09.x	C 500	19	82.6	452	17	AAQ770491	AAQ770491 HS 5372.A
C 428	19	82.6	400	17	AAQ755528	AAQ755528 HS 2210.B	C 501	19	82.6	453	17	AAQ815097	AAQ815097 HS 5261.B
C 429	19	82.6	401	9	AA048983	AA048983 DKFZp434M	C 502	19	82.6	453	17	AAQ180278	AAQ180278 HS 3209.B
C 430	19	82.6	401	17	AAQ12443	AAQ12443 RPT11-11	C 503	19	82.6	454	14	C06481	C06481 C06481 Huma
C 431	19	82.6	403	17	AAQ129179	AAQ129179 HS 3037.B	C 504	19	82.6	455	17	AAI678894	AAI678894 tu70f09.x
C 432	19	82.6	403	17	AAQ020701	AAQ020701 RPT11-57	C 505	19	82.6	457	9	BE045897	BE045897 hq54d11.x
C 433	19	82.6	404	9	AI366729	AI366729 qy95c09.x	C 506	19	82.6	458	10	BE045897	BE045897 hq54d11.x
C 434	19	82.6	404	13	BI491182	BI491182 df05a09.w	C 507	19	82.6	459	17	AAQ284359	AAQ284359 RPT11-91
C 435	19	82.6	404	14	N22161	N22161 yw33g10.s1	C 508	19	82.6	459	17	AAQ586397	AAQ586397 RPT11-4
C 436	19	82.6	404	17	AAQ733664	AAQ733664 HS 5558.A	C 509	19	82.6	460	17	AAW088563	AAW088563 xdl7f02.x
C 437	19	82.6	405	9	AA070539	AA070539 zm70b04.i	C 510	19	82.6	460	17	AAQ382314	AAQ382314 RPT11-13
C 438	19	82.6	406	12	BF871325	BF871325 CM0-ET012	C 511	19	82.6	464	9	AI571512	AI571512 tr85a12.x
C 439	19	82.6	408	14	HS7192	HS7192 y08a05.r1	C 512	19	82.6	464	17	B42459	B42459 HS-1055-B2-
C 440	19	82.6	408	17	AAQ101931	AAQ101931 HS 3017.B	C 513	19	82.6	465	17	AAQ340477	AAQ340477 HS 2236.B
C 441	19	82.6	410	14	W93102	W93102 zh45e02.s1	C 514	19	82.6	466	17	AAQ817627	AAQ817627 HS 5265.B
C 442	19	82.6	410	17	AAQ132151	AAQ132151 HS 3001.B	C 515	19	82.6	467	12	BG007715	BG007715 RC2-GN026
C 443	19	82.6	411	14	BQ778298	BQ778298 il44f02.x	C 516	19	82.6	467	17	AZ517949	AZ517949 RPT11-11-9
C 444	19	82.6	412	9	AI654529	AI654529 tq91h04.x	C 517	19	82.6	467	17	AAQ491297	AAQ491297 RPT11-11-2

C 518	19	82.6	469	14	BQ890690	BQ890690 AGENCOURT	C 591	19	82.6	517	17	AQ323115	AQ323115 RPC111-96
C 519	19	82.6	470	9	AL299694	AL299694 qm37a09.x	C 592	19	82.6	519	17	AQ678348	AQ678348 HS 5529 B
C 520	19	82.6	470	9	AL299694	AL299694 qm37a09.x	C 593	19	82.6	520	17	AL710725	AL710725 DKEZp686L
C 521	19	82.6	470	9	AL299694	AL707371 DKEZp686F	C 594	19	82.6	521	9	AL711809	AL711809 DKEZp686C
C 522	19	82.6	471	10	AW265393	AW265393 xp46d12.x	C 595	19	82.6	522	9	AL711809	AL711809 DKEZp686C
C 523	19	82.6	471	10	AW265393	AW265393 xp46d12.x	C 596	19	82.6	523	13	BQ150128	BQ150128 HS 3194 A
C 524	19	82.6	472	10	AW501334	AW501334 UI-HF-BPO	C 597	19	82.6	524	13	BQ150128	BQ150128 HS 3194 A
C 525	19	82.6	472	10	AW238345	AW238345 xp21c10.x	C 598	19	82.6	525	17	AQ370935	AQ370935 HS 5048 B
C 526	19	82.6	473	9	AQ103978	AQ103978 CIT-HSP-2	C 599	19	82.6	526	17	AQ370935	AQ370935 HS 5048 B
C 527	19	82.6	473	9	AQ103978	AQ103978 CIT-HSP-2	C 600	19	82.6	527	9	AI871225	AI871225 w180b08.x
C 528	19	82.6	474	9	AI871225	AI871225 w180b08.x	C 601	19	82.6	528	17	AQ785290	AQ785290 HS 3214 A
C 529	19	82.6	474	9	AI871225	AI871225 w180b08.x	C 602	19	82.6	529	17	AQ785290	AQ785290 HS 3214 A
C 530	19	82.6	475	17	AQ387376	AQ387376 RPC111-14	C 603	19	82.6	530	10	BE042846	BE042846 ho29f03.x
C 531	19	82.6	476	9	AI377567	AI377567 tc37f04.x	C 604	19	82.6	531	17	AQ483271	AQ483271 RPC111-2
C 532	19	82.6	477	12	BF906470	BF906470 ILO-OT012	C 605	19	82.6	532	9	AA844930	AA844930 ak61a09.s
C 533	19	82.6	478	17	AQ379236	AQ379236 CIT-HSP-2	C 606	19	82.6	533	17	AQ379236	AQ379236 CIT-HSP-2
C 534	19	82.6	479	17	AQ379236	AQ379236 CIT-HSP-2	C 607	19	82.6	534	17	AQ379236	AQ379236 CIT-HSP-2
C 535	19	82.6	480	17	AQ379236	AQ379236 CIT-HSP-2	C 608	19	82.6	535	17	AQ379236	AQ379236 CIT-HSP-2
C 536	19	82.6	481	10	AW743288	AW743288 AV743288	C 609	19	82.6	536	9	AL043804	AL043804 DKEZp343P
C 537	19	82.6	482	17	B94693	B94693 CIT-HSP-216	C 610	19	82.6	537	13	BI714785	BI714785 IC31105.X
C 538	19	82.6	483	10	AW188419	AW188419 xj98a02.x	C 611	19	82.6	538	17	AQ311201	AQ311201 CITBI-EI-
C 539	19	82.6	483	10	AW499719	AW499719 UI-HF-BRO	C 612	19	82.6	539	12	BQ291183	BQ291183 602388621
C 540	19	82.6	484	14	R12604	R12604 yf57a01.x	C 613	19	82.6	540	17	AQ391351	AQ391351 CITBI-EI-
C 541	19	82.6	484	14	R12604	R12604 yf57a01.x	C 614	19	82.6	541	17	AQ391351	AQ391351 CITBI-EI-
C 542	19	82.6	485	12	BF874197	BF874197 MR1-ET014	C 615	19	82.6	542	14	BM822753	BM822753 K-EST0092
C 543	19	82.6	485	12	BF874197	BF874197 MR1-ET014	C 616	19	82.6	543	9	AL047247	AL047247 DKEZp586A
C 544	19	82.6	486	14	C06154	C06154 C06154 Huma	C 617	19	82.6	544	9	AL047247	AL047247 DKEZp586A
C 545	19	82.6	486	14	C06154	C06154 C06154 Huma	C 618	19	82.6	545	17	AQ394650	AQ394650 CITBI-EI-
C 546	19	82.6	487	17	AQ789011	AQ789011 HS 3044 B	C 619	19	82.6	546	17	AQ789011	AQ789011 HS 3044 B
C 547	19	82.6	487	17	AQ789011	AQ789011 HS 3044 B	C 620	19	82.6	547	10	BE151208	BE151208 RC4-HT027
C 548	19	82.6	488	14	BM763572	BM763572 K-EST0044	C 621	19	82.6	548	17	AQ417654	AQ417654 RPC111-2
C 549	19	82.6	488	14	BM763572	BM763572 K-EST0044	C 622	19	82.6	549	17	AQ417654	AQ417654 RPC111-2
C 550	19	82.6	489	10	AW172908	AW172908 xj05e10.x	C 623	19	82.6	550	17	AQ363020	AQ363020 RPC111-3
C 551	19	82.6	489	17	AQ276084	AQ276084 CITBI-EI-	C 624	19	82.6	551	9	AL044688	AL044688 AU144688
C 552	19	82.6	489	17	AQ276084	AQ276084 CITBI-EI-	C 625	19	82.6	552	17	AQ333394	AQ333394 HS 5009 B
C 553	19	82.6	490	17	AQ276084	AQ276084 CITBI-EI-	C 626	19	82.6	553	17	AQ333394	AQ333394 HS 5009 B
C 554	19	82.6	491	12	BF754060	BF754060 IL5-CT052	C 627	19	82.6	554	10	BE151208	BE151208 RC4-HT027
C 555	19	82.6	491	17	AQ134773	AQ134773 HS 3053 A	C 628	19	82.6	555	14	BM688309	BM688309 UI-E-CL0-
C 556	19	82.6	492	9	AI377556	AI377556 tc37e04.x	C 629	19	82.6	556	17	B92301	B92301 CIT-HSP-217
C 557	19	82.6	493	17	AQ894221	AQ894221 HS 3114 A	C 630	19	82.6	557	17	AQ415061	AQ415061 RPC111-2
C 558	19	82.6	494	14	H29241	H29241 ym53f09.e1	C 631	19	82.6	558	17	AQ417207	AQ417207 RPC111-2
C 559	19	82.6	495	17	AQ269311	AQ269311 HS 2016 B	C 632	19	82.6	559	9	AL046713	AL046713 AU146713
C 560	19	82.6	496	17	AQ338555	AQ338555 HS 3118 B	C 633	19	82.6	560	17	AQ463998	AQ463998 HS 5087 A
C 561	19	82.6	497	12	BF814066	BF814066 MR2-CI018	C 634	19	82.6	561	12	BF916011	BF916011 MR2-CI012
C 562	19	82.6	497	12	BF814066	BF814066 MR2-CI018	C 635	19	82.6	562	17	AQ267977	AQ267977 RPC111-72
C 563	19	82.6	498	10	AW658184	AW658184 EST380379	C 636	19	82.6	563	10	AW974167	AW974167 EST386270
C 564	19	82.6	498	10	AW658184	AW658184 EST380379	C 637	19	82.6	564	17	AQ149657	AQ149657 HS 3171 B
C 565	19	82.6	499	17	B82435	B82435 RPC111-15M3	C 638	19	82.6	565	9	AL048234	AL048234 AU148234
C 566	19	82.6	499	14	BQ416803	BQ416803 iK41912.x	C 639	19	82.6	566	14	BM822827	BM822827 K-EST0093
C 567	19	82.6	500	17	AQ263708	AQ263708 CITBI-EI-	C 640	19	82.6	567	12	BG142238	BG142238 iA52802.Y
C 568	19	82.6	500	17	AQ263708	AQ263708 CITBI-EI-	C 641	19	82.6	568	17	AQ377281	AQ377281 RPC111-1
C 569	19	82.6	500	17	AQ263708	AQ263708 CITBI-EI-	C 642	19	82.6	569	17	AQ377281	AQ377281 RPC111-1
C 570	19	82.6	501	17	AQ040474	AQ040474 CIT-HSP-2	C 643	19	82.6	570	17	BI5271	BI5271 34117.TV C
C 571	19	82.6	502	17	AQ040474	AQ040474 CIT-HSP-2	C 644	19	82.6	571	17	AQ306219	AQ306219 HS 2041 A
C 572	19	82.6	504	14	BM673489	BM673489 UI-E-CRI-	C 645	19	82.6	572	17	AQ775679	AQ775679 HS 2173 B
C 573	19	82.6	505	9	AI377505	AI377505 tc37d04.x	C 646	19	82.6	573	13	BM9180	BM9180 RPC111-5C23
C 574	19	82.6	505	14	BQ640608	BQ640608 he30a04.Y	C 647	19	82.6	574	12	BG142238	BG142238 iA52802.Y
C 575	19	82.6	509	10	AW504832	AW504832 UI-HF-BNO	C 648	19	82.6	575	17	AQ377281	AQ377281 RPC111-1
C 576	19	82.6	510	17	AQ140446	AQ140446 HS 3110 B	C 649	19	82.6	576	12	BG142238	BG142238 iA52802.Y
C 577	19	82.6	511	13	BM353779	BM353779 i956a11.Y	C 650	19	82.6	577	17	BI5271	BI5271 34117.TV C
C 578	19	82.6	511	17	AQ263778	AQ263778 CITBI-EI-	C 651	19	82.6	578	17	AQ306219	AQ306219 HS 2041 A
C 579	19	82.6	511	17	AQ263778	AQ263778 CITBI-EI-	C 652	19	82.6	579	17	AQ775679	AQ775679 HS 2173 B
C 580	19	82.6	511	17	AQ488100	AQ488100 RPC111-2	C 653	19	82.6	580	13	BM9180	BM9180 RPC111-5C23
C 581	19	82.6	512	14	BQ640398	BQ640398 he28a08.Y	C 654	19	82.6	581	13	BM9180	BM9180 RPC111-5C23
C 582	19	82.6	513	10	BE151195	BE151195 RC4-HT027	C 655	19	82.6	582	17	AQ037313	AQ037313 CIT-HSP-2
C 583	19	82.6	513	17	AQ027663	AQ027663 CIT-HSP-2	C 656	19	82.6	583	17	AQ037313	AQ037313 CIT-HSP-2
C 584	19	82.6	513	17	AQ027663	AQ027663 CIT-HSP-2	C 657	19	82.6	584	17	AQ037313	AQ037313 CIT-HSP-2
C 585	19	82.6	515	9	AA665160	AA665160 nu83b08.s	C 658	19	82.6	585	12	BF916011	BF916011 MR2-CI018
C 586	19	82.6	515	14	BQ026454	BQ026454 UI-1-BB0-	C 659	19	82.6	586	17	BI5271	BI5271 34117.TV C
C 587	19	82.6	515	17	AQ738319	AQ738319 HS 2260 B	C 660	19	82.6	587	9	AI525172	AI525172 promrna-9
C 588	19	82.6	516	9	AI978650	AI978650 wr57g08.x	C 661	19	82.6	588	10	AW851317	AW851317 IL3-CT022
C 589	19	82.6	516	17	AQ293549	AQ293549 HS 3024 A	C 662	19	82.6	589	17	AQ531851	AQ531851 RPC111-3
C 590	19	82.6	516	17	AQ293549	AQ293549 HS 3024 A	C 663	19	82.6	590	10	BE045902	BE045902 hc54f03.x

664	19	82.6	585	17	AQ423630	CITBI-E1-	737	19	82.6	690	17	AG146194	Pan trogl
C 665	19	82.6	587	10	AW150781	XG39503.x	C 738	19	82.6	691	17	AQ051709	RPc111-49
666	19	82.6	588	10	AV759047	AV759047	739	19	82.6	691	17	AQ001893	Homo sapi
C 667	19	82.6	588	12	BE969845	601679417	740	19	82.6	692	17	AG010820	Homo sapi
668	19	82.6	588	14	BM992270	UT-H-DF1-	741	19	82.6	693	17	AG001472	Homo sapi
C 669	19	82.6	589	10	AV718791	AV718791	C 742	19	82.6	696	10	AV731842	AV731842
C 670	19	82.6	592	10	AA668309	ab79d02.s	C 743	19	82.6	696	17	AG009915	Homo sapi
C 671	19	82.6	594	9	AQ319274	RPc111-99	C 744	19	82.6	698	17	AQ013971	RPc111-23
C 672	19	82.6	595	17	AQ379242	RPc111-11-1	C 745	19	82.6	698	17	AQ059526	CIT-HSP-2
C 673	19	82.6	596	17	AQ350160	RPc111-10	746	19	82.6	698	17	AQ009905	Homo sapi
674	19	82.6	601	17	B83348	B83348	747	19	82.6	698	17	AQ0385631	RPc111-13
C 675	19	82.6	604	17	AQ285763	RPc111-89	748	19	82.6	699	17	AG180770	Pan trogl
C 676	19	82.6	614	17	AQ051953	AQ051953	749	19	82.6	702	17	AG171475	Pan trogl
C 677	19	82.6	621	17	AG012061	Homo sapi	C 750	19	82.6	706	17	AG124119	Pan trogl
C 678	19	82.6	624	12	BF854308	MR2-EN009	C 751	19	82.6	708	17	AG085806	Pan trogl
C 679	19	82.6	624	14	BQ287972	IK37H06.x	752	19	82.6	709	17	AG001891	Homo sapi
680	19	82.6	624	17	AQ481418	RPc11-12	C 753	19	82.6	710	17	AG010816	Homo sapi
C 681	19	82.6	626	17	AG082369	Pan trogl	754	19	82.6	710	17	AG176536	Pan trogl
682	19	82.6	627	17	AG012034	Homo sapi	C 755	19	82.6	710	17	AG179045	Pan trogl
C 683	19	82.6	630	17	AG059998	Pan trogl	756	19	82.6	711	17	AG112898	Pan trogl
C 684	19	82.6	632	17	AG012035	Homo sapi	757	19	82.6	712	17	AG001892	Homo sapi
C 685	19	82.6	633	17	AG012062	Homo sapi	C 758	19	82.6	714	17	AG166771	Pan trogl
686	19	82.6	636	17	AG065252	Pan trogl	759	19	82.6	715	17	AQ528313	RPc11-3
C 687	19	82.6	638	17	AQ897255	HS 3144.A	760	19	82.6	717	12	BG163461	602338454
C 688	19	82.6	638	17	AG091253	Pan trogl	761	19	82.6	717	14	BQ648354	AGENCOURT
689	19	82.6	639	12	BF673634	602136047	762	19	82.6	717	17	AG093169	Pan trogl
C 690	19	82.6	640	10	AW474147	Xy11d007.x	763	19	82.6	718	17	AG000907	Homo sapi
C 691	19	82.6	641	12	BG284716	602408912	C 764	19	82.6	719	17	AQ053118	RPc111-49
C 692	19	82.6	644	12	BG567733	602586525	765	19	82.6	720	17	B84881	RPc111-28K5
C 693	19	82.6	644	17	AG035980	Pan trogl	766	19	82.6	724	17	AG102986	Pan trogl
C 694	19	82.6	645	10	AW338129	xw67406.x	767	19	82.6	725	17	AG120380	Pan trogl
C 695	19	82.6	647	17	AG065332	Pan trogl	C 768	19	82.6	728	17	AG107086	Pan trogl
696	19	82.6	648	12	BG536366	602584757	769	19	82.6	736	17	AQ752879	HS 5570.B
C 697	19	82.6	651	17	AG098968	Pan trogl	C 770	19	82.6	737	9	AI377389	tc35a01.x
C 698	19	82.6	654	9	A1922539	wm89d01.x	C 771	19	82.6	740	10	AW850535	IL3-CT021
699	19	82.6	655	17	AQ109080	CIT-HSP-2	C 772	19	82.6	741	17	AQ536297	RPc11-3
C 700	19	82.6	655	17	AG146259	Pan trogl	C 773	19	82.6	742	17	AQ321762	RPc111-10
701	19	82.6	657	13	BG927683	HNC4-1-E	C 774	19	82.6	748	17	AG123667	Pan trogl
702	19	82.6	658	17	AZ527523	HSC 00214	C 775	19	82.6	753	17	AG879097	HS 3184.A
C 703	19	82.6	660	17	AG174563	Pan trogl	C 776	19	82.6	754	17	AQ85993	Pan trogl
704	19	82.6	661	9	AL707930	DKEZp686D	777	19	82.6	761	17	AQ742321	HS 5383.B
705	19	82.6	661	17	AG016064	Homo sapi	778	19	82.6	762	10	AV700768	AV700768
706	19	82.6	663	17	AG075680	Pan trogl	C 779	19	82.6	762	17	AQ746920	HS 2275.A
C 707	19	82.6	665	17	AG138387	Pan trogl	C 780	19	82.6	773	17	AG746920	HS 2275.A
708	19	82.6	667	17	AG081074	Pan trogl	C 781	19	82.6	774	10	BE279646	601157380
709	19	82.6	667	17	AQ017902	Pan trogl	782	19	82.6	777	9	AU122517	AU122517
C 710	19	82.6	667	17	AQ036759	RPc11-3	783	19	82.6	777	17	AG173117	Pan trogl
711	19	82.6	669	17	AG084645	Pan trogl	784	19	82.6	779	17	AQ343532	RPc111-12
712	19	82.6	669	17	AG115838	Pan trogl	785	19	82.6	783	10	BE387319	601275786
713	19	82.6	669	17	AG160724	Pan trogl	786	19	82.6	784	12	BE967450	601649119
714	19	82.6	669	17	AG168864	Pan trogl	787	19	82.6	794	17	AG000354	Homo sapi
715	19	82.6	669	17	AQ353227	CITBI-E1-	C 788	19	82.6	796	12	BF347269	602021016
C 716	19	82.6	672	17	AG095361	Pan trogl	789	19	82.6	797	17	AQ030520	Pan trogl
C 717	19	82.6	672	17	AQ348932	RPc111-12	C 790	19	82.6	800	17	AQ895488	HS 3133.A
C 718	19	82.6	674	17	AG062545	Pan trogl	C 791	19	82.6	819	17	AQ746249	HS 2276.A
719	19	82.6	675	17	AG041370	Pan trogl	C 792	19	82.6	822	12	BF668362	602122574
720	19	82.6	676	17	AG183410	Pan trogl	793	19	82.6	823	12	BF346539	602020151
721	19	82.6	677	9	AL707579	DKEZp686K	794	19	82.6	825	12	BF346543	602020159
C 722	19	82.6	679	17	AG088195	Pan trogl	795	19	82.6	827	12	BF105055	601822040
723	19	82.6	680	17	AG185868	Pan trogl	796	19	82.6	833	17	AQ900081	HS 2087.B
724	19	82.6	681	17	AG069820	Pan trogl	797	19	82.6	835	12	BF678011	602085045
C 725	19	82.6	682	10	AW955307	EST367377	798	19	82.6	839	17	AQ751648	HS 5566.B
726	19	82.6	682	17	AQ002321	CIT-HSP-2	799	19	82.6	848	14	BQ431499	AGENCOURT
727	19	82.6	682	17	AG076733	Pan trogl	800	19	82.6	852	17	AQ896944	HS 3134.A
728	19	82.6	684	10	AQ274779	RPc11-5-10	C 801	19	82.6	857	17	AQ749766	HS 5573.A
C 729	19	82.6	684	17	AV725274	AV725274	802	19	82.6	858	17	AQ746960	HS 5538.A
C 730	19	82.6	685	17	AG166908	Pan trogl	803	19	82.6	860	12	BG027041	602294089
C 731	19	82.6	686	17	AG001462	Homo sapi	804	19	82.6	868	17	AQ746490	HS 2273.A
732	19	82.6	687	17	AG091828	Pan trogl	C 805	19	82.6	869	17	AQ741627	HS 5572.B
733	19	82.6	687	17	AQ537592	RPc11-11-3	C 806	19	82.6	870	17	AQ745579	HS 5572.A
734	19	82.6	688	17	AQ351002	RPc111-12	807	19	82.6	880	12	BF242198	601878009
735	19	82.6	690	12	BG485117	602503738	808	19	82.6	885	14	BQ232385	AGENCOURT
C 736	19	82.6	690	17	AG145071	Pan trogl	809	19	82.6	887	17	AQ740132	HS 5504.A

810	19	82.6	899	9	AL535154	AL535154	883	18	78.3	345	10	AV754805
811	19	82.6	908	17	AQ749282	HS 5576 A	c 884	18	78.3	345	14	R00976
c 812	19	82.6	932	14	BQ940835	AGENCOURT	885	18	78.3	350	9	AI312309
c 813	19	82.6	940	12	BQ165423	602346089	886	18	78.3	350	12	BF411888
c 814	19	82.6	953	12	BG178900	602328051	887	18	78.3	352	9	AI562068
c 815	19	82.6	975	12	AQ749270	HS 5576 A	c 888	18	78.3	352	10	AW337869
c 816	19	82.6	982	12	BF683149	BF683149 602139211	889	18	78.3	356	13	BI496045
c 817	19	82.6	1024	13	BM452725	AGENCOURT	890	18	78.3	360	9	AI661358
c 818	19	82.6	1065	9	AL515292	AL515292	891	18	78.3	361	12	BF738406
c 819	19	82.6	1075	13	BM549609	AGENCOURT	892	18	78.3	362	12	BF738406
c 820	19	82.6	1100	14	BM928197	AGENCOURT	c 893	18	78.3	362	17	AQ819842
c 821	19	82.6	1137	14	BM910832	AGENCOURT	894	18	78.3	364	9	AA252641
c 822	19	82.6	1405	11	AF318347	Hom sapi	895	18	78.3	365	10	BB813752
c 823	19	82.6	1739	11	AF289552	Hom sapi	c 896	18	78.3	366	9	AA193624
c 824	19	82.6	3753	11	BC018955	Hom sapi	c 897	18	78.3	368	12	BG011114
c 825	18	78.3	1110	10	BE173049	RCO-HT055	c 898	18	78.3	368	17	AZ778949
c 826	18	78.3	122	10	AW847403	RCO-HT020	c 899	18	78.3	369	12	BG012761
c 827	18	78.3	138	13	BI042763	BI042763 CM4-OT016	c 900	18	78.3	371	13	BI496044
c 828	18	78.3	139	12	BF842076	BF842076 RC2-HT107	c 901	18	78.3	371	17	AQ136307
c 829	18	78.3	149	10	AW882207	AW882207 RC4-OT005	c 902	18	78.3	373	9	AA491002
c 830	18	78.3	150	17	AZ260123	RCI-23-1	c 903	18	78.3	373	10	AV734981
c 831	18	78.3	154	12	BF934875	BF934875 IL2-NT019	c 904	18	78.3	373	12	BF834303
c 832	18	78.3	162	13	BI042762	BI042762 CM4-OT016	c 905	18	78.3	378	10	AV724091
c 833	18	78.3	173	17	AZ092026	AZ092026 RPCI-23-7	c 906	18	78.3	379	12	BF809582
c 834	18	78.3	212	12	BF885726	BF885726 QV3-NT016	c 907	18	78.3	380	17	AQ294927
c 835	18	78.3	215	14	TI00571	hbc1286 Hum	c 908	18	78.3	381	12	BF801433
c 836	18	78.3	226	12	BG003425	BG003425 RC3-GN004	c 909	18	78.3	381	17	AQ101447
c 837	18	78.3	230	12	BG011187	BG011187 IL5-GN023	c 910	18	78.3	384	14	W95501
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c 862	18	78.3	303	12	BG011203	BG011203 IL5-GN023	c 935	18	78.3	412	9	AA365359
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c 879	18	78.3	335	9	AA492202	AA492202 ng78e08.s	c 952	18	78.3	426	17	AQ189745
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BF738406 CM3-KT003
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AA252641 z826c06.f
BB813752 BB813752
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BG012761 IL5-GN023
BI496044 df12d012.
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AA491002 aa52h04.s
BF834303 PM3-HT092
AV724091 AV724091
BF809582 QV0-CI019
AQ294927 HS 3056 A
BF801433 IL5-CI000
AQ101447 HS 3020 B
W95501 ze06a03.r1
AA323727 ES726625
W95387 ze06a03.s1
T86727 yd77f01.s1
AQ824636 HS 5292 A
AQ303918 HS 2241 B
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AA456885 aa1f09.s
BF809404 QV0-CI019
AQ093196 HS 3008 A
T90346 yd43a03.s1
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AQ338541 HS 3118 B
N63749 za18f11.s1
AQ131993 HS 2252 A
AQ181169 HS 3216 A
AI524686 th12a06.x
BE328486 hs98e08.x
AQ152190 HS 2320 A
AW868739 EST380815
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AA302759 EST10432
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BI492222 df21c07.w
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AZ837558 2M0132G23
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AW021413 df23c06.y
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AQ460579 HS 5090 A
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c 999 18 78.3 481 14 N29963
c1000 18 78.3 484 17 B74075

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ALIGNMENTS

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LOCUS HA2479 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION A0174766
VERSION A0174766.1 GI:6361145
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 217)
AUTHORS Yu.Y., Zhang.C., Luo.L., Ouyang.S., Li.W., Wu.J., Zhou.S., Liu.M.
and He.F.
TITLE Expression profile analysis of a human fetal liver cDNA library
JOURNAL Unpublished (1998)
COMMENT Contact: Chenggang Zhang
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Email: zhang.chenggang@hotmail.com.
FEATURES
source
1. .217

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 CAGCCAGGCATGGTGGCAGGTG 22
Db 44 CAGCCAGGCATGGTGGCAGGTG 65
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LOCUS EST84797 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar
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ACCESSION A0372667
VERSION A0372667.1 GI:2025175
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 237)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Shall,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li.Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Peng,D.-P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tcdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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FEATURES
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/organism="Homo sapiens"
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EcoRI; Site_2: XhoI"

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION
HS 3055 A2 C10 MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3055 Col=20 Row=E, DNA sequence.
ACCESSION
AQ102785
VERSION
AQ102785.1 GI:3473814
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 361)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
9380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3055 row: E column: 20
Class: BAC ends
High quality sequence stop: 361.
Location/Qualifiers
1. 361
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 150 AGCCAGGCATGGTGGCAGGTGT 171

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LOCUS
DEFINITION
I13-CT0674-060401-492-D11 CT0674 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG960515
VERSION
BG960515.1 GI:14378673
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0674-
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Seq primer: puc 18 forward
High quality sequence stop: 375.
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/dev_stage="Adult"
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,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 297 CAGCCAGGCATGGTGGCAGGTG 318

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LOCUS
DEFINITION
MRI-CT0529-140900-002-e06 CT0529 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF084762
VERSION
BF084762.1 GI:10878592
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 538)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

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MEDLINE
COMMENT

20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-MR1-CT0529-140
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Seq primer: puc 18 forward
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
170 a 116 c 107 g 144 t 1 others

BASE COUNT 170 a 116 c 107 g 144 t 1 others
ORIGIN

Query Match 95.7%; Score 22; DB 12; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.4;
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Genomic clone Plate=1002 Col=22 Row=O, DNA sequence.
ACCESSION A0714377
VERSION A0714377.1 GI:5463693
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 587)
Mahaithas.G.G., Wallace.J.C., Smith.K., Swartzell.S., Holzman.T.,
Keller.A., Shaker.R., Furlong.J., Young,J., Zhao.S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu
Plate: 1002 Row: O Column: 22
Seq primer: T7
Class: BAC ends
High quality sequence stop: 587.
Location/Qualifiers
1. .587
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
159 a 137 c 108 g 166 t 17 others

BASE COUNT 159 a 137 c 108 g 166 t 17 others
ORIGIN

Query Match 95.7%; Score 22; DB 17; Length 587;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCGATGGTGGCAGGTGT 23
|||||
Db 386 AGCCAGGCGATGGTGGCAGGTGT 365
|||||

RESULT 7
AG034167
LOCUS
DEFINITION Pan troglodytes DNA, clone: PTB-009G22.F, genomic survey sequence.
ACCESSION AG034167
VERSION AG034167.1 GI:16561040
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone lib:PTB Chimpanzee Male
BAC Library clone:PTB-009G22.F.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 674)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chmpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. .674
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-009G22.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
264 a 134 c 142 g 133 t 1 others

BASE COUNT 264 a 134 c 142 g 133 t 1 others

```

ORIGIN
Query Match          95.7%; Score 22; DB 17; Length 674;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 149 AGCCAGGCATGGTGGCAGGTGT 170

RESULT 8
AG096453/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: PTB-097N07.F, genomic survey sequence.
ACCESSION AG096453
VERSION AG096453.1 GI:16716970
KEYWORDS
SOURCE
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC library clone:PTB-097N07.F.
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 679)
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
Location/Qualifiers
1..679
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-097N07.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 131 a 180 c 173 g 195 t
ORIGIN

Query Match          95.7%; Score 22; DB 17; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 417 AGCCAGGCATGGTGGCAGGTGT 396

RESULT 9
BG617547
LOCUS
DEFINITION 602615028F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4733982 5',
mRNA sequence.
ACCESSION BG617547
VERSION BG617547.1 GI:13668918

KEYWORDS
EST.
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 723)
NIH-MGC http://mgi.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCMI596 row: g column: 07
High quality sequence stop: 706.
FEATURES
Location/Qualifiers
1..723
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4733982"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 235 a 138 c 137 g 213 t
ORIGIN

Query Match          95.7%; Score 22; DB 12; Length 723;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 128 AGCCAGGCATGGTGGCAGGTGT 149

RESULT 10
BF676568
LOCUS
DEFINITION 602084486F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248741 5',
mRNA sequence.
ACCESSION BF676568
VERSION BF676568.1 GI:11950463
KEYWORDS
EST.
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 766)
NIH-MGC http://mgi.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

```

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http://image.llnl.gov
Plate: LICM1067 row: 1 column: 22
High quality sequence step: 239.
Location/Qualifiers
1. 766
/organism="Homo sapiens"
/db xref="taxon:9606"
/cln="IMAGE:4248741"
/clone_lib="NIH_MGC_83"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfII (ggcgctcgcc); Site 2: SfII (ggcattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATTTAGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 207 a 186 c 211 g 162 t
ORIGIN

Query Match 95.7%; Score 22; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGGCATGGTGGCAGGTG 22
|||||
Db 128 CAGCAGGCATGGTGGCAGGTG 149

RESULT 11
AA089829
LOCUS
DEFINITION chn1495.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
CDNA 5', mRNA sequence.
ACCESSION AA089829
VERSION AA089829.1 GI:1636321
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 144)
Liew,C.C.
CDNAS from fetal heart (1996)
Unpublished (1996)
JOURNAL
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6179750995
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: 5' CCAAGTAATTGTAATACCACTCACTAAGGG 3'
Location/Qualifiers
1. 144
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI for directional cloning into
predigested lambda ZAP Express."
BASE COUNT 37 a 34 c 45 g 28 t
ORIGIN

Query Match 91.3%; Score 21; DB 9; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
|||||
Db 5 AGCCAGGCATGGTGGCAGGTG 25

RESULT 12
N84649/c
LOCUS
DEFINITION N84649 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
clone J0399 5' similar to REPETITIVE ELEMENT ALU, mRNA sequence.
ACCESSION N84649
VERSION N84649.1 GI:1260274
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 150)
Liew,C.C.
CDNAS from fetal heart (1996)
Unpublished (1996)
JOURNAL
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6179750995
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: GAAATTAACCTCACTAAGGG.
Location/Qualifiers
1. 150
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI for directional cloning into
predigested lambda ZAP Express."
BASE COUNT 35 a 40 c 31 g 44 t
ORIGIN

Query Match 91.3%; Score 21; DB 14; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
|||||
Db 72 AGCCAGGCATGGTGGCAGGTG 52

RESULT 13
T28260
LOCUS
DEFINITION T28260 Human Embryo Homo sapiens cDNA 5' end similar to
alcohol/hydroxysteroid sulfotransferase (HT:2595), mRNA sequence.
ACCESSION T28260
VERSION T28260.1 GI:610358
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 152)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

```

C.J., Lee, N., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.B., Hanna, M.C., Hedblom, E., Hinkley, P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Damke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.H.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
JOURNAL Based Upon 83 Million Basepairs of cDNA Sequence
MEDLINE Nature 377, 3-174 (1995)
COMMENT 96026280

CONTACT: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@db.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org)

Seq primer: M13 Reverse.

Location/Qualifiers
 1. .152
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):101723"
 /db_xref="taxon:9606"
 /clone_lib="Human Embryo"
 /tissue_type="embryo"
 /note="Organ: colon"

BASE COUNT 39 a 34 c 27 g 52 t

ORIGIN

Query Match 91.3%; Score 21; DB 14; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

source

RESULT 14
LOCUS AI925839
DEFINITION w052h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2459009 3', similar to contains Alu repetitive element; contains element PTR5 repetitive element ;, mRNA sequence.
ACCESSION AI925839
VERSION AI925839.1 GI:5661803
KEYWORDS EST.
SOURCE human.

BASE COUNT 39 a 34 c 27 g 52 t

ORIGIN

Query Match 91.3%; Score 21; DB 14; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGTCGCGAGGTG 22
 |||||

Db 130 AGCCAGGCATGTCGCGAGGTG 150
 |||||

RESULT 14

LOCUS AI925839/c

DEFINITION w052h09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2459009 3', similar to contains Alu repetitive element; contains element PTR5 repetitive element ;, mRNA sequence.

ACCESSION AI925839

VERSION AI925839.1 GI:5661803

KEYWORDS EST.

SOURCE human.

REFERENCE 1 (bases 1 to 170)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgap@remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert length: 2114 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 141.

Location/Qualifiers

source

1. .170
 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2459009"

/clone_lib="NCI CGAP Gas4"

/tissue_type="poorly_differentiated adenocarcinoma with signet ring cell features"

/lab_host="DH10B"

/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.69 kb. Life Technologies catalog #:

11549-011"

BASE COUNT 32 a 52 c 39 g 47 t

ORIGIN

Query Match 91.3%; Score 21; DB 9; Length 170;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGTCGCGAGGTG 22
 |||||

Db 151 AGCCAGGCATGTCGCGAGGTG 131
 |||||

RESULT 15

LOCUS BE179910/c

DEFINITION IL3-HT0618-110500-133-Fl2 HT0618 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE179910

VERSION BE179910.1 GI:8658971

KEYWORDS EST.

SOURCE human.

ORIGIN

REFERENCE 1 (bases 1 to 183)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zsgo, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

REFERENCE This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=at2=IL3-HT0618-110500-133-Fl2&t3=2000-05-11&t4=1)

AUTHORS Seq primer: puc 18 forward

TITLE High quality sequence stop: 183.

JOURNAL Location/Qualifiers

MEDLINE 1. .183

COMMENT /organism="Homo sapiens"

/db_xref="taxon:9606"

```

/clone_lib="HT0618"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 35 a 49 c 38 g 61 t
ORIGIN

```

```

Query Match 91.3%; Score 21; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22
Db 165 AGCCAGGCATGGTGGCAGGTG 145

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Search completed: June 17, 2003, 06:24:11
Job time : 74.3864 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 4429.72 Seconds
(without alignments)
15794.017 Million cell updates/sec

Title: US-09-513-888c-1_COPY_4514_6917

Perfect score: 2404

Sequence: 1 agagggagagcgaggtgc.....gacagggtctgtctgtcc 2404

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pla.*
- 35: em.htg.rod.*
- 36: em.htg.man.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2404	100.0	9108	9	AF123653 Homo sapi
2	1966	81.8	5492	9	AF123659 Homo sapi
3	1338	55.7	173264	2	AC025853 Homo sapi
4	373	15.5	1722	9	AF123658 Homo sapi
5	283	11.8	1692	9	AF123657 Homo sapi
6	254	10.6	1614	9	AF123655 Homo sapi
7	219	9.1	1515	9	AF123656 Homo sapi
8	80	3.3	633	9	AF123654 Homo sapi
9	76	3.2	231	9	AF123652 Homo sapi
10	52	2.2	227884	2	AC114995 Mus muscu
c 11	52	2.2	263546	2	AC099416 Mus muscu
12	49	2.0	162178	9	AC093491 Homo sapi
c 13	49	2.0	195952	9	AC012184 Homo sapi
14	43	1.8	129435	9	AL391314 Human DNA
c 15	43	1.8	140179	2	AC084688 Homo sapi
16	43	1.8	178785	9	AC068139 Homo sapi
17	43	1.8	203484	2	AC010194 Homo sapi
18	42	1.7	26478	9	AL445307 Human DNA
19	42	1.7	42159	9	AP000950 Homo sapi
c 20	42	1.7	104357	9	AL392123 Human DNA
21	42	1.7	138006	2	AC068246 Homo sapi
22	42	1.7	144784	9	AC009224 Homo sapi
23	42	1.7	145528	9	AC003665 Homo sapi
c 24	42	1.7	147244	9	AC005969 Homo sapi
25	42	1.7	147525	2	AC060754 Homo sapi
26	42	1.7	154708	2	AC024443 Homo sapi
27	42	1.7	157289	9	AC009234 Homo sapi
c 28	42	1.7	159070	2	AC131160 Homo sapi
29	42	1.7	160604	9	AL449305 Human DNA
30	42	1.7	167998	9	AL353662 Human DNA
31	42	1.7	168738	2	AC093632 Homo sapi
32	42	1.7	169149	9	AL445930 Human DNA
33	42	1.7	171731	2	AC091659 Papio cyn
34	42	1.7	175952	2	AC009195 Homo sapi
c 35	42	1.7	178688	9	AC068644 Homo sapi
c 36	42	1.7	180231	9	AC009161 Homo sapi
c 37	42	1.7	181049	9	AC093131 Papio cyn
38	42	1.7	187064	9	AC011476 Homo sapi
39	42	1.7	187822	9	AC015674 Homo sapi
c 40	42	1.7	203006	9	HS1145123
41	42	1.7	203912	9	AC008755 Homo sapi
42	42	1.7	204340	2	AC019238 Homo sapi
c 43	42	1.7	247335	2	AC084794 Homo sapi
c 44	42	1.7	257967	2	AL365337 Mus muscu
45	42	1.7	340000	9	AP001688 Homo sapi
46	41	1.7	87471	9	AC041005 Homo sapi
c 47	41	1.7	103819	9	HSJ775C13
48	41	1.7	122564	9	HSJ899B16
c 49	41	1.7	150829	2	AC009092 Homo sapi
c 50	41	1.7	162559	9	AL360230 Human DNA
c 51	41	1.7	164602	9	AC022001 Homo sapi
c 52	41	1.7	165398	2	AC012086 Homo sapi
c 53	41	1.7	166206	2	AC016927 Homo sapi
54	41	1.7	167238	9	AC024903 Homo sapi
55	41	1.7	167245	9	AC099521 Homo sapi
c 56	41	1.7	169969	2	AL390727 Homo sapi
c 57	41	1.7	173317	9	AC016637 Homo sapi
c 58	41	1.7	177834	9	AC018811 Homo sapi
c 59	41	1.7	181646	9	AC009162 Homo sapi
c 60	41	1.7	182452	9	AL161731 Human DNA
61	41	1.7	186202	9	AC108516 Homo sapi
c 62	41	1.7	191308	9	AC034243 Homo sapi
c 63	41	1.7	195191	9	AC024339 Homo sapi
c 64	41	1.7	201599	2	AC068790 Homo sapi
c 65	41	1.7	210067	2	AC026358 Homo sapi

C 66	41	1-7	212659	2	AL390737	AL390737 Homo sapi	C 139	38	1-6	59561	2	AC090911	AC090911 Homo sapi
C 67	41	1-7	243587	2	AL591179	AL591179 Homo sapi	C 140	38	1-6	62944	6	AX334775	AX334775 Sequence
C 68	40	1-7	135259	9	HS127820	Z83838 Human DNA s	C 141	38	1-6	62944	6	AX336090	AX336090 Sequence
C 69	39	1-6	105880	9	AL158062	AL158062 Human DNA	C 142	38	1-6	62944	9	HS127820	HS127820 Homo sapi
C 70	39	1-6	119638	9	AC024575	AC024575 Homo sapi	C 143	38	1-6	63459	9	AC115224	AC115224 Homo sapi
C 71	39	1-6	130416	9	AC008851	AC008851 Homo sapi	C 144	38	1-6	65435	9	AC104587	AC104587 Homo sapi
C 72	39	1-6	148656	9	AC005482	AC005482 Homo sapi	C 145	38	1-6	65961	2	AC090266	AC090266 Homo sapi
C 73	39	1-6	150107	2	AC025482	AC025482 Homo sapi	C 146	38	1-6	65957	2	AC090850	AC090850 Homo sapi
C 74	39	1-6	154370	2	AC108106	AC108106 Homo sapi	C 147	38	1-6	67066	2	AC126358	AC126358 Homo sapi
C 75	39	1-6	162350	9	AC008118	AC008118 Homo sapi	C 148	38	1-6	67236	2	AC021282	AC021282 Homo sapi
C 76	39	1-6	177381	2	AC083805	AC083805 Homo sapi	C 149	38	1-6	67550	2	AC016452	AC016452 Homo sapi
C 77	39	1-6	180672	9	AC011451	AC011451 Homo sapi	C 150	38	1-6	67908	2	AC103998	AC103998 Homo sapi
C 78	39	1-6	184053	9	AC011900	AC011900 Homo sapi	C 151	38	1-6	68517	2	AC107935	AC107935 Homo sapi
C 79	39	1-6	194716	2	AL136227	AL136227 Homo sapi	C 152	38	1-6	68517	2	AL107935	AL107935 Homo sapi
C 80	39	1-6	198161	9	HS232K4	AL021938 Homo sapi	C 153	38	1-6	68525	2	AL845464	AL845464 Homo sapi
C 81	39	1-6	204457	2	AC121759	AC121759 Homo sapi	C 154	38	1-6	70416	9	AC095039	AC095039 Homo sapi
C 82	39	1-6	203530	9	AC025097	AC025097 Homo sapi	C 155	38	1-6	70435	2	AC116909	AC116909 Homo sapi
C 83	39	1-6	212103	9	CNS01DV4	AL133453 Human Chr	C 156	38	1-6	70972	2	AC130332	AC130332 Homo sapi
C 84	39	1-6	217328	2	AC007513	AC007513 Homo sapi	C 157	38	1-6	71263	9	HS1014D13	HS1014D13 Human DNA
C 85	39	1-6	217668	2	AC020561	AC020561 Homo sapi	C 158	38	1-6	72461	9	AC073322	AC073322 Homo sapi
C 86	39	1-6	239008	2	AC022460	AC022460 Homo sapi	C 159	38	1-6	72754	9	AC011338	AC011338 Homo sapi
C 87	39	1-6	309805	2	AC026340	AC026340 Homo sapi	C 160	38	1-6	72847	2	AC023563	AC023563 Homo sapi
C 88	39	1-6	313264	2	AC023053	AC023053 Homo sapi	C 161	38	1-6	73201	9	AC011388	AC011388 Homo sapi
C 89	38	1-6	394	11	HUMUT6516	L306444 Human STS U	C 162	38	1-6	73845	2	AL356478	AL356478 Homo sapi
C 90	38	1-6	1408	9	AK026097	AK026097 Homo sapi	C 163	38	1-6	75001	9	AC093167	AC093167 Homo sapi
C 91	38	1-6	1513	9	BC002820	BC002820 Homo sapi	C 164	38	1-6	76200	9	AC008616	AC008616 Homo sapi
C 92	38	1-6	1566	9	HS127820	AL049434 Homo sapi	C 165	38	1-6	76200	9	AP005401	AP005401 Homo sapi
C 93	38	1-6	1636	9	AK024527	AK024527 Homo sapi	C 166	38	1-6	76702	9	HS756P4	HS756P4 Human DNA
C 94	38	1-6	2081	9	BC017096	BC017096 Homo sapi	C 167	38	1-6	76763	2	AL157705	AL157705 Human DNA
C 95	38	1-6	2131	9	AF092925	AF092925 Homo sapi	C 168	38	1-6	77313	2	AC022855	AC022855 Homo sapi
C 96	38	1-6	2306	9	AK054811	AK054811 Homo sapi	C 169	38	1-6	77425	9	AF068862	AF068862 Homo sapi
C 97	38	1-6	2340	9	HS127820	AL833636 Homo sapi	C 170	38	1-6	77529	2	AL611948	AL611948 Homo sapi
C 98	38	1-6	2467	9	HSCDGEN	X74984 H. sapiens 5	C 171	38	1-6	78233	2	AC004636	AC004636 Homo sapi
C 99	38	1-6	2598	6	BD012292	BD012292 Genes rel	C 172	38	1-6	78373	2	AC026519	AC026519 Homo sapi
C 100	38	1-6	2598	9	AK027382	AK027382 Homo sapi	C 173	38	1-6	79305	9	AC005200	AC005200 Homo sapi
C 101	38	1-6	2598	23	BD004972	BD004972 Genes rel	C 174	38	1-6	79810	9	AC005543	AC005543 Homo sapi
C 102	38	1-6	4192	9	AF305083	AF305083 Homo sapi	C 175	38	1-6	80846	9	AL512489	AL512489 Human DNA
C 103	38	1-6	4652	9	AF187725	AF187725 Homo sapi	C 176	38	1-6	80869	9	HS127820	HS127820 Homo sapi
C 104	38	1-6	4652	9	AF189367	AF189367 Homo sapi	C 177	38	1-6	82117	9	AP000338	AP000338 Homo sapi
C 105	38	1-6	6799	9	AB051447	AB051447 Homo sapi	C 178	38	1-6	83329	2	AC073860	AC073860 Homo sapi
C 106	38	1-6	8231	9	AC110808	AC110808 Homo sapi	C 179	38	1-6	84450	2	AC091431	AC091431 Homo sapi
C 107	38	1-6	8231	9	AC112176	AC112176 Homo sapi	C 180	38	1-6	85874	9	AC073150	AC073150 Homo sapi
C 108	38	1-6	8922	9	AC112176	AC112176 Homo sapi	C 181	38	1-6	86451	2	AC107037	AC107037 Pan trogl
C 109	38	1-6	20539	9	HS349E10	AL022341 Human DNA	C 182	38	1-6	89218	9	AC005902	AC005902 Homo sapi
C 110	38	1-6	26078	9	AF376770	AF376770 Homo sapi	C 183	38	1-6	89921	2	AF170802	AF170802 Homo sapi
C 111	38	1-6	27273	9	AL365206	AL365206 Homo sapi	C 184	38	1-6	89944	9	AC093127	AC093127 Papio cyn
C 112	38	1-6	28265	9	HSR314	Z69890 Human DNA s	C 185	38	1-6	90109	2	AC002557	AC002557 Homo sapi
C 113	38	1-6	30632	9	AL160051	AL160051 Human DNA s	C 186	38	1-6	90136	9	HS330012	HS330012 Human DNA
C 114	38	1-6	32269	9	HSRA36	Z69720 Human DNA s	C 187	38	1-6	90143	9	AL669876	AL669876 Human DNA
C 115	38	1-6	32918	2	AC007445	AC007445 Homo sapi	C 188	38	1-6	90780	2	AC093202	AC093202 Homo sapi
C 116	38	1-6	34182	9	HSU197H3	Z74409 Human DNA s	C 189	38	1-6	91187	9	AC023790	AC023790 Homo sapi
C 117	38	1-6	34346	9	AC090632	AC090632 Homo sapi	C 190	38	1-6	91388	9	AC005994	AC005994 Homo sapi
C 118	38	1-6	36230	9	AP001059	AP001059 Homo sapi	C 191	38	1-6	91835	9	HS26H23	HS26H23 Human DNA s
C 119	38	1-6	37718	9	AC004034	AC004034 Homo sapi	C 192	38	1-6	93285	9	AL159174	AL159174 Human DNA
C 120	38	1-6	38250	2	AC012006	AC012006 Homo sapi	C 193	38	1-6	93296	9	AL136363	AL136363 Human DNA
C 121	38	1-6	38727	9	AC006953	AC006953 Homo sapi	C 194	38	1-6	93324	9	AL139119	AL139119 Human DNA
C 122	38	1-6	3383	9	AC022149	AC022149 Homo sapi	C 195	38	1-6	93976	9	AP000474	AP000474 Homo sapi
C 123	38	1-6	40893	9	AL589952	AL589952 Human DNA	C 196	38	1-6	94060	2	AF216673	AF216673 Homo sapi
C 124	38	1-6	44544	9	AC004262	AC004262 Homo sapi	C 197	38	1-6	95484	2	AC015854	AC015854 Homo sapi
C 125	38	1-6	44733	2	AC006171	AC006171 Homo sapi	C 198	38	1-6	97218	9	AC092385	AC092385 Homo sapi
C 126	38	1-6	45373	9	AL158092	AL158092 Human DNA	C 199	38	1-6	97601	9	AC073190	AC073190 Homo sapi
C 127	38	1-6	47338	9	AL355990	AL355990 Human DNA	C 200	38	1-6	98104	9	HS127820	HS127820 Homo sapi
C 128	38	1-6	47854	9	HS839M1	AL034485 Human DNA	C 201	38	1-6	99074	9	HS560B9	HS560B9 Human DNA s
C 129	38	1-6	50651	9	AC004762	AC004762 Homo sapi	C 202	38	1-6	99799	9	AL445184	AL445184 Human DNA
C 130	38	1-6	50660	9	AP000657	AP000657 Homo sapi	C 203	38	1-6	100000	9	AB020865	AB020865 Homo sapi
C 131	38	1-6	52737	2	AC007800	AC007800 Homo sapi	C 204	38	1-6	100000	9	AP000216	AP000216 Homo sapi
C 132	38	1-6	53168	9	HS109G6	AL023879 Human DNA	C 205	38	1-6	100167	9	HSJ189G13	HSJ189G13 Human DNA
C 133	38	1-6	53415	2	AC111176	AC111176 Homo sapi	C 206	38	1-6	100793	9	AF070717	AF070717 Homo sapi
C 134	38	1-6	53942	9	HS506G2A	Z82901 Human DNA s	C 207	38	1-6	102117	9	AC098823	AC098823 Homo sapi
C 135	38	1-6	54166	9	AC126119	AC126119 Homo sapi	C 208	38	1-6	102259	2	AC015916	AC015916 Homo sapi
C 136	38	1-6	54407	2	AC021817	AC021817 Homo sapi	C 209	38	1-6	102484	9	HS510H16	HS510H16 Human DNA
C 137	38	1-6	57408	9	AL670471	AL670471 Human DNA	C 210	38	1-6	104082	9	AC011503	AC011503 Homo sapi
C 138	38	1-6	58884	9	AL359512	AL359512 Human DNA	C 211	38	1-6	104357	9	AL392123	AL392123 Human DNA

c 212	38	1.6 104679	9	AL353706	AL353706 Human DNA
c 213	38	1.6 105955	9	AC074136	AC074136 Homo sapi
c 214	38	1.6 106008	9	HS0506	HS0506 Homo sapi
c 215	38	1.6 106506	9	AL358235	AL358235 Human DNA
c 216	38	1.6 106508	9	AC005102	AC005102 Homo sapi
c 217	38	1.6 106954	9	AC104651	AC104651 Homo sapi
c 218	38	1.6 107527	9	AC005018	AC005018 Homo sapi
c 219	38	1.6 108315	9	HS41P2	HS41P2 Homo sapi
c 220	38	1.6 108500	9	AP001624	AP001624 Homo sapi
c 221	38	1.6 108965	9	AF191069	AF191069 Homo sapi
c 222	38	1.6 109239	2	AC104521	AC104521 Homo sapi
c 223	38	1.6 109488	9	HS298815	HS298815 Homo sapi
c 224	38	1.6 109864	9	AF096876	AF096876 Homo sapi
c 225	38	1.6 110000	2	AC073860	AC073860 Homo sapi
c 226	38	1.6 110000	2	AC092789	AC092789 Homo sapi
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c 228	38	1.6 110000	2	AL390072	AL390072 Homo sapi
c 229	38	1.6 110000	2	AL683885	AL683885 Homo sapi
c 230	38	1.6 110000	2	AL732359	AL732359 Homo sapi
c 231	38	1.6 110000	2	AC026673	AC026673 Homo sapi
c 232	38	1.6 110159	2	AC068178	AC068178 Homo sapi
c 233	38	1.6 110271	9	AC024576	AC024576 Homo sapi
c 234	38	1.6 111123	9	AP000365	AP000365 Homo sapi
c 235	38	1.6 111321	2	AC068718	AC068718 Homo sapi
c 236	38	1.6 111738	2	AL592304	AL592304 Homo sapi
c 237	38	1.6 111962	9	AP000890	AP000890 Homo sapi
c 238	38	1.6 113117	9	AL512288	AL512288 Human DNA
c 239	38	1.6 113213	9	AC016554	AC016554 Homo sapi
c 240	38	1.6 113370	9	AL591493	AL591493 Homo sapi
c 241	38	1.6 113929	9	AF196969	AF196969 Homo sapi
c 242	38	1.6 113982	2	AF192303	AF192303 Homo sapi
c 243	38	1.6 114231	9	HS390C10	HS390C10 Homo sapi
c 244	38	1.6 114842	9	AC002996	AC002996 Homo sapi
c 245	38	1.6 115297	2	U82207	U82207 Homo sapi
c 246	38	1.6 115644	2	AC124056	AC124056 Homo sapi
c 247	38	1.6 115928	2	AC037475	AC037475 Homo sapi
c 248	38	1.6 115948	2	AC027727	AC027727 Homo sapi
c 249	38	1.6 115958	9	AC004736	AC004736 Homo sapi
c 250	38	1.6 116311	9	AL360181	AL360181 Human DNA
c 251	38	1.6 116334	2	AC084172	AC084172 Homo sapi
c 252	38	1.6 117404	2	AC063329	AC063329 Homo sapi
c 253	38	1.6 117587	2	AC107375	AC107375 Homo sapi
c 254	38	1.6 118047	9	HS0513M9	HS0513M9 Homo sapi
c 255	38	1.6 118218	2	AP000670	AP000670 Homo sapi
c 256	38	1.6 118582	2	AC115989	AC115989 Homo sapi
c 257	38	1.6 119760	9	AC025458	AC025458 Homo sapi
c 258	38	1.6 120015	2	AL354860	AL354860 Homo sapi
c 259	38	1.6 120166	9	AC091390	AC091390 Homo sapi
c 260	38	1.6 120387	9	AC003051	AC003051 Homo sapi
c 261	38	1.6 120821	9	AC004702	AC004702 Homo sapi
c 262	38	1.6 121143	9	AF312915	AF312915 Homo sapi
c 263	38	1.6 121460	2	AC027330	AC027330 Homo sapi
c 264	38	1.6 121478	9	AL365229	AL365229 Human DNA
c 265	38	1.6 121520	9	AC006477	AC006477 Homo sapi
c 266	38	1.6 122000	9	AC003093	AC003093 Human DNA
c 267	38	1.6 122000	9	AP002414	AP002414 Homo sapi
c 268	38	1.6 122140	2	AC082647	AC082647 Homo sapi
c 269	38	1.6 123288	9	AP000547	AP000547 Homo sapi
c 270	38	1.6 123661	9	AC095048	AC095048 Homo sapi
c 271	38	1.6 125108	9	AF030453	AF030453 Homo sapi
c 272	38	1.6 125641	9	HSJ234P15	HSJ234P15 Homo sapi
c 273	38	1.6 125653	9	AL133517	AL133517 Human DNA
c 274	38	1.6 125922	9	AL731566	AL731566 Human DNA
c 275	38	1.6 126392	2	AC018785	AC018785 Homo sapi
c 276	38	1.6 126491	9	AL589764	AL589764 Human DNA
c 277	38	1.6 126615	9	AC005180	AC005180 Homo sapi
c 278	38	1.6 126792	9	AC008102	AC008102 Homo sapi
c 279	38	1.6 127661	2	AP001261	AP001261 Homo sapi
c 280	38	1.6 128398	9	AC004817	AC004817 Homo sapi
c 281	38	1.6 128779	9	HS29K1	HS29K1 Homo sapi
c 282	38	1.6 128871	9	AL157838	AL157838 Human DNA
c 283	38	1.6 128915	9	AC002418	AC002418 Human sapi
c 284	38	1.6 129350	9	AC068802	AC068802 Homo sapi
c 285	38	1.6 129435	9	AL391314	AL391314 Human DNA
c 286	38	1.6 129541	9	AC004999	AC004999 Homo sapi
c 287	38	1.6 129584	9	AL355385	AL355385 Human DNA
c 288	38	1.6 131078	9	HSU80017	HSU80017 Homo sapi
c 289	38	1.6 132070	9	AC003663	AC003663 Homo sapi
c 290	38	1.6 132290	9	AL627402	AL627402 Human DNA
c 291	38	1.6 132875	9	AC112907	AC112907 Homo sapi
c 292	38	1.6 133337	2	AC016231	AC016231 Homo sapi
c 293	38	1.6 133814	2	AC027550	AC027550 Homo sapi
c 294	38	1.6 134011	2	AC068269	AC068269 Homo sapi
c 295	38	1.6 134040	2	AC044856	AC044856 Homo sapi
c 296	38	1.6 134091	2	AC023349	AC023349 Homo sapi
c 297	38	1.6 134250	9	AL139044	AL139044 Human DNA
c 298	38	1.6 134999	2	AC040894	AC040894 Homo sapi
c 299	38	1.6 137057	9	AC004952	AC004952 Homo sapi
c 300	38	1.6 137730	9	HS365E2	HS365E2 Homo sapi
c 301	38	1.6 137806	2	AC026372	AC026372 Homo sapi
c 302	38	1.6 137922	2	AC073398	AC073398 Homo sapi
c 303	38	1.6 137935	9	AL662884	AL662884 Human DNA
c 304	38	1.6 138221	9	AL391422	AL391422 Human DNA
c 305	38	1.6 138347	9	AL389889	AL389889 Human DNA
c 306	38	1.6 138764	9	AC006387	AC006387 Homo sapi
c 307	38	1.6 138932	9	AL662828	AL662828 Human DNA
c 308	38	1.6 139327	2	AC025017	AC025017 Homo sapi
c 309	38	1.6 139966	9	AC004820	AC004820 Homo sapi
c 310	38	1.6 140207	9	AL356390	AL356390 Human DNA
c 311	38	1.6 140403	2	AC109444	AC109444 Homo sapi
c 312	38	1.6 140446	9	AL355581	AL355581 Human DNA
c 313	38	1.6 140974	9	AC088533	AC088533 Homo sapi
c 314	38	1.6 140999	9	AL356415	AL356415 Human DNA
c 315	38	1.6 141003	2	AC016463	AC016463 Homo sapi
c 316	38	1.6 141266	9	AC004671	AC004671 Homo sapi
c 317	38	1.6 141790	9	AL590636	AL590636 Human DNA
c 318	38	1.6 141794	2	AC093455	AC093455 Homo sapi
c 319	38	1.6 141969	2	AC073242	AC073242 Homo sapi
c 320	38	1.6 143065	9	HS20208	HS20208 Human DNA
c 321	38	1.6 143096	9	HS140C12	HS140C12 Homo sapi
c 322	38	1.6 143428	9	AL162587	AL162587 Human DNA
c 323	38	1.6 143485	9	AC099678	AC099678 Homo sapi
c 324	38	1.6 143697	2	AL358572	AL358572 Homo sapi
c 325	38	1.6 143860	9	AC009155	AC009155 Homo sapi
c 326	38	1.6 143967	9	AL365366	AL365366 Human DNA
c 327	38	1.6 144314	2	AP000835	AP000835 Homo sapi
c 328	38	1.6 144388	2	AC091433	AC091433 Homo sapi
c 329	38	1.6 144392	9	HS67K17	HS67K17 Homo sapi
c 330	38	1.6 144444	9	HSJ365119	HSJ365119 Human DNA
c 331	38	1.6 144578	9	AC016588	AC016588 Homo sapi
c 332	38	1.6 144620	9	AC023787	AC023787 Homo sapi
c 333	38	1.6 144735	2	AL161458	AL161458 Homo sapi
c 334	38	1.6 145097	2	AC018888	AC018888 Homo sapi
c 335	38	1.6 145100	2	AC024641	AC024641 Homo sapi
c 336	38	1.6 145173	9	AC005599	AC005599 Homo sapi
c 337	38	1.6 145299	2	AF228728	AF228728 Homo sapi
c 338	38	1.6 145414	9	HSJ392M18	HSJ392M18 Human DNA
c 339	38	1.6 145550	9	AC092851	AC092851 Homo sapi
c 340	38	1.6 145580	9	AC097373	AC097373 Homo sapi
c 341	38	1.6 145726	2	AC021807	AC021807 Homo sapi
c 342	38	1.6 146004	9	AC019144	AC019144 Homo sapi
c 343	38	1.6 146309	9	AL645565	AL645565 Human DNA
c 344	38	1.6 146572	2	AC024983	AC024983 Homo sapi
c 345	38	1.6 146776	2	AC093486	AC093486 Homo sapi
c 346	38	1.6 146954	9	AL590640	AL590640 Human DNA
c 347	38	1.6 147088	2	AC104422	AC104422 Homo sapi
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c 350	38	1.6 148045	9	AC021860	AC021860 Homo sapi
c 351	38	1.6 148507	2	AC011263	AC011263 Homo sapi
c 352	38	1.6 148606	9	AC104692	AC104692 Homo sapi
c 353	38	1.6 148819	9	AC006996	AC006996 Homo sapi
c 354	38	1.6 148980	2	AC105105	AC105105 Homo sapi
c 355	38	1.6 149170	2	AC110603	AC110603 Homo sapi
c 356	38	1.6 149271	9	AC022144	AC022144 Homo sapi
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C 363	38	1.6 150222	9	AC092296	Homo sapi
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C 367	38	1.6 150668	9	AC027314	Homo sapi
C 368	38	1.6 150681	9	AP001251	Homo sapi
C 369	38	1.6 150681	9	AC006011	Homo sapi
C 370	38	1.6 151133	9	AC013355	Homo sapi
C 371	38	1.6 151358	2	AL590437	Homo sapi
C 372	38	1.6 151445	9	AL354943	Human DNA
C 373	38	1.6 151606	9	AC087441	Homo sapi
C 374	38	1.6 151630	9	AC005154	Homo sapi
C 375	38	1.6 151736	2	AC024439	Homo sapi
C 376	38	1.6 151739	2	AC020691	Homo sapi
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C 378	38	1.6 152454	2	AC067909	Homo sapi
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C 380	38	1.6 152867	9	AC027671	Homo sapi
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C 385	38	1.6 154518	2	AC011619	Homo sapi
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C 395	38	1.6 156249	2	AC016458	Homo sapi
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C 400	38	1.6 156929	2	AC026854	Homo sapi
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C 418	38	1.6 160039	9	AC094109	Homo sapi
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C 422	38	1.6 160359	9	AC007262	Homo sapi
C 423	38	1.6 160433	9	AC093296	Homo sapi
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C 435	38	1.6 161920	2	AP002502	Homo sapi
C 436	38	1.6 161990	2	AL357313	Homo sapi
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C 438	38	1.6 162377	9	AL683870	Human DNA
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C 440	38	1.6 162728	9	AP002906	Homo sapi
C 441	38	1.6 162959	2	AC019255	Homo sapi
C 442	38	1.6 163076	2	AC107885	Homo sapi
C 443	38	1.6 163711	2	AC013245	Homo sapi
C 444	38	1.6 164168	9	AL135927	Human DNA
C 445	38	1.6 164176	2	AC080147	Homo sapi
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C 450	38	1.6 164598	2	AC093212	Homo sapi
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C 453	38	1.6 165197	9	AC002070	Human BAC
C 454	38	1.6 165282	2	AC027117	Homo sapi
C 455	38	1.6 165341	2	AC092037	Homo sapi
C 456	38	1.6 165434	9	AC022448	Homo sapi
C 457	38	1.6 165531	2	AC023038	Homo sapi
C 458	38	1.6 165562	2	AC116004	Homo sapi
C 459	38	1.6 165866	2	AC087273	Homo sapi
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C 464	38	1.6 166218	2	AC092993	Homo sapi
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C 519	38	1.6 173346	9	AC112184	AC112184 Homo sapi
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C 521	38	1.6 173717	9	AC012236	AC012236 Homo sapi
C 522	38	1.6 173893	9	AC010150	AC010150 Homo sapi
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C 525	38	1.6 174539	9	AC103558	AC103558 Homo sapi
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C 528	38	1.6 174991	2	AC015935	AC015935 Homo sapi
C 529	38	1.6 175011	2	AC105339	AC105339 Homo sapi
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C 531	38	1.6 175265	2	AC063964	AC063964 Homo sapi
C 532	38	1.6 175339	9	AC005772	AC005772 Homo sapi
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C 535	38	1.6 175550	2	AC009863	AC009863 Homo sapi
C 536	38	1.6 175562	2	AC012636	AC012636 Homo sapi
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C 539	38	1.6 176155	2	AC012149	AC012149 Homo sapi
C 540	38	1.6 176222	9	AC011825	AC011825 Homo sapi
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C 542	38	1.6 176616	2	AC114489	AC114489 Homo sapi
C 543	38	1.6 176634	2	AC116163	AC116163 Homo sapi
C 544	38	1.6 176636	2	AC024936	AC024936 Homo sapi
C 545	38	1.6 176845	2	AC023509	AC023509 Homo sapi
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C 547	38	1.6 177019	9	AL158194	AL158194 Human DNA
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C 549	38	1.6 177160	9	AC019089	AC019089 Homo sapi
C 550	38	1.6 177178	2	AC013791	AC013791 Homo sapi
C 551	38	1.6 177257	2	AL807789	AL807789 Homo sapi
C 552	38	1.6 177379	2	AC079826	AC079826 Homo sapi
C 553	38	1.6 177384	9	AC097639	AC097639 Homo sapi
C 554	38	1.6 177444	2	AC024617	AC024617 Homo sapi
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C 577	38	1.6 181858	2	AC079822	AC079822 Homo sapi
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C 586	38	1.6 183382	9	AL157388	AL157388 Human DNA
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C 596	38	1.6 184439	2	AP003085	AP003085 Homo sapi
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C 627	38	1.6 187960	9	AP000866	AP000866 Homo sapi
C 628	38	1.6 188119	9	AC119673	AC119673 Homo sapi
C 629	38	1.6 188207	9	AC027644	AC027644 Homo sapi
C 630	38	1.6 188255	2	AC061991	AC061991 Homo sapi
C 631	38	1.6 188257	2	AC118755	AC118755 Homo sapi
C 632	38	1.6 188353	9	AC009480	AC009480 Homo sapi
C 633	38	1.6 188460	9	AC010542	AC010542 Homo sapi
C 634	38	1.6 188478	9	CNS05TF4	AL1365294 Human chr
C 635	38	1.6 188582	2	AC013720	AC013720 Homo sapi
C 636	38	1.6 188784	2	AC090154	AC090154 Homo sapi
C 637	38	1.6 189174	9	AC092687	AC092687 Homo sapi
C 638	38	1.6 189786	2	AC068015	AC068015 Homo sapi
C 639	38	1.6 190162	9	AC009244	AC009244 Homo sapi
C 640	38	1.6 190189	2	AC027181	AC027181 Homo sapi
C 641	38	1.6 190357	2	AC012259	AC012259 Homo sapi
C 642	38	1.6 190385	9	AC012305	AC012305 Homo sapi
C 643	38	1.6 190739	2	AP001361	AP001361 Homo sapi
C 644	38	1.6 190773	9	AC018513	AC018513 Homo sapi
C 645	38	1.6 190848	9	AC113416	AC113416 Homo sapi
C 646	38	1.6 190871	9	AC044797	AC044797 Homo sapi
C 647	38	1.6 191027	2	AC022271	AC022271 Homo sapi
C 648	38	1.6 191141	2	AC069374	AC069374 Homo sapi
C 649	38	1.6 191923	2	AP001846	AP001846 Homo sapi

650	38	1.6	191970	2	AC073334	AC073334 Homo sapi	C 723	38	1.6	222106	2	AC018570	AC018570 Homo sapi
C 651	38	1.6	192298	9	AP000943	AP000943 Homo sapi	C 724	38	1.6	223284	2	AC108373	AC108373 Pan trogl
C 652	38	1.6	192404	9	CNS01DWO	AL136296 Human chr	C 725	38	1.6	223606	2	AC013479	AC013479 Homo sapi
C 653	38	1.6	192491	2	AC103705	AC103705 Homo sapi	C 726	38	1.6	224068	9	CNS01DOU	AL133246 BAC seque
C 654	38	1.6	192799	9	AL583841	AL583841 Human DNA	C 727	38	1.6	226171	9	AP003730	AP003730 Homo sapi
C 655	38	1.6	192834	2	AC069503	AC069503 Homo sapi	C 728	38	1.6	229379	9	AC010746	AC010746 Homo sapi
C 656	38	1.6	193118	2	AC067728	AC067728 Homo sapi	C 729	38	1.6	230392	9	AC026672	AC026672 Homo sapi
C 657	38	1.6	193589	2	AC130473	AC130473 Homo sapi	C 730	38	1.6	231379	2	AC091717	AC091717 Pan trogl
C 658	38	1.6	193605	2	AC130472	AC130472 Homo sapi	C 731	38	1.6	233250	9	AC053527	AC053527 Homo sapi
C 659	38	1.6	194197	9	AC064871	AC064871 Homo sapi	C 732	38	1.6	233877	9	AC093798	AC093798 Homo sapi
C 660	38	1.6	194523	9	HS3233M2	AL022476 Human DNA	C 733	38	1.6	234481	2	AC022214	AC022214 Homo sapi
C 661	38	1.6	194523	9	HS3233M2	AL022476 Human DNA	C 734	38	1.6	235968	9	AC087393	AC087393 Homo sapi
C 662	38	1.6	195029	2	AC018642	AC018642 Homo sapi	C 735	38	1.6	235968	9	AC087393	AC087393 Homo sapi
C 663	38	1.6	195029	2	AC007902	AC007902 Homo sapi	C 736	38	1.6	239008	2	AC022460	AC022460 Homo sapi
C 664	38	1.6	195323	2	AC026612	AC026612 Homo sapi	C 737	38	1.6	241674	2	AC068641	AC068641 Homo sapi
C 665	38	1.6	195325	2	AC125616	AC125616 Homo sapi	C 737	38	1.6	252015	9	AC008382	AC008382 Homo sapi
C 666	38	1.6	195766	9	CNS01DVC	AL135744 Human chr	C 738	38	1.6	256073	9	AE006464	AE006464 Homo sapi
C 667	38	1.6	195900	2	AC021164	AC021164 Homo sapi	C 739	38	1.6	258002	9	AE006462	AE006462 Homo sapi
C 668	38	1.6	196973	9	AP000926	AP000926 Homo sapi	C 740	38	1.6	273403	9	AC011498	AC011498 Homo sapi
C 669	38	1.6	197811	2	AC009833	AC009833 Homo sapi	C 741	38	1.6	273403	9	AC011498	AC011498 Homo sapi
C 670	38	1.6	198068	9	AC087240	AC087240 Homo sapi	C 742	38	1.6	283396	2	AC093024	AC093024 Homo sapi
C 671	38	1.6	198248	2	AP001487	AP001487 Homo sapi	C 743	38	1.6	297235	2	AL499603	AL499603 Homo sapi
C 672	38	1.6	198418	9	AC007496	AC007496 Homo sapi	C 744	38	1.6	298575	2	HSBA2284	AL080244 Homo sapi
C 673	38	1.6	198888	9	AC087728	AC087728 Papio cyn	C 745	38	1.6	304623	2	AC021052	AC021052 Homo sapi
C 674	38	1.6	199208	2	AC019236	AC019236 Homo sapi	C 746	38	1.6	320902	2	AL161456	AL161456 Homo sapi
C 675	38	1.6	199240	2	AC010287	AC010287 Homo sapi	C 747	38	1.6	321438	2	AC104989	AC104989 Homo sapi
C 676	38	1.6	199287	2	AC068659	AC068659 Homo sapi	C 748	38	1.6	330250	9	AF049895	AF049895 Homo sapi
C 677	38	1.6	199906	2	AC021764	AC021764 Homo sapi	C 749	38	1.6	340000	9	AP001679	AP001679 Homo sapi
C 678	38	1.6	200045	2	AC069454	AC069454 Homo sapi	C 750	38	1.6	340000	9	AP001684	AP001684 Homo sapi
C 679	38	1.6	200477	2	AC105137	AC105137 Homo sapi	C 751	38	1.6	340000	9	AP001689	AP001689 Homo sapi
C 680	38	1.6	200493	9	AP005270	AP005270 Homo sapi	C 752	38	1.6	340000	9	AP001707	AP001707 Homo sapi
C 681	38	1.6	200680	2	AC023891	AC023891 Homo sapi	C 753	38	1.6	340000	9	AP001753	AP001753 Homo sapi
C 682	38	1.6	200685	2	AP001455	AP001455 Homo sapi	C 754	38	1.6	340000	9	AP001760	AP001760 Homo sapi
C 683	38	1.6	200771	9	AC093668	AC093668 Homo sapi	C 755	38	1.6	345524	9	AF235103	AF235103 Homo sapi
C 684	38	1.6	200799	2	AL445648	AL445648 Homo sapi	C 756	37	1.5	1808	9	AK094860	AK094860 Homo sapi
C 685	38	1.6	201948	2	AP001026	AP001026 Homo sapi	C 757	37	1.5	3107	9	AK023883	AK023883 Homo sapi
C 686	38	1.6	202544	9	AC104447	AC104447 Homo sapi	C 758	37	1.5	6458	9	AY033285S1	AY033285 Homo sapi
C 687	38	1.6	202889	9	AC010552	AC010552 Homo sapi	C 759	37	1.5	10304	9	AY032750	AY032750 Homo sapi
C 688	38	1.6	203010	9	AC008530	AC008530 Homo sapi	C 760	37	1.5	13472	9	AF020057	AF020057 Homo sapi
C 689	38	1.6	203038	9	AC076968	AC076968 Homo sapi	C 761	37	1.5	14266	9	HSE14065	HSE14065 Homo sapi
C 690	38	1.6	203040	2	AC128674	AC128674 Homo sapi	C 762	37	1.5	18368	9	AB034990	AB034990 Homo sapi
C 691	38	1.6	203050	2	HS44N10	Z97197 Homo sapien	C 763	37	1.5	26550	9	AF421855	AF421855 Homo sapi
C 692	38	1.6	203169	9	AL390785	AL390785 Human DNA	C 764	37	1.5	28567	9	HS132695	HS132695 Homo sapi
C 693	38	1.6	203228	9	AC092718	AC092718 Homo sapi	C 765	37	1.5	35122	9	AP000302	AP000302 Homo sapi
C 694	38	1.6	203790	9	AC010422	AC010422 Homo sapi	C 766	37	1.5	36542	9	AC006117	AC006117 Homo sapi
C 695	38	1.6	203838	2	AC026840	AC026840 Homo sapi	C 767	37	1.5	36705	9	AC005340	AC005340 Homo sapi
C 696	38	1.6	203926	2	AC011122	AC011122 Homo sapi	C 768	37	1.5	38939	9	AC004678	AC004678 Homo sapi
C 697	38	1.6	204340	2	AC019238	AC019238 Homo sapi	C 769	37	1.5	39673	9	AL672238	AL672238 Human DNA
C 698	38	1.6	204917	9	AC008040	AC008040 Homo sapi	C 770	37	1.5	40149	9	AC109818	AC109818 Homo sapi
C 699	38	1.6	205715	2	AC007604	AC007604 Homo sapi	C 771	37	1.5	40198	9	HSL261H12	Z54072 Human DNA s
C 700	38	1.6	205866	2	AC055833	AC055833 Homo sapi	C 772	37	1.5	41055	9	AC006930	AC006930 Homo sapi
C 701	38	1.6	206624	9	AC097662	AC097662 Homo sapi	C 773	37	1.5	41220	9	AC004777	AC004777 Homo sapi
C 702	38	1.6	207086	2	AC034290	AC034290 Homo sapi	C 774	37	1.5	41229	9	AC079742	AC079742 Homo sapi
C 703	38	1.6	208024	9	AC010900	AC010900 Homo sapi	C 775	37	1.5	42513	9	AL592438	AL592438 Human DNA
C 704	38	1.6	208612	2	AC108668	AC108668 Homo sapi	C 776	37	1.5	43237	9	AC005578	AC005578 Homo sapi
C 705	38	1.6	208823	2	AC022532	AC022532 Homo sapi	C 777	37	1.5	44145	9	AC010129	AC010129 Homo sapi
C 706	38	1.6	209307	2	AC078778	AC078778 Homo sapi	C 778	37	1.5	44145	9	AL589691	AL589691 Human DNA
C 707	38	1.6	210805	2	AC026333	AC026333 Homo sapi	C 779	37	1.5	46955	2	AC006183	AC006183 Homo sapi
C 708	38	1.6	211767	2	AC110813	AC110813 Homo sapi	C 780	37	1.5	47833	9	AF334400	AF334400 Homo sapi
C 709	38	1.6	212505	2	AC027220	AC027220 Homo sapi	C 781	37	1.5	48032	9	AC003963	AC003963 Homo sapi
C 710	38	1.6	212656	9	AC007957	AC007957 Homo sapi	C 782	37	1.5	48680	9	AC091799	AC091799 Homo sapi
C 711	38	1.6	213599	2	AC104785	AC104785 Homo sapi	C 783	37	1.5	51932	9	AC114275	AC114275 Homo sapi
C 712	38	1.6	215081	2	AC087501	AC087501 Homo sapi	C 784	37	1.5	56386	9	AC002117	AC002117 Genomic s
C 713	38	1.6	215399	9	AL160278	AL160278 Human DNA	C 785	37	1.5	57729	9	AL449284	AL449284 Human DNA
C 714	38	1.6	215509	2	AC079794	AC079794 Homo sapi	C 786	37	1.5	60136	2	AC129510	AC129510 Homo sapi
C 715	38	1.6	216268	2	AC026986	AC026986 Homo sapi	C 787	37	1.5	60610	9	AL591470	AL591470 Human DNA
C 716	38	1.6	216877	9	AC106791	AC106791 Homo sapi	C 788	37	1.5	61958	9	AC092067	AC092067 Homo sapi
C 717	38	1.6	217900	9	AC091809	AC091809 Homo sapi	C 789	37	1.5	62195	9	HSJ664K17	AL109952 Human DNA
C 718	38	1.6	218445	2	AC083959	AC083959 Homo sapi	C 790	37	1.5	62466	9	AC093785	AC093785 Homo sapi
C 719	38	1.6	220719	2	AC116353	AC116353 Homo sapi	C 791	37	1.5	64183	9	HSJ429G5	AL078596 Human DNA
C 720	38	1.6	220995	2	AC010687	AC010687 Homo sapi	C 792	37	1.5	65583	2	AC103997	AC103997 Homo sapi
C 721	38	1.6	221222	2	AC023794	AC023794 Homo sapi	C 793	37	1.5	66539	9	HSJ583K24	AL049576 Human DNA
C 722	38	1.6	221673	2	AC012183	AC012183 Homo sapi	C 794	37	1.5	67197	9	AF510423S1	AF510423 Homo sapi
C 723	38	1.6	221673	2	AC012183	AC012183 Homo sapi	C 795	37	1.5	67543	9	AC100776	AC100776 Homo sapi

C 796	37	1.5	68001	9	AP001442	Homo sapi
C 797	37	1.5	68443	2	AC124292	Homo sapi
C 798	37	1.5	70111	9	AP000263	Homo sapi
C 799	37	1.5	71120	2	AC124800	Homo sapi
C 800	37	1.5	73666	9	HS0J581P3	Homo sapi
C 801	37	1.5	74516	2	AC025641	Homo sapi
C 802	37	1.5	74516	2	AC025641	Homo sapi
C 803	37	1.5	75446	2	AC084204	Homo sapi
C 804	37	1.5	76163	9	AP001436	Homo sapi
C 805	37	1.5	80142	9	AL645465	Homo sapi
C 806	37	1.5	80338	2	AC114939	Homo sapi
C 807	37	1.5	80869	9	HS0J54N4	Homo sapi
C 808	37	1.5	81364	2	AC021072	Homo sapi
C 809	37	1.5	81437	2	AC002353	Homo sapi
C 810	37	1.5	82939	9	AL135928	Homo sapi
C 811	37	1.5	83463	9	AL161644	Homo sapi
C 812	37	1.5	83463	9	AL161644	Homo sapi
C 813	37	1.5	83549	9	AC004752	Homo sapi
C 814	37	1.5	85195	9	AL136093	Homo sapi
C 815	37	1.5	86975	2	AC048340	Homo sapi
C 816	37	1.5	87034	9	AC004587	Homo sapi
C 817	37	1.5	87543	9	HSWRNG2	Homo sapi
C 818	37	1.5	87974	2	AC021283	Homo sapi
C 819	37	1.5	90108	2	AC021611	Homo sapi
C 820	37	1.5	90476	9	AC015910	Homo sapi
C 821	37	1.5	91202	2	AC006186	Homo sapi
C 822	37	1.5	94727	9	AL591034	Homo sapi
C 823	37	1.5	94770	9	HS0J570F3	Homo sapi
C 824	37	1.5	95002	9	AF233390	Homo sapi
C 825	37	1.5	95467	9	AL390122	Homo sapi
C 826	37	1.5	95565	9	AC000379	Homo sapi
C 827	37	1.5	95930	9	AC106033	Homo sapi
C 828	37	1.5	96201	9	AC079601	Homo sapi
C 829	37	1.5	96227	9	AC008026	Homo sapi
C 830	37	1.5	97465	9	AL157820	Homo sapi
C 831	37	1.5	98804	2	AC106723	Homo sapi
C 832	37	1.5	99500	6	AR211954	Sequence
C 833	37	1.5	100000	9	AP000046	Homo sapi
C 834	37	1.5	100000	9	AP000089	Homo sapi
C 835	37	1.5	100000	9	AP000100	Homo sapi
C 836	37	1.5	100000	9	AP000114	Homo sapi
C 837	37	1.5	100000	9	AP000141	Homo sapi
C 838	37	1.5	100000	9	AP000156	Homo sapi
C 839	37	1.5	100000	9	AP000176	Homo sapi
C 840	37	1.5	100000	9	AP000190	Homo sapi
C 841	37	1.5	100259	9	AC005800	Homo sapi
C 842	37	1.5	100743	9	AC073472	Homo sapi
C 843	37	1.5	100836	2	AC087298	Homo sapi
C 844	37	1.5	100921	9	AC004996	Homo sapi
C 845	37	1.5	101041	2	AP002079	Homo sapi
C 846	37	1.5	102112	9	AC005231	Homo sapi
C 847	37	1.5	106277	9	AC068792	Homo sapi
C 848	37	1.5	106623	9	AL355979	Homo sapi
C 849	37	1.5	106729	9	AC008467	Homo sapi
C 850	37	1.5	107017	9	AC012510	Homo sapi
C 851	37	1.5	107264	9	AP002078	Homo sapi
C 852	37	1.5	107652	9	HS0J259N9	Homo sapi
C 853	37	1.5	107819	9	AL589685	Homo sapi
C 854	37	1.5	107967	9	AL353701	Homo sapi
C 855	37	1.5	108182	9	AC009308	Homo sapi
C 856	37	1.5	108460	9	HS111C20	Homo sapi
C 857	37	1.5	108822	2	AC112164	Homo sapi
C 858	37	1.5	109239	2	AC104521	Homo sapi
C 859	37	1.5	109609	9	AL138785	Homo sapi
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C 861	37	1.5	110526	9	HS0J81H24	Homo sapi
C 862	37	1.5	110753	9	AC100216	Homo sapi
C 863	37	1.5	110794	9	AC107071	Homo sapi
C 864	37	1.5	111496	9	AC069351	Homo sapi
C 865	37	1.5	112309	9	AC003025	Homo sapi
C 866	37	1.5	112424	9	AC092838	Homo sapi
C 867	37	1.5	112542	2	AC090777	Homo sapi
C 868	37	1.5	113515	9	HS0J944F13	Homo sapi

C 869	37	1.5	113744	2	AC008884	Homo sapi
C 870	37	1.5	113872	9	HS57G9	Homo sapi
C 871	37	1.5	114127	9	AC008683	Homo sapi
C 872	37	1.5	114467	9	AP000462	Homo sapi
C 873	37	1.5	116106	2	AL162611	Homo sapi
C 874	37	1.5	116457	9	AL137845	Homo sapi
C 875	37	1.5	117160	9	AC021803	Homo sapi
C 876	37	1.5	118929	2	AC025976	Homo sapi
C 877	37	1.5	119104	9	AL157788	Homo sapi
C 878	37	1.5	119238	9	AC078871	Homo sapi
C 879	37	1.5	119249	9	AC114810	Homo sapi
C 880	37	1.5	119350	9	HS12803	Homo sapi
C 881	37	1.5	119638	9	AC024575	Homo sapi
C 882	37	1.5	120664	9	AP000887	Homo sapi
C 883	37	1.5	122279	9	HS215D11	Homo sapi
C 884	37	1.5	122289	9	AL389925	Homo sapi
C 885	37	1.5	123230	9	HS215E10	Homo sapi
C 886	37	1.5	124343	2	AC079188	Homo sapi
C 887	37	1.5	125304	9	AC008044	Homo sapi
C 888	37	1.5	125515	2	AC100803	Homo sapi
C 889	37	1.5	126779	9	AL603882	Homo sapi
C 890	37	1.5	127565	2	AL161611	Homo sapi
C 891	37	1.5	128379	9	HS0J73A18	Homo sapi
C 892	37	1.5	128615	2	AL450329	Homo sapi
C 893	37	1.5	129423	9	AC006362	Homo sapi
C 894	37	1.5	129641	9	AC008560	Homo sapi
C 895	37	1.5	129898	9	AC104008	Homo sapi
C 896	37	1.5	129992	9	AL354897	Homo sapi
C 897	37	1.5	130020	9	HUAC004525	Homo sapi
C 898	37	1.5	130572	2	AC024096	Homo sapi
C 899	37	1.5	130985	9	HS243213	Homo sapi
C 900	37	1.5	131607	9	HS894K16	Homo sapi
C 901	37	1.5	131839	9	AC112166	Homo sapi
C 902	37	1.5	133475	9	AC006254	Homo sapi
C 903	37	1.5	133683	2	AC084857	Homo sapi
C 904	37	1.5	134030	2	AF064861	Homo sapi
C 905	37	1.5	134514	2	AC025192	Homo sapi
C 906	37	1.5	134814	2	AL831787	Homo sapi
C 907	37	1.5	135046	9	HSU91325	Homo sapi
C 908	37	1.5	135202	2	AC124061	Homo sapi
C 909	37	1.5	135240	9	AL136362	Homo sapi
C 910	37	1.5	136021	9	AL662799	Homo sapi
C 911	37	1.5	136372	9	AC103828	Homo sapi
C 912	37	1.5	136655	9	AC004843	Homo sapi
C 913	37	1.5	137074	9	AF130248	Homo sapi
C 914	37	1.5	138613	9	AC092538	Homo sapi
C 915	37	1.5	138969	9	AC104600	Homo sapi
C 916	37	1.5	139035	9	AC113996	Homo sapi
C 917	37	1.5	139388	9	AC007666	Homo sapi
C 918	37	1.5	139388	9	AC007666	Homo sapi
C 919	37	1.5	139971	9	AC007425	Homo sapi
C 920	37	1.5	140053	2	AC007873	Homo sapi
C 921	37	1.5	140469	2	AC025066	Homo sapi
C 922	37	1.5	140469	2	AC025066	Homo sapi
C 923	37	1.5	141119	2	AC027324	Homo sapi
C 924	37	1.5	141222	2	AC034224	Homo sapi
C 925	37	1.5	141339	9	AL1356318	Homo sapi
C 926	37	1.5	141905	9	CNS01DUL	Homo sapi
C 927	37	1.5	141905	9	CNS01DUL	Homo sapi
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C 930	37	1.5	142281	9	AL157397	Homo sapi
C 931	37	1.5	142326	2	AC024047	Homo sapi
C 932	37	1.5	142357	9	AC011416	Homo sapi
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946	37	1.5	145253	9	AC006329	Homo sapi
947	37	1.5	145538	9	HS245G319	
948	37	1.5	145616	9	HS108K11	
949	37	1.5	145899	2	AC016611	Homo sapi
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971	37	1.5	153023	2	AL355880	Homo sapi
972	37	1.5	153026	9	AL391280	Human DNA
973	37	1.5	153081	9	AC009774	Homo sapi
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980	37	1.5	153900	2	AC092525	Papio cyn
981	37	1.5	154470	2	AC027820	Homo sapi
982	37	1.5	155084	9	AC008753	Homo sapi
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992	37	1.5	156897	9	AC018782	Homo sapi
993	37	1.5	157248	9	AC002312	Human Chr
994	37	1.5	157324	9	AC013643	Homo sapi
995	37	1.5	157750	2	AC006097	Homo sapi
996	37	1.5	157807	9	AC037573	Homo sapi
997	37	1.5	157814	2	AC037460	Homo sapi
998	37	1.5	157978	2	AP001444	Homo sapi
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ALIGNMENTS

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LOCUS	AF123653				
DEFINITION	Homo sapiens FEZ1 (FEZ1) gene, complete cds.				
ACCESSION	AF123653				
VERSION	AF123653.1				
KEYWORDS	GI:4572463				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				

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Qy	481	TGAGGACCCAGGACCTGGAGGGCCCTGCGCACCAAGGGCTCGAGCTGAGGTCTGTG	540
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Qy	541	AGATGAGCTGCAGCGCAAGAAAGACGAGCGGAGCTGCTGCGGGAGAAAGTGAACCTGC	600
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Qy	721	TGCGGAGGAGCGCAAGGCCATGACAGATGTCTCCGGGCTTCAGCATGAGCGGCTCG	780
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Qy	901	ACAGCGCGGGAGCCCTTGAGAGTTGACCTGGAAGGGGCTGACATCCCTACGAGGACA	960
Db	5474	ACAGCGCGGGAGCCCTTGAGAGTTGACCTGGAAGGGGCTGACATCCCTACGAGGACA	5533
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Db	5534	TCATAGCCACTGAGATCTGAGGGGCTGCTGGAGAGCGAGTCTGGGGACCTGGCACTGG	5593
Qy	1021	GAGCAGGGCTCTCCCGTGATCCCGCTGCTCAGCAATTCAGACCCCTCTGAGAGACGC	1080
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Db	5714	TCCTGTATGTCCAGTCTCAGAGCCCTGAGGCCACAGACCTGAGGCCCTGACTCCT	5773
Qy	1201	CTGGCTTTCCAGGAGATGGTCCAGGGTCTGTCTGCTTGTGTTAAGGGCTCCCTAAAC	1260
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RESULT 2
AF123659
LOCUS

AF123659 5492 bp mRNA linear PRI 07-APR-1999

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DEFINITION Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.
ACCESSION AF123659
VERSION AF123659.1 GI:4572475
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5492)
AUTHORS Ichihi.H., Baffa.R., Numata,S.I., Murakumo.Y., Rattan,S., Inoue,H.,
            Mori.M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
            and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 5492)
AUTHORS Ichihi.H., Baffa.R., Numata,S.I., Murakumo.Y., Rattan,S., Inoue,H.,
            Mori.M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
            Institute, 233S 10th street, Philadelphia, PA 19107, USA
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        /map="8p22"
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     112..1902
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        /db_xref="GI:4572476"
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        ELKPLGSLGALSDGRMSLSLTHSTSSITOLDPLVTPVPTSPRFGSAHNTQGLV
        LODSNMMSLKALSPDSGLGSHNKADKGPSCVRSPISTDECSIQLEOKLLERGA
        LKQRFSEELASLAYERPRRCRDELPKPGKNLQKASQSORAQOVLHIQ
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        LLKQLESOTEVNAKASEILGLAQLKDTGKLEGLRLTDLEGALRTKGLLEVC
        ENELQRKNEALLREKVNILLEQLRAQALARDMPPTPEDVPALQRELERLR
        AELREKQHDQMSGFGOHERKLVWKEKERYIQKQLQGSYVAMYNORLEKALQQ
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BASE COUNT 1137 a 1704 c 1565 g 1086 t
ORIGIN
Query Match      81.8%; Score 1966; DB 9; Length 5492;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2066; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 397 CGGAGGTGAACGCCAAGCTGACGAGATCTCTGGGTCTCAAGGCACAGCTGAAGGACAGC 456
DB 1319 CGGAGGTGAACGCCAAGCTGACGAGATCTCTGGGTCTCAAGGCACAGCTGAAGGACAGC 1378
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DB 1379 GGGCAAGCTCGAGGCTCGAGCTGAGGACCCAGGACCTGAGGGGCCCTCGCGCACCA 1438
QY 517 AGGGCTCGAGCTGAGGCTCTGTGAGATGAGCTGACGCGCAAGAAAGAACGAGCGGAGC 576
DB 1439 AGGGCTCGAGCTGAGGCTCTGTGAGATGAGCTGACGCGCAAGAAAGAACGAGCGGAGC 1498
QY 577 TGCTCGGGAGAGAGGTGAACCTGCTGGAGCAGGAGCTGACGAGCTCGGGGCCCGAGCCG 636
DB 1499 TGCTCGGGAGAGAGGTGAACCTGCTGGAGCAGGAGCTGACGAGCTCGGGGCCCGAGCCG 1558

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Db 2699 GGGTCTGGGAGGAGGTTGAACACCACTGTAACAGAGGGTGTGGCTTCCAGGAC 2758
Qy 1837 CCTCAGGAGCCTCCCATCTGTCCAGCTGGGGCCAGAGGCTGGAGTCCCTACTCTCTT 1896
Db 2759 CCTCAGGAGCCTCCCATCTGTCCAGCTGGGGCCAGAGGCTGGAGTCCCTACTCTCTT 2818
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Db 2819 CAGTTGGCGGGCTACTCTGGAATGTTTTTCCCTCCAGAGTCCAGAGTCTTGTCTTG 2878
Qy 1957 ATCCAGAAGACCCATATCACTAGATGGCATATGTGATCTGGGCAATTTCTCTCTCT 2016
Db 2879 ATCCAGAAGACCCATATCACTAGATGGCATATGTGATCTGGGCAATTTCTCTCTCT 2938
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Qy 2137 GAAAAGAGCCATACACAGCAGTGTGAATAGCTGGCCAGCCAGCCATCTCCCTCCAC 2196
Db 3059 GAAAAGAGCCATACACAGCAGTGTGAATAGCTGGCCAGCCAGCCATCTCCCTCCAC 3118
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DEFINITION IN PROGRESS ***, 3 unordered pieces.
AC025853
VERSION AC025853.13 GI:21431202
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
Boguslavskiy,L., Boukhaltier,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collimore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N.,
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Meneus,L., Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C.,
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O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupbach,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Straus,N., Subramanian,A., Talanas,J., Testaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,C., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talanas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE

JOURNAL

Submitted (16-WAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

3 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhaltier,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collimore,A., Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C., Nicoli,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talanas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 17, 2002 this sequence version replaced gi:21321864.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L7454

Center clone name: 353_K12

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved

* 1 39461: contig of 39461 bp in length

* 39462 39561: gap of 100 bp

* 39562 108347: contig of 68786 bp in length

* 108348 108447: gap of 100 bp

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Location/Qualifiers

1. 173264

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FEATURES

source

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DEFINITION complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1722)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1722)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1692)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1692)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1614)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1614)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
JOURNAL Institute, 233S 10th street, Philadelphia, PA 19107, USA
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LOCUS Homo sapiens clone D14 FEZ1 (FEZ1) mRNA, alternatively spliced,
DEFINITION complete cds.
ACCESSION AF123656
VERSION AF123656.1 GI:4572469
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1515)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
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and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1515)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
JOURNAL Institute, 233S 10th street, Philadelphia, PA 19107, USA
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Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 939 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCT 990
Db 87977 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCT 88028

RESULT 11
AC099416/c
LOCUS AC099416 263546 bp DNA linear HTG 23-MAY-2002
DEFINITION Mus musculus chromosome UNK clone RP23-122M11, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
AC099416
VERSION AC099416.2 GI:21105058
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
2 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (14-NOV-2001) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On May 23, 2002 this sequence version replaced gi:16924178.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
----- Project Information -----
Center project name: M BA0122M11
----- Summary Statistics -----
Sequencing vector: M13; 32%
Sequencing vector: plasmid; 68%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 278310 bases at least Q40
Consensus quality: 282938 bases at least Q30
Consensus quality: 286149 bases at least Q20
Insert size: 250000; agarose-fp
Insert size: 387570; sum-of-contigs
Quality coverage: 25.74 in Q20 bases; agarose-fp
Quality coverage: 16.86 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently

```

* consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

* 1 1204: contig of 1204 bp in length
* 1205 1304: gap of unknown length
* 1305 2524: contig of 1220 bp in length
* 2525 2624: gap of unknown length
* 2625 4136: contig of 1512 bp in length
* 4137 4236: gap of unknown length
* 4237 16434: contig of 12198 bp in length
* 16435 32106: gap of unknown length
* 32107 32206: contig of 15572 bp in length
* 32207 140224: contig of 108018 bp in length
* 140225 140324: gap of unknown length
* 140325 262693: contig of 122369 bp in length
* 262694 262793: gap of unknown length
* 262794 263546: contig of 753 bp in length.

```

FEATURES

source

```

1..263546
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-122M11"

```

misc_feature

```

1..1204
/note="assembly_name:Contig127"

```

misc_feature

```

1305..2524
/note="assembly_name:Contig157"

```

misc_feature

```

2625..4136
/note="assembly_name:Contig360"

```

misc_feature

```

4237..16434
/note="assembly_name:Contig396"

```

misc_feature

```

16535..32106
/note="assembly_name:Contig397"

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misc_feature

```

32207..140224
/note="assembly_name:Contig398"

```

misc_feature

```

140325..262693
/note="assembly_name:Contig399"

```

misc_feature

```

262794..263546
/note="assembly_name:Contig154"

```

BASE COUNT

```

76628 a 56149 c 55623 g 74436 t 710 others
ORIGIN

```

Query Match

```

2.2%; Score 52; DB 2; Length 263546;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY

```

939 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCT 990

```

Db

```

246909 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCT 246958

```

RESULT 12

AC093491

LOCUS

```

AC093491 162178 bp DNA linear PRI 02-NOV-2001

```

DEFINITION

```

Homo sapiens chromosome 16 clone RP11-410N2, complete sequence.

```

ACCESSION

```

AC093491 AC024237

```

VERSION

```

AC093491.2 GI:16596544

```

KEYWORDS

```

HTG.

```

SOURCE

```

Homo sapiens.

```

ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

```

1 (bases 1 to 162178)
DOE Joint Genome Institute.

```

AUTHORS

```

Sequencing of Human Chromosome 16

```

TITLE

```

Unpublished

```

JOURNAL

```

2 (bases 1 to 162178)
DOE Joint Genome Institute.

```

REFERENCE

```

2 (bases 1 to 162178)
DOE Joint Genome Institute.

```

AUTHORS

```

DOE Joint Genome Institute.

```

TITLE Direct Submission
JOURNAL Submitted (28-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 162178)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 2, 2001 this sequence version replaced gi:15320919.

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

FEATURES
source Location/Qualifiers
1. 162178
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-410N2"
BASE COUNT 41546 a 39076 c 39454 g 42102 t
ORIGIN

Query Match 2.0%; Score 49; DB 9; Length 162178;
Best Local Similarity 100.0%; Pred. No. 4.6e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACTACACCCAGCCT 54
DB 100265 GGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACTACACCCAGCCT 100313

RESULT 13
AC012184/c
LOCUS AC012184 195952 bp DNA linear PRI 07-MAY-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-529K1, complete sequence.
ACCESSION AC012184.6 GI:20486391
VERSION
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 195952)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 195952)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 195952)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On May 7, 2002 this sequence version replaced gi:13786348.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

FEATURES
source Location/Qualifiers
1. 195952
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-529K1"
BASE COUNT 48977 a 48735 c 48253 g 49987 t
ORIGIN

Query Match 2.0%; Score 49; DB 9; Length 195952;
Best Local Similarity 100.0%; Pred. No. 4.6e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACTACACCCAGCCT 54
DB 32583 GGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACTACACCCAGCCT 32535

RESULT 14
AL391314
LOCUS AL391314 129435 bp DNA linear PRI 06-DEC-2001
DEFINITION Human DNA sequence from clone RP11-477H7 on chromosome 10, complete sequence.
ACCESSION AL391314.21 GI:17426471
VERSION
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 129435)
AUTHORS Tracey, A.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
COMMENT On Dec 8, 2001 this sequence version replaced gi:17402352. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP

database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>
 RP11-477H7 is from the library RPI-11.2 constructed by the group
 of Pictet de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone
 RP11-477H7 It may be shorter because we sequence overlapping
 sections only once, except for a short overlap.
 The true right end of clone RP11-477H7 is at 129435 in this
 sequence. The true left end of clone RP11-481B7 is at 30248 in this
 sequence. The true right end of clone RP11-186N15 is at 2000 in
 this sequence.

FEATURES
 source
 1..129435
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-477H7"
 /clone_lib="RPI-11.2"
 99418..99422
 /note="Sequence from uni-directional dGTP big dye
 terminator reads only."
 misc_feature
 32508 a 29205 c 30709 g 37013 t

Query Match 1.8%; Score 43; DB 9; Length 129435;
 Best Local Similarity 100.0%; Pred. No. 9.7e-12;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GGGGAGCGGAGGTTGCAGTCAGCCAGATCAGCCACTACAC 46
 |||||
 Db 92566 GGGGAGCGGAGGTTGCAGTCAGCCAGATCAGCCACTACAC 92508

RESULT 15
 AC084688/c
 LOCUS
 DEFINITION Homo sapiens chromosome 1 clone RP11-25F12 map 1, WORKING DRAFT
 SEQUENCE, 41 unordered pieces.

AC084688
 AC084688.2 GI:11875300
 HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE
 human.

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 140179)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 1, clone RP11-25F12
 Unpublished

2 (bases 1 to 140179)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Bida,F., Boguslavskiy,L.,
 Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
 Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
 FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
 Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
 Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
 Lamazares,R., Landers,T., Leoczky,J., Levine,R., Lieu,C., Liu,G.,
 Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
 McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
 O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
 Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
 Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
 Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Submitted (05-NOV-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 140179)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
 Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
 Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
 Leoczky,J., Levine,R., Liu,G., Maclean,C., Macdonald,P.,
 Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
 McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
 Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
 Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
 Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Dec 16, 2000 this sequence version replaced gi:11095466.
 All repeats were identified using RepeatMasker:
 Smit, A.P.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L11244
 Center clone name: 25_F_12

Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 122426 bases at least Q40
 Consensus quality: 130754 bases at least Q30
 Consensus quality: 133913 bases at least Q20
 Insert size: 165000; agarose-fp
 Insert size: 136179; sum-of-contigs
 Quality coverage: 3.4 in Q20 bases; agarose-fp
 Quality coverage: 4.2 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 41 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1280: contig of 1280 bp in length
 * 1381 1380: gap of 100 bp
 * 1381 2040: contig of 660 bp in length
 * 2041 2140: gap of 100 bp
 * 2141 2814: contig of 674 bp in length
 * 2815 2914: gap of 100 bp
 * 2915 3574: contig of 660 bp in length
 * 3575 3674: gap of 100 bp
 * 3675 4354: contig of 680 bp in length
 * 4355 4454: gap of 100 bp

```

* 4455 5092: contig of 638 bp in length
* 5093 5192: gap of 100 bp
* 5193 5842: contig of 850 bp in length
* 5843 5942: gap of 100 bp
* 5943 6720: contig of 778 bp in length
* 6721 6820: gap of 100 bp
* 6821 7633: contig of 813 bp in length
* 7634 7733: gap of 100 bp
* 7734 8605: contig of 872 bp in length
* 8606-8705: gap of 100 bp
* 8706 9428: contig of 723 bp in length
* 9429 9528: gap of 100 bp
* 9529 10366: contig of 838 bp in length
* 10367 10466: gap of 100 bp
* 10467 11579: contig of 1113 bp in length
* 11580 11679: gap of 100 bp
* 11680 12821: contig of 1142 bp in length
* 12822 12921: gap of 100 bp
* 12922 14646: contig of 1725 bp in length
* 14647 14746: gap of 100 bp
* 14747 27804: contig of 13058 bp in length
* 27805 27904: gap of 100 bp
* 27905 29117: contig of 1213 bp in length
* 29118 29217: gap of 100 bp
* 29218 30146: contig of 929 bp in length
* 30147 30246: gap of 100 bp
* 30247 32128: contig of 1882 bp in length
* 32129 32228: gap of 100 bp
* 32229 33798: contig of 1570 bp in length
* 33799 33898: gap of 100 bp
* 33899 35326: contig of 1428 bp in length
* 35327 35426: gap of 100 bp
* 35427 37354: contig of 1928 bp in length
* 37355 37454: gap of 100 bp
* 37455 39096: contig of 1642 bp in length
* 39097 39196: gap of 100 bp
* 39197 40669: contig of 1473 bp in length
* 40670 40769: gap of 100 bp
* 40770 43457: contig of 2688 bp in length
* 43458 43557: gap of 100 bp
* 43558 45192: contig of 1635 bp in length
* 45193 45292: gap of 100 bp
* 45293 47751: contig of 2459 bp in length
* 47752 47851: gap of 100 bp
* 47852 51681: contig of 3830 bp in length
* 51682 51781: gap of 100 bp
* 51782 54378: contig of 2597 bp in length
* 54379 54478: gap of 100 bp
* 54479 57216: contig of 2738 bp in length
* 57217 57316: gap of 100 bp
* 57317 62124: contig of 4808 bp in length
* 62125 62224: gap of 100 bp
* 62225 65448: contig of 3224 bp in length
* 65449 65548: gap of 100 bp
* 65549 70639: contig of 5091 bp in length
* 70640 70739: gap of 100 bp
* 70740 76462: contig of 5723 bp in length
* 76463 76562: gap of 100 bp
* 76563 84079: contig of 7517 bp in length
* 84080 84179: gap of 100 bp
* 84180 91013: contig of 6834 bp in length
* 91014 91113: gap of 100 bp
* 91114 101538: contig of 10422 bp in length
* 101539 101638: gap of 100 bp
* 101639 109093: contig of 7458 bp in length
* 109094 109193: gap of 100 bp
* 109194 125678: contig of 16485 bp in length
* 125679 125778: gap of 100 bp
* 125779 139277: contig of 13493 bp in length
* 139278 139377: gap of 100 bp
* 139378 140179: contig of 802 bp in length.
Location/Qualifiers
1. .140179

```

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chrnosome="1"
/map="1"
/clone="RP11-25F12"
/clone_lib="RPC1-11 Human Male BAC"
1. .1280
/note="assembly_fragment"
clone_end:SP6
vector_side:left
1381. .2040
/note="assembly_fragment"
2141. .2814
/note="assembly_fragment"
2915. .3574
/note="assembly_fragment"
3675. .4354
/note="assembly_fragment"
4455. .5092
/note="assembly_fragment"
5193. .5842
/note="assembly_fragment"

Query Match 1.8%; Score 43; DB 2; Length 140179;
Best Local Similarity 100.0%; Pred.No. 9.7e-12;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGGGAGCGGAGGTTGCGAGTGAGCCCAAGATCAGCCCACTACAC 46
Db 131623 GGGGAGCGGAGGTTGCGAGTGAGCCCAAGATCAGCCCACTACAC 131581
|||||

```

Search completed: June 17, 2003, 03:57:56
Job time : 4484.72 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.									
OM nucleic - nucleic search, using sw model									
Run on: June 16, 2003, 11:19:01 ; Search time 424.399 Seconds (without alignments) 12756.396 Million cell updates/sec									
Title: US-09-513-888C-1_COPY_4514_6917									
Perfect score: 2404									
Sequence: 1 agagggagcggaggtgc.....gacagggtctgtctgtctc 2404									
Scoring table: OLIGO NUC									
Gapop 60.0 , Gapext 60.0									
Searched: 2185239 seqs, 1125999159 residues									
Word size : 0									
Total number of hits satisfying chosen parameters: 4370478									
Minimum DB seq length: 0									
Maximum DB seq length: 2000000000									
Post-processing: Listing first 1000 summaries									
Database : N Geneseq_101002.*									
1: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*									
2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*									
3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*									
4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*									
5: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*									
6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*									
7: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*									
8: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*									
9: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*									
10: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*									
11: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*									
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24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result	Query	Match	Length	DB	ID	Description			
No.									
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2	1966	81.8	5492	21	AAA64508	cdna sequence of t			
3	644	26.8	1791	21	AAA64509	cdna sequence enco			
4	373	15.5	1722	21	AAA64515	Nucleotide sequenc			
5	283	11.8	1692	21	AAA64514	Nucleotide sequenc			
6	254	10.6	1614	21	AAA64512	Nucleotide sequenc			
7	249	10.4	404	21	AAA64510	Nucleotide sequenc			
8	219	9.1	1512	21	AAA64513	Nucleotide sequenc			
9	80	3.3	633	21	AAA64511	Nucleotide sequenc			

83	36	1.5	1655	22	AAL35996	Human musculooskele	c 156	33	1.4	14260	22	AAK83183	Human immune/haema
c 84	36	1.5	2031	22	ABA09088	Human secreted pro	c 157	33	1.4	14260	22	AAK83217	Human immune/haema
c 86	36	1.5	2432	22	AAH18662	Human cDNA sequenc	c 158	33	1.4	15295	22	AAL37039	Human musculooskele
c 87	36	1.5	3819	22	AAH18644	Human cDNA sequenc	c 159	33	1.4	15364	22	AAK83152	Human immune/haema
c 88	36	1.5	10912	22	AAK72629	Human immune/haema	c 160	33	1.4	15772	22	AAK83220	Human immune/haema
c 89	36	1.5	15037	22	AAI99283	Human excretory re	c 161	33	1.4	18488	22	AAK83173	Human immune/haema
c 90	36	1.5	15037	22	AAI63633	Human kidney relat	c 162	33	1.4	31405	22	AAK67293	Human immune/haema
c 91	36	1.5	22655	22	AAK70122	Human immune/haema	c 163	33	1.4	31405	22	AAK74865	Human immune/haema
c 92	36	1.5	30110	22	AAK89230	Human digestive sy	c 164	33	1.4	31405	22	AAK83153	Human immune/haema
c 93	36	1.5	33923	22	AAK67071	Human immune/haema	c 165	33	1.4	33147	22	AAK67282	Human immune/haema
c 94	35	1.5	168	22	ABA14469	Human nervous syst	c 166	33	1.4	68356	22	AAK67283	Human immune/haema
c 95	35	1.5	318	24	ABL80033	Human ovarian canc	c 167	33	1.4	68356	22	AAK83212	Ovary cancer relat
c 96	35	1.5	383	21	AAL22590	Human secreted pro	c 168	33	1.4	174424	24	ABL68122	Human immune/haema
c 97	35	1.5	416	24	ABL68776	Kidney cancer rela	c 169	32	1.3	112	22	AAK78243	Human immune/haema
c 98	35	1.5	488	22	AAI92918	Human polynucleoti	c 170	32	1.3	143	21	AAK20411	Human secreted pro
c 99	35	1.5	564	22	AAL22733	Human breast cance	c 171	32	1.3	146	21	AAC20386	Human secreted pro
c 100	35	1.5	570	22	AAH10591	Human cDNA clone (c 172	32	1.3	167	22	AAK79634	Human immune/haema
c 101	35	1.5	657	22	AAF22599	Human breast cance	c 173	32	1.3	271	22	AAK78277	Human immune/haema
c 102	35	1.5	2021	22	AAH15705	Human cDNA sequenc	c 174	32	1.3	309	21	AAC13762	Human secreted pro
c 103	35	1.5	2849	22	AAH14716	Human cDNA sequenc	c 175	32	1.3	309	21	AAC14038	Human secreted pro
c 104	35	1.5	2857	22	AAH17701	Human cDNA sequenc	c 176	32	1.3	338	24	ABL86327	Human ovarian canc
c 105	35	1.5	4397	22	AAK84921	Human immune/haema	c 177	32	1.3	370	22	AAL89800	Human polynucleoti
c 106	35	1.5	8911	22	ABA06809	Human genomic DNA	c 178	32	1.3	406	21	AAC28834	Human secreted pro
c 107	35	1.5	8911	22	AAS41748	Genomic sequence #	c 179	32	1.3	414	24	ABL85195	Human ovarian canc
c 108	35	1.5	14103	22	AAI99350	Human excretory re	c 180	32	1.3	449	24	ABL85964	Human ovarian canc
c 109	35	1.5	14103	22	AAK81278	Human immune/haema	c 181	32	1.3	455	24	ABL83611	Human ovarian canc
c 110	35	1.5	29629	24	ABL58699	Human kidney relat	c 182	32	1.3	503	23	ABV48891	Human prostate exp
c 111	35	1.5	32082	22	AAL06991	Human kinase encod	c 183	32	1.3	517	23	ABV38966	Human prostate exp
c 112	35	1.5	32184	22	AAL05850	Human reproductive	c 184	32	1.3	551	23	ABV05711	Human prostate exp
c 113	35	1.5	32184	23	ABL98414	Human reproductive	c 185	32	1.3	554	24	ABN63242	Human cancer relat
c 114	35	1.5	32204	22	AAI05849	Human testicular a	c 186	32	1.3	560	23	ABV05765	Human prostate exp
c 115	35	1.5	32204	23	ABL05849	Human reproductive	c 187	32	1.3	586	23	ABV02013	Human prostate exp
c 116	35	1.5	38358	22	AAK73535	Human testicular a	c 188	32	1.3	600	23	ABV14934	Human prostate exp
c 117	35	1.5	38771	22	AAK81036	Human immune/haema	c 189	32	1.3	611	23	ABV11182	Human prostate exp
c 118	35	1.5	160552	21	AAD02697	Human glycosyl sul	c 190	32	1.3	637	23	ABV39019	Human prostate exp
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c 120	35	1.5	227968	24	ABK83497	Human cDNA differe	c 192	32	1.3	661	23	ABV41258	Human prostate exp
c 121	34	1.4	339	22	AAI80178	Human polynucleoti	c 193	32	1.3	661	23	ABV44754	Human prostate exp
c 122	34	1.4	1401	22	AAK82687	Human immune/haema	c 194	32	1.3	681	22	ABV44806	Human prostate exp
c 123	34	1.4	2204	21	AAAS3270	Human phospholipas	c 195	32	1.3	792	24	ABQ89530	Human immune/haema
c 124	34	1.4	5629	23	ABK42275	Genomic sequence #	c 196	32	1.3	838	23	ABQ81480	Human prostate exp
c 125	34	1.4	6265	23	ABK42274	Genomic sequence #	c 197	32	1.3	1154	21	AAH51628	Human prostate exp
c 126	34	1.4	8517	21	AAZ88756	Human PLA2 DNA. H	c 198	32	1.3	1301	21	AAH51627	Human g35018 cDNA
c 127	34	1.4	8517	22	AAK90487	Human phospholipas	c 199	32	1.3	1386	21	AAH51631	Human g35018 cDNA
c 128	34	1.4	8517	22	AAK74998	Phospholipase A2 (c 200	32	1.3	1412	22	AAK85854	Human immune/haema
c 129	34	1.4	11837	22	AAK99070	Human digestive sy	c 201	32	1.3	1412	22	AAK85855	Human immune/haema
c 130	34	1.4	11837	22	AAS33429	DNA encoding human	c 202	32	1.3	1669	21	AAK65263	Human secreted pro
c 131	34	1.4	302250	24	ABL67703	Oesophagus cancer	c 203	32	1.3	1754	22	AAK94142	Human full-length
c 132	33	1.4	550	22	AAH13500	Human cDNA clone (c 204	32	1.3	2113	22	AAH17397	Human cDNA sequenc
c 133	33	1.4	2088	22	AAH16743	Human cDNA sequenc	c 205	32	1.3	2133	22	AAH17953	Human cDNA sequenc
c 134	33	1.4	3956	22	ABA21203	Human nervous syst	c 206	32	1.3	2205	22	AAK68629	Human immune/haema
c 135	33	1.4	4283	22	AAK83180	Human immune/haema	c 207	32	1.3	2571	22	AAL35850	Human musculooskele
c 136	33	1.4	6286	22	AAK83148	Human immune/haema	c 208	32	1.3	2571	22	AAL35851	Human musculooskele
c 137	33	1.4	6751	22	AAK83163	Human immune/haema	c 209	32	1.3	4316	22	AAK82458	Human musculooskele
c 138	33	1.4	7633	22	AAK83159	Human immune/haema	c 210	32	1.3	4316	22	AAK82461	Human lung antigen
c 139	33	1.4	7858	22	AAK67290	Human immune/haema	c 211	32	1.3	2892	22	AAS29933	Genomic sequence #
c 140	33	1.4	7858	22	AAK83149	Human immune/haema	c 212	32	1.3	3351	23	ABK42251	Human nervous syst
c 141	33	1.4	7906	22	AAK83154	Human immune/haema	c 213	32	1.3	4288	22	ABA20895	Human immune/haema
c 142	33	1.4	8331	22	AAK67308	Human immune/haema	c 214	32	1.3	4288	22	AAK69392	Human immune/haema
c 143	33	1.4	8331	22	AAK83167	Human immune/haema	c 215	32	1.3	4316	22	AAK82458	Human immune/haema
c 144	33	1.4	9133	22	AAK83165	Human immune/haema	c 216	32	1.3	4317	22	AAK82456	Human immune/haema
c 145	33	1.4	9217	22	AAK83151	Human immune/haema	c 217	32	1.3	4512	22	ABA07396	Human pancreatic c
c 146	33	1.4	9439	22	AAK67312	Human immune/haema	c 218	32	1.3	4512	22	ABA07394	Human digestive sy
c 147	33	1.4	9439	22	AAK83168	Human immune/haema	c 219	32	1.3	4512	22	AAK89941	Human bone marrow
c 148	33	1.4	9832	22	AAK83150	Human immune/haema	c 220	32	1.3	4864	22	ABA09670	Human immune/haema
c 149	33	1.4	10497	22	AAK67302	Human immune/haema	c 221	32	1.3	5577	22	AAK79789	Human immune/haema
c 150	33	1.4	10497	22	AAK83166	Human immune/haema	c 222	32	1.3	5632	23	ABL04707	Human reproductive
c 151	33	1.4	11428	22	AAK83156	Human immune/haema	c 223	32	1.3	5632	23	ABL97614	Human testicular a
c 152	33	1.4	11744	22	AAK83160	Human immune/haema	c 224	32	1.3	6943	22	AAK83198	Human immune/haema
c 153	33	1.4	11853	22	AAK67297	Human immune/haema	c 225	32	1.3	8606	22	AAK80122	Human immune/haema
c 154	33	1.4	11853	22	AAK83162	Human immune/haema	c 226	32	1.3	13315	22	ABA07371	Human pancreatic c
c 155	33	1.4	14258	22	AAK83210	Human immune/haema	c 227	32	1.3	13315	22	AAS30064	Human lung antigen
c 155	33	1.4	14258	22	AAK83210	Human immune/haema	c 228	32	1.3	13315	22	AAK65415	Human immune/haema

229	32	1.3	13315	22	AAK91102	Human digestive sy	c 302	31	1.3	760	22	AAI244464	Human breast cance
c 230	32	1.3	13409	22	ABA08135	Human ovarian and	c 303	31	1.3	792	22	AAH04417	Human cDNA clone (
c 231	32	1.3	13409	22	AAI06913	Human reproductive	c 304	31	1.3	952	24	ABA96565	Human tyrosinase 9
c 232	32	1.3	13912	22	AAK82686	Human immune/haema	c 305	31	1.3	1074	22	AAK80190	Human immune/haema
c 233	32	1.3	14543	24	ABK15798	Human von Hippel-L	c 306	31	1.3	1074	22	AAK80191	Human immune/haema
c 234	32	1.3	14598	22	AAK79627	Human immune/haema	c 307	31	1.3	1332	21	AAK79685	Human secreted pro
c 235	32	1.3	14598	22	AAK80690	Human immune/haema	c 308	31	1.3	1484	24	ABA96607	Human hexokinase p
c 236	32	1.3	14718	22	AAI03293	Human reproductive	c 309	31	1.3	1497	22	AAK87499	Human immune/haema
c 237	32	1.3	16062	22	AAI05359	Human reproductive	c 310	31	1.3	1548	22	AAH15300	Human cDNA sequenc
c 238	32	1.3	16062	23	ABL98228	Human testicular a	c 311	31	1.3	1552	22	AAH15300	Human secreted pro
c 239	32	1.3	19696	22	AAK40722	DNA encoding human	c 312	31	1.3	1593	21	AAK79951	Human secreted pro
c 240	32	1.3	19696	22	AAI06639	Human reproductive	c 313	31	1.3	1682	21	AAK72218	Human 251967 cDNA.
c 241	32	1.3	20261	22	ABA07368	Human pancreatic c	c 314	31	1.3	1755	22	AAK67934	Human immune/haema
c 242	32	1.3	20261	22	AAK30061	Human lung antigen	c 315	31	1.3	1856	22	AAH44344	Human DNA polymera
c 243	32	1.3	20261	22	AAK65412	Human immune/haema	c 316	31	1.3	2194	22	AAI04793	Human reproductive
c 244	32	1.3	20261	22	AAK91099	Human digestive sy	c 317	31	1.3	2194	22	ABL97687	Human testicular a
c 245	32	1.3	26496	22	ABAI9696	Human nervous syst	c 318	31	1.3	2195	22	AAI04794	Human reproductive
c 246	32	1.3	27154	22	AAI05708	Human reproductive	c 319	31	1.3	2195	23	ABL97688	Human testicular a
c 247	32	1.3	28180	22	AAK68939	Human immune/haema	c 320	31	1.3	2197	22	AAI04795	Human reproductive
c 248	32	1.3	31168	22	ABA07295	Human pancreatic c	c 321	31	1.3	2197	23	ABL97689	Human testicular a
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c 250	32	1.3	31168	22	AAK527804	DNA encoding novel	c 323	31	1.3	2306	17	AAI31377	Human alpha-1C2 ad
c 251	32	1.3	31168	22	AAK64760	Human immune/haema	c 324	31	1.3	2422	22	AAH99069	Human EST-derived
c 252	32	1.3	31168	22	AAK89940	Human digestive sy	c 325	31	1.3	2624	22	AAH17299	Human cDNA sequenc
c 253	32	1.3	31813	22	ABA08137	Human ovarian and	c 326	31	1.3	2810	21	AAI20997	Human low adenosin
c 254	32	1.3	31813	22	AAI06997	Human reproductive	c 327	31	1.3	2810	21	AAK34875	Human adenosine re
c 255	32	1.3	34488	22	AAK97854	Human neuroblastom	c 328	31	1.3	3023	20	AAK03036	Human IL-1ra BAC c
c 256	32	1.3	44211	22	AAK85974	Human immune/haema	c 329	31	1.3	3045	20	AAI19787	Human cytochrome p
c 257	32	1.3	73465	24	ABQ88161	Human osteoblast d	c 330	31	1.3	3045	20	AAI207812	Human cytochrome p
c 258	32	1.3	106746	21	AAI10225	Human PCTA-1 genom	c 331	31	1.3	3045	24	ABN95821	Gene #2319 used to
c 259	32	1.3	121162	21	AAK66548	Human kinesin-like	c 332	31	1.3	3045	24	ABN95821	Lung cancer relate
c 260	32	1.3	143306	24	ABK49586	Human transporter	c 333	31	1.3	3286	21	AAI61870	Human ASE-1 cDNA.
c 261	32	1.3	154465	24	AAI28763	Human AKAP allelic	c 334	31	1.3	3593	22	AAI07532	Human GABA(b) rece
c 262	32	1.3	158245	24	AAI28762	Human AKAP allelic	c 335	31	1.3	3903	22	AAI28781	Human GABA(b) rece
c 263	32	1.3	161425	22	AAH02340	Human AKAP10 gene	c 336	31	1.3	4025	22	AAI355975	Human musculoskele
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c 265	32	1.3	162025	24	AAH028758	Human AKAP allelic	c 338	31	1.3	4025	22	AAI355980	Human musculoskele
c 266	32	1.3	162025	24	AAH28759	Human AKAP allelic	c 339	31	1.3	4082	22	AAK79954	Human immune/haema
c 267	32	1.3	167343	24	ABL64403	Stomach cancer rel	c 340	31	1.3	4082	22	AAK82476	Human immune/haema
c 268	32	1.3	167343	24	ABL67239	Thyroid cancer rel	c 341	31	1.3	4085	22	AAK79956	Human immune/haema
c 269	32	1.3	227968	24	ABK83497	Human cDNA differe	c 342	31	1.3	4085	22	AAK82478	Human immune/haema
c 270	32	1.3	319608	21	AAH51601	Human chromosome 1	c 343	31	1.3	4086	22	AAK79955	Human immune/haema
c 271	32	1.3	319608	22	AAH05301	Human chizophreni	c 344	31	1.3	4086	22	AAK82477	Human immune/haema
c 272	32	1.3	368004	24	ABK79909	Human transporter	c 345	31	1.3	4090	22	AAI35891	Human immune/haema
c 273	31	1.3	51	22	AAI73861	Human silent SNP c	c 346	31	1.3	4124	22	AAI01154	5'-untranslated re
c 274	31	1.3	51	22	AAI79585	Human silent SNP c	c 347	31	1.3	4169	21	AAK09331	Human cancer assoc
c 275	31	1.3	88	22	ABA19011	Human nervous syst	c 348	31	1.3	4171	22	AAH18676	Human cDNA sequenc
c 276	31	1.3	114	22	AAK31531	Human DNA for a no	c 349	31	1.3	4334	22	ABA07081	Human pancreatic c
c 277	31	1.3	114	22	ABQ66855	Human polynucleoti	c 350	31	1.3	4334	22	AAK89291	Human digestive sy
c 278	31	1.3	129	22	AAK70596	Human immune/haema	c 351	31	1.3	4380	22	ABA14731	Human nervous syst
c 279	31	1.3	139	22	AAK74457	Human immune/haema	c 352	31	1.3	4696	22	ABA07079	Human pancreatic c
c 280	31	1.3	146	22	AAK35889	Human cardiovascular	c 353	31	1.3	4696	22	AAK89289	Human digestive sy
c 281	31	1.3	153	21	AAI17493	Human secreted pro	c 354	31	1.3	4699	22	ABA07080	Human pancreatic c
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c 283	31	1.3	159	22	AAK39647	Genomic sequence #	c 356	31	1.3	4744	22	AAK65959	Human immune/haema
c 284	31	1.3	159	22	AAK89051	Human digestive sy	c 357	31	1.3	4745	22	AAK65958	Human immune/haema
c 285	31	1.3	165	22	AAK73573	Human immune/haema	c 358	31	1.3	4941	22	AAI98901	Human kidney relat
c 286	31	1.3	292	21	AAA45872	Human secreted exp	c 359	31	1.3	4941	22	AAI63251	Human immune/haema
c 287	31	1.3	341	21	AAK13943	Human secreted pro	c 360	31	1.3	4958	22	AAK67565	Human immune/haema
c 288	31	1.3	369	21	AAK76655	Human ORFX ORF210	c 361	31	1.3	4958	22	AAK68610	Human immune/haema
c 289	31	1.3	396	22	AAK66882	Novel human polynu	c 362	31	1.3	5102	24	ABK81380	Human immune/haema
c 290	31	1.3	417	21	AAK06169	Human secreted pro	c 363	31	1.3	5176	22	AAK66814	DNA encoding small
c 291	31	1.3	436	24	ABL77451	Human ovarian canc	c 364	31	1.3	5352	22	AAK04049	Human ABC1 gene, p
c 292	31	1.3	443	22	AAK70807	Human immune/haema	c 365	31	1.3	5702	22	ABA20798	Human nervous syst
c 293	31	1.3	450	22	ABN62921	Human cancer relat	c 366	31	1.3	6346	22	AAK74144	Human immune/haema
c 294	31	1.3	483	22	ABAI4579	Human nervous syst	c 367	31	1.3	6727	20	AAK02993	Human IL-1ra BAC c
c 295	31	1.3	493	22	AAI81410	Human polynucleoti	c 368	31	1.3	8902	24	ABL51551	Human NAG-1 promot
c 296	31	1.3	514	22	AAI15620	Human breast cance	c 369	31	1.3	9615	22	AAI36590	Human musculoskele
c 297	31	1.3	538	24	ABN62997	Human cancer relat	c 370	31	1.3	9691	22	AAK76929	Human immune/haema
c 298	31	1.3	585	22	AAH09225	Human cDNA clone (c 371	31	1.3	9732	22	AAI36439	Human musculoskele
c 299	31	1.3	693	22	AAK83933	BAP28 genomic ampl	c 372	31	1.3	9780	22	AAK72360	Human immune/haema
c 300	31	1.3	700	22	AAH92793	Human inflammatory	c 373	31	1.3	10119	22	AAK87559	Human immune/haema
c 301	31	1.3	745	24	ABK34389	Human cDNA for nov	c 374	31	1.3	10646	22	AAK42119	Genomic sequence #

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376	31	1.3	10669	22	AAK61696	Human immune/haema
C 377	31	1.3	10985	22	AAK86420	Human immune/haema
C 378	31	1.3	10985	22	AAK86421	Human immune/haema
C 379	31	1.3	10985	22	AAK86422	Human immune/haema
C 380	31	1.3	11715	22	ABAI6244	Human nervous syst
C 381	31	1.3	11977	22	AAK76752	Human genomic DNA
C 382	31	1.3	12149	22	AAK36758	Human cardiovascular
C 383	31	1.3	12247	22	AAK73076	Human immune/haema
C 384	31	1.3	12247	22	AAK87543	Human immune/haema
C 385	31	1.3	12409	22	AAK30238	DNA encoding rena
C 386	31	1.3	13058	22	AAK29194	Genomic sequence #
C 387	31	1.3	13058	22	AAK73075	Human immune/haema
C 388	31	1.3	13216	22	AAK05122	Human reproductive
C 389	31	1.3	13216	22	ABL98014	Human testicular a
C 390	31	1.3	13774	23	AAK83209	Human immune/haema
C 391	31	1.3	13973	24	ABK50459	Human caspase 5, a
C 392	31	1.3	14617	22	ABAI19132	Human nervous syst
C 393	31	1.3	14627	22	ABAI19130	Human nervous syst
C 394	31	1.3	14874	22	AAK04984	Human reproductive
C 395	31	1.3	14874	22	AAK89726	Human digestive sy
C 396	31	1.3	14874	23	ABL97877	Human testicular a
C 397	31	1.3	14969	22	AAK78763	Human immune/haema
C 398	31	1.3	14983	22	AAK73075	Human immune/haema
C 399	31	1.3	14983	22	AAK87542	Human immune/haema
C 400	31	1.3	15201	22	AAK83176	Human immune/haema
C 401	31	1.3	15531	22	AAK31521	Human nervous syst
C 402	31	1.3	15531	22	AAK31521	Human DNA for a no
C 403	31	1.3	15531	24	ABQ66845	Human polynucleoti
C 404	31	1.3	15765	24	AAD32179	Human NFkB gene
C 405	31	1.3	15765	24	AAK32327	Human NFkB gene
C 406	31	1.3	15808	22	ABAI18444	Human nervous syst
C 407	31	1.3	16596	22	AAK83767	Human immune/haema
C 408	31	1.3	16596	22	AAK33396	DNA encoding human
C 409	31	1.3	16748	22	AAK65193	Human immune/haema
C 410	31	1.3	16862	20	AAK58060	Genomic DNA for Hu
C 411	31	1.3	17073	21	AAK20998	Human low adenosin
C 412	31	1.3	17073	21	AAK34876	Human adenosine re
C 413	31	1.3	17138	22	AAK14757	Human protease gen
C 414	31	1.3	17138	22	ABL41524	Entire genomic seq
C 415	31	1.3	17170	22	AAK77880	Human immune/haema
C 416	31	1.3	17173	22	AAK77881	Human immune/haema
C 417	31	1.3	17200	22	AAK73025	Human musculoskele
C 418	31	1.3	18887	22	AAK18543	DNA encoding UDP g
C 419	31	1.3	19125	22	AAK136440	Human musculoskele
C 420	31	1.3	19191	22	AAK67485	Human immune/haema
C 421	31	1.3	19883	21	AAK20999	Human low adenosin
C 422	31	1.3	19943	21	AAK34877	Human adenosine re
C 423	31	1.3	20188	22	AAK73082	Human immune/haema
C 424	31	1.3	20188	22	AAK87550	Human nervous syst
C 425	31	1.3	20869	22	ABAI6245	Human cardiovascular
C 426	31	1.3	20869	22	AAK36927	Human immune/haema
C 427	31	1.3	20869	22	AAK85001	Human immune/haema
C 428	31	1.3	20991	22	AAK87545	Human immune/haema
C 429	31	1.3	21358	22	AAK39919	Genomic sequence #
C 430	31	1.3	21358	22	AAK06419	Human reproductive
C 431	31	1.3	21358	22	AAK73090	Human immune/haema
C 432	31	1.3	21358	22	AAK87446	Human immune/haema
C 433	31	1.3	21358	22	AAK87558	Human immune/haema
C 434	31	1.3	21358	22	AAK90363	Human digestive sy
C 435	31	1.3	21676	22	AAK39918	Genomic sequence #
C 436	31	1.3	21676	22	AAK06418	Human reproductive
C 437	31	1.3	21676	22	AAK73081	Human immune/haema
C 438	31	1.3	21676	22	AAK87445	Human immune/haema
C 439	31	1.3	21676	22	AAK87549	Human digestive sy
C 440	31	1.3	21676	22	AAK90362	Human immune/haema
C 441	31	1.3	22401	22	AAK71911	Human immune/haema
C 442	31	1.3	22402	22	AAK71912	Human immune/haema
C 443	31	1.3	22645	22	AAK04985	Human reproductive
C 444	31	1.3	22645	22	AAK05495	Human reproductive
C 445	31	1.3	22645	22	AAK89727	Human digestive sy
C 446	31	1.3	22645	23	ABL97878	Human testicular a
C 447	31	1.3	22645	23	ABL98348	Human testicular a
448	31	1.3	23075	22	ABAI19112	Human nervous syst
449	31	1.3	23580	22	AAK66230	Human immune/haema
C 450	31	1.3	23580	22	AAK83578	Human immune/haema
C 451	31	1.3	23603	22	AAK71829	Human immune/haema
C 452	31	1.3	23603	22	AAK73089	Human immune/haema
C 453	31	1.3	23603	22	AAK87557	Human immune/haema
C 454	31	1.3	23603	22	AAI62936	Human genomic DNA
C 455	31	1.3	23613	22	AAK71823	Human immune/haema
C 456	31	1.3	23613	22	AAK73085	Human immune/haema
C 457	31	1.3	23613	22	AAK87553	Human immune/haema
C 458	31	1.3	23613	22	AAI62930	Human genomic DNA
C 459	31	1.3	24102	22	AAK74877	Human immune/haema
C 460	31	1.3	24218	22	AAK71828	Human immune/haema
C 461	31	1.3	24218	22	AAK73088	Human immune/haema
C 462	31	1.3	24218	22	AAK87556	Human immune/haema
C 463	31	1.3	24218	22	AAI62935	Human genomic DNA
C 464	31	1.3	25837	22	AAK85952	Human immune/haema
C 465	31	1.3	25837	22	AAK77832	Human immune/haema
C 466	31	1.3	26928	22	ABA82620	Human HBM gene reg
C 467	31	1.3	26928	24	ABK22779	Human high bone ma
C 468	31	1.3	26928	22	AAK22779	Human lung antigen
C 469	31	1.3	26928	22	AAK22779	Human reproductive
C 470	31	1.3	29163	22	ABL98013	Human testicular a
C 471	31	1.3	29449	22	AAI6646	Human novel protei
C 472	31	1.3	29449	22	AAK30243	DNA encoding rena
C 473	31	1.3	31871	23	ABK42516	Genomic sequence #
C 474	31	1.3	32145	22	AAK68491	Human immune/haema
C 475	31	1.3	32145	22	AAK68575	Human immune/haema
C 476	31	1.3	32187	22	AAK89946	Human digestive sy
C 477	31	1.3	32190	22	AAI62927	Human genomic DNA
C 478	31	1.3	32195	22	AAK36517	Human cardiovascular
C 479	31	1.3	32207	22	ABAI19666	Human nervous syst
C 480	31	1.3	32219	22	AAK36516	Human cardiovascular
C 481	31	1.3	32249	22	AAI62932	Human genomic DNA
C 482	31	1.3	33795	24	ABN95686	Gene #184 used to
C 483	31	1.3	33968	22	AAK71820	Human immune/haema
C 484	31	1.3	33968	22	AAK73078	Human immune/haema
C 485	31	1.3	39068	22	AAK85294	Human immune/haema
C 486	31	1.3	39068	22	AAK87544	Human immune/haema
C 487	31	1.3	39110	22	AAK71825	Human immune/haema
C 488	31	1.3	39110	22	AAK73087	Human immune/haema
C 489	31	1.3	39110	22	AAK87555	Human immune/haema
C 490	31	1.3	39887	22	AAK79153	Human immune/haema
C 491	31	1.3	39887	22	AAK81263	Human immune/haema
C 492	31	1.3	40742	22	AAK68089	Human immune/haema
C 493	31	1.3	40742	22	AAK79886	Human immune/haema
C 494	31	1.3	42324	22	AAK84724	Human immune/haema
C 495	31	1.3	44354	22	AAK77833	Human immune/haema
C 496	31	1.3	44354	22	AAK77836	Human immune/haema
C 497	31	1.3	44354	22	AAK77837	Human immune/haema
C 498	31	1.3	45300	22	AAK12437	DNA encoding 1-ami
C 499	31	1.3	45300	22	AAK73079	Human immune/haema
C 500	31	1.3	45300	22	AAK87547	Human immune/haema
C 501	31	1.3	47090	22	AAK68725	Human immune/haema
C 502	31	1.3	47090	22	AAK78219	Human immune/haema
C 503	31	1.3	48037	22	AAK84729	Human immune/haema
C 504	31	1.3	48037	22	AAK85983	Human immune/haema
C 505	31	1.3	48045	22	AAK84730	Human immune/haema
C 506	31	1.3	48045	22	AAK85984	Human immune/haema
C 507	31	1.3	49998	20	AAK23518	Human kidney amino
C 508	31	1.3	50849	24	ABN87883	Human glutathione
C 509	31	1.3	51402	22	AAK72363	Human immune/haema
C 510	31	1.3	53552	22	AAK13655	Genomic DNA sequen
C 511	31	1.3	57236	22	AAK78170	Human immune/haema
C 512	31	1.3	57236	22	AAK78847	Human immune/haema
C 513	31	1.3	57236	22	AAK79364	Human immune/haema
C 514	31	1.3	57236	22	AAK86799	Human immune/haema
C 515	31	1.3	62944	24	ABL66947	Lung cancer relate
C 516	31	1.3	62944	24	ABL68262	Kidney cancer rela
C 517	31	1.3	65854	22	AAK86282	Human immune/haema
C 518	31	1.3	66566	21	AAK53450	Human thioredoxin
C 519	31	1.3	72928	20	AAK21835	Human ASTHJ 5' ge
C 520	31	1.3	72928	21	AAA80253	Human ASTHJ 5' ge

C 521	31	1.3	81001	22	AAF30035	Human apolipoprote	c 594	30	1.2	402	22	AAI91321	Human polynucleoti
C 522	31	1.3	97835	24	ABK84796	Human CDNA differe	c 595	30	1.2	404	23	ABV43752	Human prostate exp
C 523	31	1.3	100301	24	ABQ88176	Human osteoblast d	c 596	30	1.2	405	23	ABV34903	Human prostate exp
524	31	1.3	107820	22	AAI16230	Human ATP-binding	c 597	30	1.2	412	24	ABL83673	Human ovarian canc
525	31	1.3	109906	24	ABK94411	DNA encoding endoc	c 598	30	1.2	420	24	ABV36507	Human prostate exp
526	31	1.3	110096	24	ABN95044	Gene #1542 used to	c 599	30	1.2	431	22	AAK84332	Human immune/haema
527	31	1.3	125439	24	ABQ88177	Human osteoblast d	c 600	30	1.2	432	22	AAK84331	Human immune/haema
528	31	1.3	136284	24	ABK83575	Human CDNA differe	c 601	30	1.2	432	23	AAK75410	DNA encoding novel
C 529	31	1.3	139389	24	ABK84795	Human CDNA differe	c 602	30	1.2	436	21	AAK25662	Human secreted pro
C 530	31	1.3	139904	24	ABK83562	Human CDNA differe	c 603	30	1.2	437	24	ABN65729	Human cancer relat
C 531	31	1.3	143899	24	AAI38336	Genomic sequence e	c 604	30	1.2	448	22	AAK57663	Human immune/haema
C 532	31	1.3	145831	24	ABL62309	Colon adenocarcino	c 605	30	1.2	465	22	AAK56418	Human immune/haema
C 533	31	1.3	145831	24	ABL66806	Lung cancer relate	c 606	30	1.2	470	22	AAH10091	Human CDNA clone (
C 534	31	1.3	145831	24	ABL68588	Kidney cancer rela	c 607	30	1.2	471	23	ABV35684	Human prostate exp
C 535	31	1.3	145831	24	ABL69213	Prostate cancer re	c 608	30	1.2	471	23	ABV44489	Human prostate exp
536	31	1.3	147708	24	ABQ88154	Human osteoblast d	c 609	30	1.2	477	23	ABV04621	Human prostate exp
537	31	1.3	160755	23	AAH88704	Human DNA sequence	c 610	30	1.2	478	22	AAK67984	Human immune/haema
538	31	1.3	160771	24	ABQ88179	Human osteoblast d	c 611	30	1.2	478	22	AAK67985	Human immune/haema
C 539	31	1.3	183999	22	AAF92831	Human ABC1 genomic	c 612	30	1.2	482	24	ABL85825	Human ovarian canc
C 540	31	1.3	198161	24	ABK93564	Human CDNA differe	c 613	30	1.2	485	23	ABV38047	Human prostate exp
541	31	1.3	220895	24	ABK84798	Human CDNA differe	c 614	30	1.2	495	23	ABV53854	Human prostate exp
C 542	31	1.3	235033	19	AAV57926	Hereditary haemoch	c 615	30	1.2	496	22	ABA14124	Human nervous syst
C 543	31	1.3	237326	19	AAV57903	Hereditary haemoch	c 616	30	1.2	496	24	ABN62961	Human cancer relat
C 544	31	1.3	465237	24	ABQ87681	Human oestrogen re	c 617	30	1.2	527	24	ABN64923	Human cancer relat
C 545	31	1.3	465237	24	ABA90193	Human oestrogen re	c 618	30	1.2	536	24	ABN61361	Human cancer relat
C 546	31	1.3	1503900	22	AAK95240	Human neuroregulin-1	c 619	30	1.2	538	23	ABV16597	Human prostate exp
C 547	31	1.3	1503900	22	AAK96733	Human neuroregulin-1	c 620	30	1.2	544	23	ABV50544	Human prostate exp
548	30	1.2	51	22	AAI76249	Human silent SNP c	c 621	30	1.2	546	24	ABL85722	Human ovarian canc
549	30	1.2	51	22	AAI76251	Human silent SNP c	c 622	30	1.2	550	22	AAH09740	Human CDNA clone (
C 550	30	1.2	51	22	AAH89405	Human coding sequ	c 623	30	1.2	553	23	ABV57690	Human prostate exp
C 551	30	1.2	73	22	AAK90007	Human upstream Alu	c 624	30	1.2	564	22	AAH10031	Human CDNA clone (
C 552	30	1.2	101	22	AAK82622	Human immune/haema	c 625	30	1.2	566	22	AAH10007	Human CDNA clone (
C 553	30	1.2	103	22	AAK73577	Human immune/haema	c 626	30	1.2	569	22	AAH13412	Human CDNA clone (
554	30	1.2	107	22	AAI04735	Human reproductive	c 627	30	1.2	574	24	ABL66172	Lung cancer relate
555	30	1.2	107	22	AAI04738	Human reproductive	c 628	30	1.2	585	23	ABV51184	Human prostate exp
556	30	1.2	107	23	ABL97640	Human testicular a	c 629	30	1.2	586	22	AAK36781	Human cardiovascular
557	30	1.2	107	23	ABL97643	Human testicular a	c 630	30	1.2	586	23	ABV08133	Human prostate exp
C 558	30	1.2	110	22	AAK85751	Human immune/haema	c 631	30	1.2	587	23	ABV23699	Human prostate exp
C 559	30	1.2	111	22	AAK73576	Human immune/haema	c 632	30	1.2	587	23	ABV29568	Human prostate exp
C 560	30	1.2	113	22	AAK73582	Human immune/haema	c 633	30	1.2	592	22	AAK72482	Human immune/haema
561	30	1.2	114	22	AAK36217	Human cardiovascular	c 634	30	1.2	593	22	AAK36778	Human cardiovascular
C 562	30	1.2	116	22	AAK73326	Human immune/haema	c 635	30	1.2	593	22	AAK36780	Human cardiovascular
C 563	30	1.2	119	22	AAK73566	Human immune/haema	c 636	30	1.2	593	22	AAK72483	Human immune/haema
C 564	30	1.2	119	22	AAK73569	Human immune/haema	c 637	30	1.2	604	22	ABA21237	Human nervous syst
C 565	30	1.2	127	22	AAI36925	Human musculoskele	c 638	30	1.2	611	24	ABN62702	Human cancer relat
C 566	30	1.2	127	22	AAK32717	Human genomic DNA	c 639	30	1.2	619	23	ABV05824	Human prostate exp
567	30	1.2	127	22	AAK65153	Human immune/haema	c 640	30	1.2	620	23	ABV14993	Human prostate exp
C 568	30	1.2	133	22	AAK77877	Human immune/haema	c 641	30	1.2	622	23	ABV51983	Human prostate exp
C 569	30	1.2	133	22	AAK77879	Human immune/haema	c 642	30	1.2	632	22	AAK70386	Human immune/haema
570	30	1.2	134	22	ABA16899	Human nervous syst	c 643	30	1.2	661	23	ABV39076	Human prostate exp
571	30	1.2	134	22	ABA18331	Human nervous syst	c 644	30	1.2	661	23	ABV44862	Human prostate exp
C 572	30	1.2	136	22	AAK68049	Human nervous syst	c 645	30	1.2	671	23	ABV46395	Human prostate exp
C 573	30	1.2	140	22	AAK65590	Human immune/haema	c 646	30	1.2	691	22	AAK56390	Human immune/haema
C 574	30	1.2	151	22	AAK86194	Human immune/haema	c 647	30	1.2	700	22	AAH92156	Human inflammatory
C 575	30	1.2	157	20	AAH86639	Human single nucle	c 648	30	1.2	700	22	AAH92420	Human inflammatory
C 576	30	1.2	167	22	AAI89783	Human polynucleoti	c 649	30	1.2	700	22	AAH92572	Human inflammatory
577	30	1.2	248	22	AAI98905	Human excretory re	c 650	30	1.2	708	22	AAH07283	Human CDNA clone (
C 578	30	1.2	248	22	AAI63255	Human kidney relat	c 651	30	1.2	723	22	AAK54060	hFIX gene AB3' age
C 579	30	1.2	294	21	AAI63305	Human secreted pro	c 652	30	1.2	726	22	AAK89244	Human digestive sy
C 580	30	1.2	308	22	AAI63305	Human musculoskele	c 653	30	1.2	739	22	AAH98158	Human EST-derived
581	30	1.2	312	24	ABL35400	Human ovarian canc	c 654	30	1.2	763	22	AAI95299	Human neuroblastom
582	30	1.2	313	24	ABL84842	Human ovarian canc	c 655	30	1.2	791	23	AAK568432	DNA encoding novel
C 583	30	1.2	321	22	AAI223397	Human breast canc	c 656	30	1.2	797	23	ABV13790	Human prostate exp
C 584	30	1.2	323	24	ABK45452	cDNA encoding colo	c 657	30	1.2	800	22	AAH04460	Human CDNA clone (
C 585	30	1.2	335	14	AAQ59473	Human brain expres	c 658	30	1.2	847	22	AAK67359	Human immune/haema
586	30	1.2	341	22	AAI88329	Human polynucleoti	c 659	30	1.2	856	23	ABV14606	Human prostate exp
C 587	30	1.2	341	22	AAH19245	Human secreted pro	c 660	30	1.2	1000	20	AAZ27733	Human DNA marker c
C 588	30	1.2	351	22	AAK73657	Novel human diagno	c 661	30	1.2	1001	21	AAH51279	Human SSHS related
589	30	1.2	358	22	AAI84944	Human polynucleoti	c 662	30	1.2	1001	21	AAH51293	Human GLCL related
590	30	1.2	369	22	ABA15271	Human nervous syst	c 663	30	1.2	1001	21	AAH51294	Human GLCL related
C 591	30	1.2	380	24	ABL84503	Human ovarian canc	c 664	30	1.2	1001	21	AAH51559	Human GLCL related
C 592	30	1.2	401	22	AAK96009	Human neuroregulin g	c 665	30	1.2	1001	21	AAH51564	Human GLCL related
593	30	1.2	401	22	AAK97502	Human neuroregulin g	c 666	30	1.2	1002	22	AAI06938	Human reproductive

C 813	30	1.2	13824	22	AAL37127	Human musculoskele	886	30	1.2	24887	24	ABK14141	Human aminolevulin
C 814	30	1.2	14040	22	ABA08209	Human ovarian and	C 887	30	1.2	25012	22	ABA15431	Human nervous syst
C 815	30	1.2	14040	22	AAL02790	Human reproductive	C 888	30	1.2	25715	22	AAS33462	DNA encoding human
C 816	30	1.2	14040	22	AAL07517	Human reproductive	C 889	30	1.2	25785	22	AAK78465	Human immune/haema
C 817	30	1.2	14063	22	AAK82933	Human immune/haema	C 890	30	1.2	25971	22	AAK86336	Human immune/haema
C 818	30	1.2	14063	22	AAK82934	Human immune/haema	C 891	30	1.2	26191	22	AAK86339	Human immune/haema
C 819	30	1.2	14175	22	AAS27814	DNA encoding novel	C 892	30	1.2	26201	24	ABK14039	Human 3-hydroxy-3-
C 820	30	1.2	14175	22	AAK78859	Human immune/haema	C 893	30	1.2	26201	24	ABK14446	Human HMGCL gene,
C 821	30	1.2	14299	22	AAK90955	Human digestive sy	C 894	30	1.2	26372	22	AAK77103	Human immune/haema
C 822	30	1.2	14299	22	AAS31990	Human liver associ	C 895	30	1.2	27289	22	AAS34624	Human DNA for a no
C 823	30	1.2	14299	22	ABN90345	Human liver antige	C 896	30	1.2	27435	22	AAK65476	Human immune/haema
C 824	30	1.2	14403	22	AAL07146	Human reproductive	C 897	30	1.2	27435	22	AAK65476	Human immune/haema
C 825	30	1.2	14633	22	ABA10066	Human nervous syst	C 898	30	1.2	27841	22	AAS29820	Human cytoskeletal
C 826	30	1.2	14633	22	AAK83608	Human immune/haema	C 899	30	1.2	27841	22	AAS29827	Human cytoskeletal
C 827	30	1.2	14970	22	AAS42037	Genomic sequence #	C 900	30	1.2	28772	24	ABK83555	Human cDNA differe
C 828	30	1.2	14976	22	AAS42038	Genomic sequence #	C 901	30	1.2	28974	22	AAS32821	Human genomic DNA
C 829	30	1.2	15554	22	AAK73537	Human immune/haema	C 902	30	1.2	28974	22	AAK69977	Human immune/haema
C 830	30	1.2	15555	22	AAK73539	Human immune/haema	C 903	30	1.2	29411	22	AAK76613	Human immune/haema
C 831	30	1.2	15558	22	AAK73538	Human immune/haema	C 904	30	1.2	30568	22	AAK37486	Human musculoskele
C 832	30	1.2	15580	22	ABA15958	Human nervous syst	C 905	30	1.2	30709	24	ABK87217	Human lipase, horm
C 833	30	1.2	15589	22	AAK80921	Human immune/haema	C 906	30	1.2	30967	17	AAT32454	Calpain large subu
C 834	30	1.2	15610	22	AAL07072	Human reproductive	C 907	30	1.2	31853	22	AAI98993	Human excretory re
C 835	30	1.2	15610	22	AAK80920	Human immune/haema	C 908	30	1.2	31853	22	AAI63343	Human kidney relat
C 836	30	1.2	15650	22	ABA15903	Human nervous syst	C 909	30	1.2	32167	22	AAI05509	Human reproductive
C 837	30	1.2	15650	22	ABA16364	Human nervous syst	C 910	30	1.2	32188	22	AAS28365	Genomic sequence #
C 838	30	1.2	15651	22	AAK81510	Human immune/haema	C 911	30	1.2	32190	22	AAS29937	Human lung antigen
C 839	30	1.2	15734	22	AAS36422	Human cardiovascular	C 912	30	1.2	32190	22	AAK89689	Human digestive sy
C 840	30	1.2	15843	22	AAS36896	Human cardiovascular	C 913	30	1.2	32192	22	AAI37292	Human musculoskele
C 841	30	1.2	15843	22	AAK67635	Human immune/haema	C 914	30	1.2	32192	22	AAI07103	Human reproductive
C 842	30	1.2	16057	22	AAS35935	Human immune/haema	C 915	30	1.2	32193	22	AAS29936	Human lung antigen
C 843	30	1.2	16086	22	AAL36020	Human cardiovascular	C 916	30	1.2	32249	22	AAS29938	Human lung antigen
C 844	30	1.2	16086	22	AAK69721	Human musculoskele	C 917	30	1.2	33513	22	AAK78746	Human immune/haema
C 845	30	1.2	16106	22	AAK83468	Human immune/haema	C 918	30	1.2	34634	24	AAD31198	Human WKL-1 Genomi
C 846	30	1.2	16161	22	AAK83469	Human immune/haema	C 919	30	1.2	34917	22	AAK70686	Human immune/haema
C 847	30	1.2	16181	22	AAL04268	Human reproductive	C 920	30	1.2	36221	22	AAK00624	Human death-associ
C 848	30	1.2	16181	23	ABK42539	Genomic sequence #	C 921	30	1.2	36797	24	AAD26738	Human synaptosomal
C 849	30	1.2	16774	22	AAS36895	Human cardiovascular	C 922	30	1.2	36797	24	AAD26830	Human SNAP29 gene
C 850	30	1.2	16774	22	AAS36898	Human cardiovascular	C 923	30	1.2	37314	22	AAK71358	Human immune/haema
C 851	30	1.2	16774	22	AAK67634	Human immune/haema	C 924	30	1.2	37449	22	AAK66874	Human immune/haema
C 852	30	1.2	16774	22	AAK67637	Human immune/haema	C 925	30	1.2	37925	22	AAK72372	Human immune/haema
C 853	30	1.2	17000	22	AAK86254	Human immune/haema	C 926	30	1.2	38059	22	AAK54018	Human factor IX (h
C 854	30	1.2	17000	22	AAK90956	Human digestive sy	C 927	30	1.2	38059	24	ABN95627	Gene #2125 used to
C 855	30	1.2	17000	22	AAS31991	Human liver associ	C 928	30	1.2	38186	20	AAZ32028	Human METH1 relate
C 856	30	1.2	17000	24	ABN90346	Human liver associ	C 929	30	1.2	38186	22	AAZ32028	AC004449 cDNA clon
C 857	30	1.2	17047	22	AAK81251	Human liver antige	C 930	30	1.2	38844	24	AAL40255	Genomic DNA encodi
C 858	30	1.2	17197	22	AAK79870	Human immune/haema	C 931	30	1.2	41159	22	AAK65631	Human immune/haema
C 859	30	1.2	17245	22	AAK83897	Human immune/haema	C 932	30	1.2	41159	22	AAK76675	Human immune/haema
C 860	30	1.2	17245	22	AAK83897	Human immune/haema	C 933	30	1.2	41772	22	AAK76676	Human immune/haema
C 861	30	1.2	17286	22	AAK36869	Human musculoskele	C 934	30	1.2	43950	24	AAD36022	Human kinase genom
C 862	30	1.2	17462	22	ABA15655	Human nervous syst	C 935	30	1.2	43950	24	AAS19703	Reference sequence
C 863	30	1.2	17538	21	AAZ29204	Human myelin oligo	C 936	30	1.2	44820	24	AAS19703	Reference sequence
C 864	30	1.2	18534	24	ABK84757	Human cDNA differe	C 937	30	1.2	45546	20	AAZ23520	Human kidney amino
C 865	30	1.2	18564	22	AAK65368	Human immune/haema	C 938	30	1.2	45993	24	AAD36070	Human liver glucok
C 866	30	1.2	18564	22	AAK65368	Human immune/haema	C 939	30	1.2	47319	22	AAK64813	Human immune/haema
C 867	30	1.2	18576	22	AAS29819	Human cytoskeletal	C 940	30	1.2	47319	22	AAK72230	Human immune/haema
C 868	30	1.2	18660	22	AAK79108	Human immune/haema	C 941	30	1.2	48203	22	AAK70161	Human immune/haema
C 869	30	1.2	18671	22	AAK90763	Human digestive sy	C 942	30	1.2	48203	22	AAK81663	Human immune/haema
C 870	30	1.2	18925	22	ABA81553	Human phospholipid	C 943	30	1.2	48203	22	AAK82628	Human immune/haema
C 871	30	1.2	18925	24	AAS94555	Human phospholipid	C 944	30	1.2	48204	22	AAK70164	Human immune/haema
C 872	30	1.2	18925	24	AAS94555	Human phospholipid	C 945	30	1.2	48204	22	AAK81666	Human immune/haema
C 873	30	1.2	19596	22	AAK73967	Human phospholipid	C 946	30	1.2	48204	22	AAK82630	Human immune/haema
C 874	30	1.2	19596	22	AAK73968	Human immune/haema	C 947	30	1.2	48908	22	AAK82338	Human immune/haema
C 875	30	1.2	19597	22	AAK78483	Human immune/haema	C 948	30	1.2	50196	22	AAK79598	Human immune/haema
C 876	30	1.2	20067	22	AAK66735	Human immune/haema	C 949	30	1.2	51474	22	AAK79846	Human neuroblastom
C 877	30	1.2	20068	22	AAK66733	Human immune/haema	C 950	30	1.2	52216	22	AAH28355	Nucleotide sequenc
C 878	30	1.2	20323	22	AAK66731	Human immune/haema	C 951	30	1.2	52216	22	AAH28355	Human musashi prom
C 879	30	1.2	21596	22	AAK71582	Human immune/haema	C 952	30	1.2	54863	22	AAK86025	Human immune/haema
C 880	30	1.2	21982	22	AAK67644	Human immune/haema	C 953	30	1.2	54877	22	AAK86026	Human immune/haema
C 881	30	1.2	22081	22	AAK79862	Human neuroblastom	C 954	30	1.2	57248	24	AAK83563	Human cDNA differe
C 882	30	1.2	22786	22	AAL137362	Human musculoskele	C 955	30	1.2	59065	24	ABJ42416	Human serine/threo
C 883	30	1.2	22916	22	AAK55305	Human immune/haema	C 956	30	1.2	59747	24	ABQ88209	Human osteoblast d
C 884	30	1.2	23164	22	AAK79678	Human immune/haema	C 957	30	1.2	65608	24	ABL62910	Breast cancer rela
C 885	30	1.2	24843	24	AAS17764	Human Genomic DNA	C 958	30	1.2	65608	24	ABL64414	Stomach cancer rel
												ABL67668	Oesophagus cancer

[illegible]

D	b	6134	GGGTTGAGAGCCAGTGGCGGGTGATGGCCAGCCCCCTGGGGCCAGCCCCCTGTTTACTGGT	6193
Q	y	1681	TCATTGCAAAATGGGAGCTGACAGCCTCTGGACAGCCAGTACCTTTTACCTCGGTGACCA	1740
D	b	6194	TCATTGCAAAATGGGAGCTGACAGCCTCTGGACAGCCAGTACCTTTTACCTCGGTGACCA	6253
Q	y	1741	CTCTTCTTTTAAAGCCATAGACCTCGAGCCCTGGGCTGGGTCTGGGAAGGAGAGGTTGAA	1800
D	b	6254	CTCTTCTTTTAAAGCCATAGACCTCGAGCCCTGGGCTGGGTCTGGGAAGGAGAGGTTGAA	6313
Q	y	1801	ACACCGTGAACGAGGGTGTGGCTTTTCAGKACCCCTCAGGGAGCCTCCCAATCTGTC	1860
D	b	6314	ACCACCGTGAACGAGGGTGTGGCTTTTCAGKACCCCTCAGGGAGCCTCCCAATCTGTC	6373
Q	y	1861	CAGCTGGGGCCAGAGGCTGGAGTCCCTACTGCTTCACTGCTTCCAGCTTGGCCGGCGCTACTCTGG	1920
D	b	6374	CAGCTGGGGCCAGAGGCTGGAGTCCCTACTGCTTCCAGCTTGGCCGGCGCTACTCTGG	6433
Q	y	1921	AATGTTTTTCCCTCCCAAGAAATCAAGCTTTTGTGTATCCAGAAAGCCCATATCACTAA	1980
D	b	6434	AATGTTTTTCCCTCCCAAGAAATCAAGCTTTTGTGTATCCAGAAAGCCCATATCACTAA	6493
Q	y	1981	GATGGCATATATGTGATCTGGGCAATTTTCTCTCTGCTTACAGCCAGGTTTAGCGGAA	2040
D	b	6494	GATGGCATATATGTGATCTGGGCAATTTTCTCTCTGCTTACAGCCAGGTTTAGCGGAA	6553
Q	y	2041	ACCTTTCCCTTTAGCACCTTCAGGCGTGAGTTCTGGGTTTCTAGAGGTGAGNACGGCTC	2100
D	b	6554	ACCTTTCCCTTTAGCACCTTCAGGCGTGAGTTCTGGGTTTCTAGAGGTGAGNACGGCTC	6613
Q	y	2101	CTCAGAGCGCCAGGAAGCCAGAGCCCCCAAGCAGGACGAAAAAGAGGCATACACACAGCAG	2160
D	b	6614	CTCAGAGCGCCAGGAAGCCAGAGCCCCCAAGCAGGACGAAAAAGAGGCATACACACAGCAG	6673
Q	y	2161	TGTGAATPAGCCTGGCCACGAGCCATCTCTCTTCACTCAAGACCCCAATTTGTCCSAGA	2220
D	b	6674	TGTGAATPAGCCTGGCCACGAGCCATCTCTCTTCACTCAAGACCCCAATTTGTCCSAGA	6733
Q	y	2221	CTAAGGATCCAGAGCAGCTCCCTTTCTCAGGAGCTTGGGAGTGCCCCAGGGAGTCC	2280
D	b	6734	CTAAGGATCCAGAGCAGCTCCCTTTCTCAGGAGCTTGGGAGTGCCCCAGGGAGTCC	6793
Q	y	2281	AGGGTTTCTCTGACAGATGTCGGAGCGGAGCGGTGTAGAGAGATAAAAGTGGAG	2340
D	b	6794	AGGGTTTCTCTGACAGATGTCGGAGCGGAGCGGTGTAGAGAGATAAAAGTGGAG	6853
Q	y	2341	TTTCTCTGTTGTTGGTTCAGGATTTATTTTAAATTTTATGACAGAGGCTTGTCTCT	2400
D	b	6854	TTTCTCTGTTGTTGGTTCAGGATTTATTTTAAATTTTATGACAGAGGCTTGTCTCT	6913
Q	y	2401	GTCC 2404	
D	b	6914	GTCC 6917	
RESULT 2				
AAA64508				
ID	AAA64508 standard; cDNA; 5492 BP.			
XX	AAA64508;			
XX	AC			
XX	AC			
DT	02-JAN-2001 (first entry)			
DE	cDNA sequence of the wild type human FEZ1 gene.			
XX				
KW	Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;			
KW	tumour proliferation; tubulin; microtubule; protein EPI-gamma;			
KW	tubulin polymerisation disorder; mitosis initiation; cell proliferation;			
KW	cell growth; cell shape; cell rigidity; cell motility; DNA replication;			
XX	tumorigenesis; tumour survival; metastasis; ss.			
OS	Homo sapiens.			

XX WO200050565-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US04950.
XX 25-FEB-1999; 99US-0121537.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Croce CM, Ishii H;
XX WPI; 2000-558396/51.
XX New polynucleotide homologous with a portion of one strand of the human
XX FEZ1 gene, useful for alleviating abnormal cell proliferation such as
XX cancer -
XX
XX Example 2; Fig 5B; 255pp; English.
XX
XX The present sequence represents the cDNA sequence of the human FEZ1 gene.
XX FEZ1 is a tumour suppressor gene, located at chromosome location 9p22.
XX Decreased or no expression of FEZ1 is detected in a variety of cancer
XX cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
XX also interacts with tubulin, with microtubules, and with protein
XX EPI-gamma. Post-translational phosphorylation and dephosphorylation
XX modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
XX expression are useful for inducing cells to proliferate. Compounds
XX which modulate FEZ1 association with tubulin are useful for alleviating
XX tubulin hyper- or hypo- polymerisation disorders, such as those
XX associated with aberrant initiation of mitosis, modulation of the
XX initiation and rate of cell proliferation and cell growth, modulation of
XX cell shape, cell rigidity, cell motility, rate and stage of cellular
XX DNA replication, intracellular distribution of organelles, metastatic
XX potential of cell and cellular transformation from a non-cancerous to
XX cancerous phenotype. Compounds which modulate FEZ1 binding and
XX phosphorylation are also useful for alleviating a disorder, such as
XX tumorigenesis, tumour survival, growth and metastasis.
XX
XX Sequence 5492 BP; 1137 A; 1704 C; 1565 G; 1086 T; 0 other;
XX
XX Query Match 81.8%; Score 1966; DB 21; Length 5492;
XX Best Local Similarity 99.9%; Pred No. 0;
XX Matches 2066; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 337 AGGTGTGCCAGAGTCAGCGAGATCTCCCTCTTGAAGCAGCAGCTGAAGAGTCCCAGA 396
XX 1259 AGGTGTGCCAGAGTCAGCGAGATCTCCCTCTTGAAGCAGCAGCTGAAGAGTCCCAGA 1318
XX 397 CGGAGGTGAACCCNAGGCTAGCGAGATCTGGGTCTCAAGGCACAGCTGAAGCAGCGC 456
XX 1319 CGGAGGTGAACCCNAGGCTAGCGAGATCTGGGTCTCAAGGCACAGCTGAAGCAGCGC 1378
XX 457 GGGGCAAGCTGGAGGCTTGAAGCTGAGGATCCAGGACCTGGAGGCGCCCTGGCGCACCA 516
XX 1379 GGGGCAAGCTGGAGGCTTGAAGCTGAGGATCCAGGACCTGGAGGCGCCCTGGCGCACCA 1438
XX 517 AGGGCTTGGAGCTGGAGTCTGTGAGATAGTGTGAGCGCAAGCAAGAACGAGCGGAGC 576
XX 1439 AGGGCTTGGAGCTGGAGTCTGTGAGATAGTGTGAGCGCAAGCAAGAACGAGCGGAGC 1498
XX 577 TGCTGCGGGAGAGGTGAACCTGTGGAGCAGGAGCTGCAGAGCTGGGCGCCAGGCGCG 636
XX 1499 TGCTGCGGGAGAGGTGAACCTGTGGAGCAGGAGCTGCAGAGCTGGGCGCCAGGCGCG 1558
XX 637 CCCTGGCGCGGACATGGGCGCGCCACCTTTCCCGAGGAGCTCCCTGCCCTGCAGCGGG 696
XX 1559 CCCTGGCGCGGACATGGGCGCGCCACCTTTCCCGAGGAGCTCCCTGCCCTGCAGCGGG 1618
XX 697 AGCTGGAGCGGCTGGCGGCGGAGCTGCGGAGGAGCGGCAAGGCGCATGACCATGTCTCT 756
XX 1619 AGCTGGAGCGGCTGGCGGCGGAGCTGCGGAGGAGCGGCAAGGCGCATGACCATGTCTCT 1678

QY	757	CGGGCTTCCAGCATGAGCGCTCGTGTGGAGGAGGAGGAGAGGTGATTTCAGTACC	816
DB	1679	CGGGCTTCCAGCATGAGCGCTCGTGTGGAGGAGGAGGAGAGGTGATTTCAGTACC	1738
QY	817	AGAAACAGCTGCAGCAGAGCTACCTGGCCATGTATACACAGCGAAACACAGCGCTCGAGAAAG	876
DB	1739	AGAAACAGCTGCAGCAGAGCTACCTGGCCATGTATACACAGCGAAACACAGCGCTCGAGAAAG	1798
QY	877	CCCTGCAGCAGCTGGCACTGGGGACAGCCCGGGGAGCCCTTGGAGGTTGACCTGGAAG	936
DB	1799	CCCTGCAGCAGCTGGCACTGGGGACAGCCCGGGGAGCCCTTGGAGGTTGACCTGGAAG	1858
QY	937	GGCTGCATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTCCCTGGGAAG	996
DB	1859	GGCTGCATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTCCCTGGGAAG	1918
QY	997	GCAGTCTGGGGACCTGGCACTGGGGAGCGGGCTCTCCCGTGCATCCCCCTCTGCAGC	1056
DB	1919	GCAGTCTGGGGACCTGGCACTGGGGAGCGGGCTCTCCCGTGCATCCCCCTCTGCAGC	1978
QY	1057	AATTCAGACCCCTCTGAGAGACGCCACTCCCTGGGACACAGACCAGGACCCCGAGGGG	1116
DB	1979	AATTCAGACCCCTCTGAGAGACGCCACTCCCTGGGACACAGACCAGGACCCCGAGGGG	2038
QY	1117	AGGCGAGGATGGCTTCTTCCCTCTCTCATGTGCCAGTGTCCACGAGCCCTGCAGCCC	1176
DB	2039	AGGCGAGGATGGCTTCTTCCCTCTCTCATGTGCCAGTGTCCACGAGCCCTGCAGCCC	2098
QY	1177	ACCAGAGCTCAGGCGCTGACTCTCTGGCTTTCCAGGAGATGGTCCAGGGGTCTGTCT	1236
DB	2099	ACCAGAGCTCAGGCGCTGACTCTCTGGCTTTCCAGGAGATGGTCCAGGGGTCTGTCT	2158
QY	1237	GCTTTGGTTAAGGCTCCCTAAACTTTGGCTTTTGTTCGAAATAGATATCTCTCCCTCT	1296
DB	2159	GCTTTGGTTAAGGCTCCCTAAACTTTGGCTTTTGTTCGAAATAGATATCTCTCCCTCT	2218
QY	1297	CTTCCAGGAGGTGGCCACAGCAAGAACAGCGCTCCCTCCGCTTCTCATCCCAACCT	1356
DB	2219	CTTCCAGGAGGTGGCCACAGCAAGAACAGCGCTCCCTCCGCTTCTCATCCCAACCT	2278
QY	1357	CTTTTCTCTCTGACACATTTGGAATGCTTGGAAATAGAAAGAGGCATATATGACCAG	1416
DB	2279	CTTTTCTCTCTGACACATTTGGAATGCTTGGAAATAGAAAGAGGCATATATGACCAG	2338
QY	1417	AGCCTTGGAAACAGCCCCCATCAGAACCTGAGCTATTTTCTCTGGCGCGCAGAGGTGTAG	1476
DB	2339	AGCCTTGGAAACAGCCCCCATCAGAACCTGAGCTATTTTCTCTGGCGCGCAGAGGTGTAG	2398
QY	1477	GGGTGGAATGAGCGCGGGGAAGCTGGCTTTTGAACCTCAGGGGTGTCCAGCCCCGGCA	1536
DB	2399	GGGTGGAATGAGCGCGGGGAAGCTGGCTTTTGAACCTCAGGGGTGTCCAGCCCCGGCA	2458
QY	1537	AGCCACAGGAGGAGGAGAGACAGCAGCCACAGCAGTGTGGAGACCTTGCCACAGCCA	1596
DB	2459	AGCCACAGGAGGAGGAGAGACAGCAGCCACAGCAGTGTGGAGACCTTGCCACAGCCA	2518
QY	1597	GAGGAGGCGAGGGGAATCCAAAGGTTGAGAGCCAGTGGCGGGTGTATGCGCAGCCCCCT	1656
DB	2519	GAGGAGGCGAGGGGAATCCAAAGGTTGAGAGCCAGTGGCGGGTGTATGCGCAGCCCCCT	2578
QY	1657	GGGCGCCAGCCCTGTTTACTGGTTCTTGCAATGGGAGCTGAGCAGCCTCTGACACAGCC	1716
DB	2579	GGGCGCCAGCCCTGTTTACTGGTTCTTGCAATGGGAGCTGAGCAGCCTCTGACACAGCC	2638
QY	1717	AGTGACCTTTGACCTCGGTGACCACTCTTTTAAGCCATAGACCTTGAGGCCCTGGGCT	1776
DB	2639	AGTGACCTTTGACCTCGGTGACCACTCTTTTAAGCCATAGACCTTGAGGCCCTGGGCT	2698
QY	1777	GGGTGCTGGGAAGGAGGTTGAAACCAACCGTGAACAGAGGGTGTGGCTTTCAGKAC	1836
DB	2699	GGGTGCTGGGAAGGAGGTTGAAACCAACCGTGAACAGAGGGTGTGGCTTTCAGGAC	2758

QY 877 CCCTGCGACGCTGGCAGCTGGGACAGCGCCGGGGAGCCCTTGAGGTTGACCTGGAAG 936
|||||
Db 1688 CCCTGCGACGCTGGCAGCTGGGACAGCGCCGGGGAGCCCTTGAGGTTGACCTGGAAG 1747
|||||
QY 937 GGGCTGACATCCCTTACGAGGACATCATAGCCACTGAGATCTGA 980
|||||
Db 1748 GGGCTGACATCCCTTACGAGGACATCATAGCCACTGAGATCTGA 1791
|||||

RESULT 4

AAA64515
ID AAA64515 standard; cDNA; 1722 BP.

XX AC AAA64515;

XX DT 02-JAN-2001 (first entry)

XX DE Nucleotide sequence of truncated FEZ1 transcript G3612.

XX KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
tumour proliferation; tubulin; microtubule; protein Efi-gamma;
tubulin polymerisation disorder; mitosis initiation; cell proliferation;
cell growth; cell shape; cell rigidity; cell motility; DNA replication;
tumorigenesis; tumour survival; metastasis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT 1..1722
XX FT CDS /*tag= a
XX FT /product= "truncated FEZ1"

XX FT

XX PN WO200050565-A2.

XX XX 31-AUG-2000.

XX XX 25-FEB-2000; 2000WO-US04950.

XX XX 25-FEB-1999; 99US-0121537.

XX XX (UYJE-) UNIV JEFFERSON THOMAS.

XX XX Croce CM, Ishii H;

XX XX WPI; 2000-558396/51.

XX XX P-PSDB; AAB08722.

XX XX New polynucleotide homologous with a portion of one strand of the human
FEZ1 gene, useful for alleviating abnormal cell proliferation such as
cancer -

XX PS Disclosure; Fig 5H; 255pp; English.

XX CC The present sequence encodes a truncated human FEZ1 polypeptide. The
encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour
suppressor gene, located at chromosome location 8p22. Decreased
or no expression of FEZ1 is detected in a variety of cancer cells.
XX CC Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
also interacts with tubulin, with microtubules, and with protein
Efi-gamma. Post-translational phosphorylation and dephosphorylation
modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
expression are useful for inducing cells to proliferate. Compounds
XX CC which modulate FEZ1 association with tubulin are useful for alleviating
tubulin hyper- or hypo- polymerisation disorders, such as those
XX CC associated with aberrant initiation of mitosis, modulation of the
initiation and rate of cell proliferation and cell growth, modulation of
cell shape, cell rigidity, cell motility, rate and stage of cellular
XX CC DNA replication, intracellular distribution of organelles, metastatic
potential of cell and cellular transformation from a non-cancerous to
XX CC cancerous phenotype. Compounds which modulate FEZ1 binding and
phosphorylation are also useful for alleviating a disorder, such as
XX CC tumorigenesis, tumour survival, growth and metastasis.

SQ Sequence 1722 BP; 381 A; 541 C; 563 G; 237 T; 0 other;
Query Match 15.5%; Score 373; DB 21; Length 1722;
Best Local Similarity 100.0%; Pred. No. 5e-160;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AGGTGTGCCAGAAAGTCAGGCGAGATCTCCTCTCTGAAGCAGCAGCTGAAGGAGTCCCGA 396
|||||
Db 1148 AGGTGTGCCAGAAAGTCAGGCGAGATCTCCTCTCTGAAGCAGCAGCTGAAGGAGTCCCGA 1207
|||||

QY 397 CGGAGGTGAACGCCAAGGCTAGCGAGATCTTGGGTCTCAAGGCACACAGCTGAAGGACACGC 456
|||||
Db 1208 CGGAGGTGAACGCCAAGGCTAGCGAGATCTTGGGTCTCAAGGCACACAGCTGAAGGACACGC 1267
|||||

QY 457 GGGGCAAGCTGGAGGCGCTGGAGCTGAGGACCCAGGACCTGGAGGGGCGCTGGGACCA 516
|||||
Db 1268 GGGGCAAGCTGGAGGCGCTGGAGCTGAGGACCCAGGACCTGGAGGGGCGCTGGGACCA 1327
|||||

QY 517 AGGGCTTGGAGCTGGAGGCTGTGTGAGATGAGCTGCAGCGCAAGAAAGACGAGCGGAGC 576
|||||
Db 1328 AGGGCTTGGAGCTGGAGGCTGTGTGAGATGAGCTGCAGCGCAAGAAAGACGAGCGGAGC 1387
|||||

QY 577 TGCTGGGGGAGAAAGGTGAACCTCTCTGGAGCAGGAGCTGCAGGAGCTGCGGGCCCGAGCCG 636
|||||
Db 1388 TGCTGGGGGAGAAAGGTGAACCTCTCTGGAGCAGGAGCTGCAGGAGCTGCGGGCCCGAGCCG 1447
|||||

QY 637 CCCTGGCCCGCGACATGGGGCCGCCACCTTCCCGGAGGACGTCCTGCGCTGCAGCGGG 696
|||||
Db 1448 CCCTGGCCCGCGACATGGGGCCGCCACCTTCCCGGAGGACGTCCTGCGCTGCAGCGGG 1507
|||||

QY 697 AGCTGGAGCGGCT 709

Db 1508 AGCTGGAGCGGCT 1520

RESULT 5

AAA64514

ID AAA64514 standard; cDNA; 1692 BP.

XX AC AAA64514;

XX DT 02-JAN-2001 (first entry)

XX DE Nucleotide sequence of truncated FEZ1 transcript G3611.

XX KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
tumour proliferation; tubulin; microtubule; protein Efi-gamma;
tubulin polymerisation disorder; mitosis initiation; cell proliferation;
cell growth; cell shape; cell rigidity; cell motility; DNA replication;
tumorigenesis; tumour survival; metastasis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT 1..1692
XX FT CDS /*tag= a
XX FT /product= "truncated FEZ1"

XX FT

XX PN WO200050565-A2.

XX XX 31-AUG-2000.

XX XX 25-FEB-2000; 2000WO-US04950.

XX XX 25-FEB-1999; 99US-0121537.

XX XX (UYJE-) UNIV JEFFERSON THOMAS.

XX XX Croce CM, Ishii H;

XX XX WPI; 2000-558396/51.

XX XX P-PSDB; AAB08721.

XX XX

CC cell shape, cell rigidity, cell motility, rate and stage of cellular
CC DNA replication, intracellular distribution of organelles, metastatic
CC potential of cell and cellular transformation from a non-cancerous to
CC cancerous phenotype. Compounds which modulate FEZ1 binding and
CC phosphorylation are also useful for alleviating a disorder, such as
CC tumorigenesis, tumour survival, growth and metastasis.

XX Sequence 1512 BP; 335 A; 483 C; 481 G; 213 T; 0 other;

Query Match 9.1%; Score 219; DB 21; Length 1512;
Best Local Similarity 100.0%; Pred. No. 9.6e-30; Mismatches 0; Indels 0; Gaps 0;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AGGTGTCAGAGTCCAGGAGATCTCCCTCTGAAGCAGCAGCTGAAGAGTCCAGCA 396
DB 1148 AGGTGTCAGAGTCCAGGAGATCTCCCTCTGAAGCAGCAGCTGAAGAGTCCAGCA 1207

QY 397 CGGAGGTGAACCCAGGCTAGCGAGATCTGGTCTCAAGGCACAGCTGAAGACAGC 456
DB 1208 CGGAGGTGAACCCAGGCTAGCGAGATCTGGTCTCAAGGCACAGCTGAAGACAGC 1267

QY 457 GGGCAAGCTGGAGGGCTTGAGCTGAGGACCCAGGACCTGGAGGGCCCTGCGCACCA 516
DB 1268 GGGCAAGCTGGAGGGCTTGAGCTGAGGACCCAGGACCTGGAGGGCCCTGCGCACCA 1327

QY 517 AGGCGCTGGAGCTGGAGGTCTGTGAGATGAGCTGCAGC 555
DB 1328 AGGCGCTGGAGCTGGAGGTCTGTGAGATGAGCTGCAGC 1366

RESULT 9
AAA64511
ID AAA64511 standard; cDNA; 633 BP.
AC AAA64511;
XX
XX 02-JAN-2001 (first entry)
DE Nucleotide sequence of truncated FEZ1 transcript E264162.
XX
XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
XX tumour proliferation; tubulin; microtubule; protein EPI-gamma;
XX tubulin polymerisation disorder; mitosis initiation; cell proliferation;
XX cell growth; cell shape; cell rigidity; cell motility; DNA replication;
XX tumorigenesis; tumour survival; metastasis; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..633
XX /*tag= a
XX /product= "truncated FEZ1"
XX
XX WO2000050565-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US04950.
XX
XX 25-FEB-1999; 99US-0121537.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Croce CM, Ishii H;
XX
XX WPI; 2000-558396/51.
XX P-PSDB; AAB08718.
XX
XX New polynucleotide homologous with a portion of one strand of the human
XX FEZ1 gene, useful for alleviating abnormal cell proliferation such as
XX cancer -
XX
XX Disclosure; Fig 5D; 255pp; English.

XX The present sequence encodes a truncated human FEZ1 polypeptide. The
CC encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour
CC suppressor gene, located at chromosome location 8p22. Decreased
CC or no expression of FEZ1 is detected in a variety of cancer cells.
CC Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
CC also interacts with tubulin, with microtubules, and with protein
CC EPI-gamma. Post-translational phosphorylation and dephosphorylation
CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
CC expression are useful for inducing cells to proliferate. Compounds
CC which modulate FEZ1 association with tubulin are useful for alleviating
CC tubulin hyper- or hypo- polymerisation disorders, such as those
CC associated with aberrant initiation of mitosis, modulation of the
CC initiation and rate of cell proliferation and cell growth, modulation of
CC cell shape, cell rigidity, cell motility, rate and stage of cellular
CC DNA replication, intracellular distribution of organelles, metastatic
CC potential of cell and cellular transformation from a non-cancerous to
CC cancerous phenotype. Compounds which modulate FEZ1 binding and
CC phosphorylation are also useful for alleviating a disorder, such as
CC tumorigenesis, tumour survival, growth and metastasis.

XX Sequence 633 BP; 136 A; 217 C; 175 G; 105 T; 0 other;

Query Match 3.3%; Score 80; DB 21; Length 633;
Best Local Similarity 100.0%; Pred. No. 2.7e-26;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 901 ACAGCGCCGGGAGCCCTTGGAGTTGACCTGGAAGGGCTGACATCCCTACGAGGACA 960
DB 554 ACAGCGCCGGGAGCCCTTGGAGTTGACCTGGAAGGGCTGACATCCCTACGAGGACA 613

QY 961 TCATAGCCACTGAGATCTGA 980
DB 614 TCATAGCCACTGAGATCTGA 633

RESULT 10
AAK8622/c
ID AAK8622 standard; cDNA; 687 BP.
XX
XX AAK8622;
XX
XX 05-NOV-2001 (first entry)
XX Human digestive system antigen coding sequence SEQ ID NO: 938.
XX
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
XX ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
XX digestive system disorder; Meckel's diverticulum; ss.
XX
XX Homo sapiens.
XX
XX WO200155314-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01324.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.

Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGGGAGCGGAGGTTGCAGTGAGCCAAAGATCACGCCACT 42
|||||
Db 309 GGGGAGCGGAGGTTGCAGTGAGCCAAAGATCACGCCACT 271
|||||

RESULT 11
ABK83564
ID ABK83564 standard; cDNA; 198161 BP.
AC ABK83564;
XX
XX
XX 14-AUG-2002 (first entry)
XX Human cDNA differentially expressed in granulocytic cells #135.
XX
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
XX Homo sapiens.
XX
XX W0200228999-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US30821.
XX
XX 03-OCT-2000; 2000US-237189P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX Claim 1; SEQ ID No 135; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC. Where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 198161 BP; 61561 A; 45946 C; 41360 G; 49294 T; 0 other;
Query Match 1.6%; Score 39; DB 24; Length 198161;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGGGAGCGGAGGTTGCAGTGAGCCAAAGATCACGCCACT 42
|||||
Db 150070 GGGGAGCGGAGGTTGCAGTGAGCCAAAGATCACGCCACT 150108
|||||

RESULT 12
AAC04727/c
ID AAC04727 standard; cDNA; 141 BP.
XX
XX AC AAC04727;
XX
XX DT 06-OCT-2000 (first entry)
XX
XX DE Human secreted protein 5' EST, SEQ ID NO: 8802.
XX
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1033401-A2.
XX
XX PD 06-SEP-2000.
XX
XX PF 21-FEB-2000; 2000EP-0200610.
XX
XX PR 26-FEB-1999; 99US-0122487.
XX
XX PA (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX PS Claim 1; SEQ ID 8802; 71pp + CD-ROM; English.
XX
XX CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design

```
CC expression and secretion vectors.
XX Sequence 141 BP; 20 A; 40 C; 37 G; 44 T; 0 other;
SQ Query Match 1.6%; Score 38; DB 21; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
Db 106 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 69

RESULT 13
AAI90310
ID AAI90310 standard; cDNA; 343 BP.
XX AC AAI90310;
XX DT 06-NOV-2001 (first entry)
XX Human polynucleotide SEQ ID NO 10370.
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation; ss.
XX OS Homo sapiens.
XX WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US04927.
XX PR 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX (HYSE-) HYSEQ INC.
XX Tang Yt, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX P-PSDB; AAO10379.
XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX Claim 1; SEQ ID NO 10370; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The vaccines or
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 343 BP; 122 A; 65 C; 68 G; 87 T; 1 other;
XX Query Match 1.6%; Score 38; DB 22; Length 343;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-07;
XX Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC expression and secretion vectors.
XX Sequence 141 BP; 20 A; 40 C; 37 G; 44 T; 0 other;
SQ Query Match 1.6%; Score 38; DB 24; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
Db 88 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 51

RESULT 14
ABL85949/c
ID ABL85949 standard; cDNA; 438 BP.
XX AC ABL85949;
XX DT 17-MAY-2002 (first entry)
XX Human ovarian cancer related cDNA clone SEQ ID NO:8927.
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX OS Homo sapiens.
XX PN WO200192581-A2.
XX PD 06-DEC-2001.
XX PF 29-MAY-2001; 2001WO-US17756.
XX PR 26-MAY-2000; 2000US-207484P.
XX PA (CORI-) CORIXA CORP.
XX Algate PA, Harlocker SL, Jones R;
XX WPI; 2002-122075/16.
XX Composition for therapy and diagnosis of ovarian cancer comprising
XX polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
XX polypeptide, antibody specific to polypeptide or T cell expressing
XX polypeptide -
XX Claim 1; SEQ ID 8927; 489pp; English.
XX The present invention describes a composition (I) comprising: carriers
XX and immunostimulants; and a polypeptide (II) of a ovarian tumour
XX polypeptide encoded by a polynucleotide (III) having a cDNA sequence
XX (S1) from the 10912 nucleotide sequences as given in ABL77023 to
XX ABL87934, (III) encoding (II) having a sequence (S2), a T cell
XX population of (III), or antigen presenting cells that express (II).
XX (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
XX (S1) can be used for detecting ovarian cancer in a patient's biological
XX sample preferably serum or ovarian tissue. The method comprises
XX contacting a biological sample from a patient with (IV), detecting the
XX amount of polynucleotide hybridising to (IV) and comparing the amount to
XX a predetermined cutoff value and thereby detecting ovarian cancer in the
XX patient, where the amount of polynucleotide hybridising to (IV) is
XX detected preferably by polymerase chain reaction (PCR). (I) comprising
XX (III) and/or (II) is useful for stimulating and/or expanding T cells
XX specific for an ovarian tumour protein comprising contacting T cells
XX with (III) or (II). (III) is useful in design and preparation of
XX ribozyme molecules for inhibiting expression of the tumour polypeptides
XX and proteins in tumour cells; and to isolate a full length gene from a
XX suitable library e.g., a tumour cDNA library using well known
XX techniques.
XX Sequence 438 BP; 67 A; 133 C; 102 G; 131 T; 5 other;
XX Query Match 1.6%; Score 38; DB 24; Length 438;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-07;
XX Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	37	1.5	87350	3	US-08-781-891-79	Sequence 79, Appl
C 2	37	1.5	87543	4	US-09-791-211-3	Sequence 3, Appli
C 3	37	1.5	99500	4	US-09-798-096-10	Sequence 10, Appl
C 4	35	1.5	29629	4	US-09-729-995-3	Sequence 3, Appli
C 5	35	1.5	162450	4	US-09-345-882-1	Sequence 1, Appli
C 6	34	1.4	8517	3	US-08-827-208-1	Sequence 1, Appli
C 7	34	1.4	8517	3	US-09-500-358-1	Sequence 1, Appli
C 8	34	1.4	8517	4	US-09-498-809-1	Sequence 1, Appli
C 9	32	1.3	62804	4	US-09-800-960-3	Sequence 3, Appli
C 10	31	1.3	3286	4	US-09-211-417-2	Sequence 2, Appli
C 11	31	1.3	4169	4	US-09-166-350-32	Sequence 32, Appl
C 12	31	1.3	15652	4	US-09-422-936-60	Sequence 60, Appl
C 13	31	1.3	17138	4	US-09-813-819-3	Sequence 3, Appli
C 14	31	1.3	17138	4	US-09-920-048-3	Sequence 3, Appli
C 15	31	1.3	38564	4	US-09-734-673-3	Sequence 3, Appli
C 16	31	1.3	50000	4	US-09-146-053-4	Sequence 4, Appli
C 17	31	1.3	72928	3	US-09-009-913-1	Sequence 1, Appli
C 18	31	1.3	81001	4	US-09-750-580-1	Sequence 1, Appli
C 19	31	1.3	152331	3	US-09-128-155-16	Sequence 16, Appl
C 20	31	1.3	176373	3	US-09-128-155-17	Sequence 17, Appl
C 21	31	1.3	246240	2	US-08-724-394A-20	Sequence 20, Appl
C 22	31	1.3	246240	2	US-08-724-394A-21	Sequence 21, Appl
C 23	31	1.3	246240	2	US-08-724-394A-22	Sequence 22, Appl
C 24	30	1.2	73	3	US-09-056-762-8	Sequence 8, Appli
C 25	30	1.2	1000	4	US-09-018-584A-33	Sequence 33, Appl
C 26	30	1.2	13158	4	US-08-687-080-105	Sequence 105, App
C 27	30	1.2	38844	4	US-09-734-675-3	Sequence 3, Appli

c 101	25	1.0	531	4	US-09-404-879A-24	Sequence 24, Appl	174	24	1.0	11298	4	US-09-103-663-31	Sequence 31, Appl
102	25	1.0	1001	4	US-09-641-638-175	Sequence 175, App	c 175	24	1.0	11811	4	US-09-078-294-7	Sequence 7, Appl
103	25	1.0	2503	4	US-09-198-122-7	Sequence 7, Appl	c 176	24	1.0	12143	4	US-09-423-744A-1	Sequence 1, Appl
104	25	1.0	16063	4	US-09-801-052-3	Sequence 3, Appl	c 177	24	1.0	14636	4	US-09-173-914-6	Sequence 6, Appl
105	25	1.0	17041	1	US-08-076-011-1	Sequence 1, Appl	c 178	24	1.0	14636	4	US-08-173-914-6	Sequence 35, Appl
106	25	1.0	87350	3	US-08-781-891-79	Sequence 79, Appl	c 179	24	1.0	14796	4	US-08-975-080-35	Sequence 10, Appl
107	25	1.0	87543	4	US-09-791-211-3	Sequence 3, Appl	c 180	24	1.0	14796	4	US-09-630-706-10	Sequence 3, Appl
108	25	1.0	112132	4	US-09-741-150-3	Sequence 3, Appl	c 181	24	1.0	14796	4	US-09-496-694B-3	Sequence 33, Appl
109	24	1.0	565	4	US-09-328-111-267	Sequence 267, App	c 182	24	1.0	15328	2	US-08-888-497-33	Sequence 33, Appl
c 110	24	1.0	629	4	US-09-385-982-204	Sequence 204, App	c 183	24	1.0	15328	2	US-09-362-230-33	Sequence 33, Appl
111	24	1.0	652	4	US-09-328-111-717	Sequence 717, App	c 184	24	1.0	15328	5	PCT-US94-07926-33	Sequence 15, Appl
112	24	1.0	689	4	US-08-105-542A-14	Sequence 14, Appl	c 185	24	1.0	17327	1	US-07-906-871-15	Sequence 4, Appl
113	24	1.0	700	4	US-08-991-789A-174	Sequence 174, App	c 186	24	1.0	17606	4	US-08-943-731-4	Sequence 36, Appl
114	24	1.0	700	4	US-09-062-451-174	Sequence 174, App	c 187	24	1.0	19011	1	US-08-310-356-36	Sequence 1, Appl
115	24	1.0	700	4	US-09-598-326-174	Sequence 174, App	c 188	24	1.0	19557	5	PCT-US92-06300-1	Sequence 3, Appl
c 116	24	1.0	798	4	US-09-288-143-21	Sequence 21, Appl	c 189	24	1.0	19806	4	US-09-740-028A-3	Sequence 6, Appl
117	24	1.0	825	2	US-08-486-148B-1	Sequence 1, Appl	c 190	24	1.0	20303	1	US-08-370-975B-6	Sequence 1, Appl
118	24	1.0	1001	4	US-09-641-638-208	Sequence 208, App	c 191	24	1.0	26764	1	US-08-370-975B-1	Sequence 3, Appl
119	24	1.0	1363	1	US-08-776-088-21	Sequence 21, Appl	c 192	24	1.0	36651	4	US-09-738-894A-3	Sequence 3, Appl
120	24	1.0	1363	5	PCT-US95-09145A-21	Sequence 5, Appl	c 193	24	1.0	36741	4	US-09-301-665-3	Sequence 6, Appl
121	24	1.0	1491	4	US-08-913-014A-5	Sequence 13, Appl	c 194	24	1.0	45546	4	US-09-146-053-6	Sequence 3, Appl
122	24	1.0	1534	1	US-08-480-784-13	Sequence 13, Appl	c 195	24	1.0	50000	4	US-09-146-053-3	Sequence 3, Appl
123	24	1.0	1534	1	US-08-483-553-13	Sequence 13, Appl	c 196	24	1.0	50000	4	US-09-146-053-3	Sequence 3, Appl
124	24	1.0	1534	1	US-08-487-002-13	Sequence 13, Appl	c 197	24	1.0	59065	4	US-09-813-817-3	Sequence 3, Appl
125	24	1.0	1534	1	US-08-483-554B-13	Sequence 13, Appl	c 198	24	1.0	59065	4	US-09-978-197-3	Sequence 3, Appl
126	24	1.0	1534	1	US-08-488-011B-13	Sequence 13, Appl	c 199	24	1.0	70000	4	US-09-851-896-3	Sequence 7, Appl
127	24	1.0	1534	4	US-08-850-727-13	Sequence 13, Appl	c 200	24	1.0	72604	4	US-09-268-992-7	Sequence 7, Appl
128	24	1.0	1534	5	PCT-US95-10202-13	Sequence 13, Appl	c 201	24	1.0	72604	4	US-09-657-474-7	Sequence 7, Appl
129	24	1.0	1534	5	PCT-US95-10203-13	Sequence 13, Appl	c 202	24	1.0	80246	4	US-09-078-294-4	Sequence 4, Appl
130	24	1.0	1534	5	PCT-US95-10220-13	Sequence 13, Appl	c 203	24	1.0	80595	4	US-09-078-294-3	Sequence 3, Appl
c 131	24	1.0	1656	1	US-08-324-465-2	Sequence 2, Appl	c 204	24	1.0	90050	4	US-09-245-041-5	Sequence 5, Appl
132	24	1.0	1656	2	US-08-465-981-2	Sequence 2, Appl	c 205	23	1.0	330	3	US-09-157-177-114	Sequence 114, App
c 133	24	1.0	1656	5	PCT-US93-11915-2	Sequence 2, Appl	c 206	23	1.0	586	4	US-08-906-156A-20	Sequence 20, Appl
c 134	24	1.0	1690	1	US-08-943-731-166	Sequence 166, App	c 207	23	1.0	587	4	US-08-906-156A-68	Sequence 68, Appl
c 135	24	1.0	1725	1	US-08-324-465-5	Sequence 5, Appl	c 208	23	1.0	609	4	US-09-385-982-237	Sequence 237, App
c 136	24	1.0	1725	5	PCT-US93-11915-5	Sequence 5, Appl	c 209	23	1.0	737	2	US-08-257-963B-41	Sequence 41, Appl
c 137	24	1.0	1725	5	PCT-US93-11915-5	Sequence 5, Appl	c 210	23	1.0	737	4	US-08-367-841A-41	Sequence 41, Appl
c 138	24	1.0	1901	5	PCT-US93-05000-32	Sequence 32, Appl	c 211	23	1.0	737	5	PCT-US95-07201-41	Sequence 41, Appl
139	24	1.0	1924	1	US-08-480-784-14	Sequence 14, Appl	c 212	23	1.0	955	4	US-09-641-638-22	Sequence 22, Appl
140	24	1.0	1924	1	US-08-483-553-14	Sequence 14, Appl	c 213	23	1.0	956	4	US-09-641-638-35	Sequence 35, Appl
141	24	1.0	1924	1	US-08-487-002-14	Sequence 14, Appl	c 214	23	1.0	1001	4	US-09-641-638-40A	Sequence 40A, App
142	24	1.0	1924	1	US-08-483-554B-14	Sequence 14, Appl	c 215	23	1.0	1001	4	US-09-641-638-522	Sequence 522, App
143	24	1.0	1924	1	US-08-488-011B-14	Sequence 14, Appl	c 216	23	1.0	1116	4	US-09-177-325-1	Sequence 1, Appl
144	24	1.0	1924	4	US-08-850-727-14	Sequence 14, Appl	c 217	23	1.0	1116	4	US-09-411-812A-1	Sequence 1, Appl
145	24	1.0	1924	5	PCT-US95-10202-14	Sequence 14, Appl	c 218	23	1.0	1116	4	US-09-590-113-1	Sequence 1, Appl
146	24	1.0	1924	5	PCT-US95-10203-14	Sequence 14, Appl	c 219	23	1.0	1278	2	US-08-309-965C-4	Sequence 4, Appl
c 147	24	1.0	1924	5	PCT-US95-10220-14	Sequence 14, Appl	c 220	23	1.0	1295	4	US-09-254-465A-8	Sequence 8, Appl
c 148	24	1.0	2022	2	US-08-464-517-32	Sequence 32, Appl	c 221	23	1.0	1410	5	PCT-US95-15428-14	Sequence 14, Appl
c 149	24	1.0	2022	2	US-08-246-361A-32	Sequence 32, Appl	c 222	23	1.0	1804	1	US-08-306-691B-40	Sequence 40, Appl
c 150	24	1.0	2022	3	US-08-463-772-32	Sequence 32, Appl	c 223	23	1.0	1804	4	US-09-167-322-14	Sequence 14, Appl
c 151	24	1.0	2334	4	US-09-493-565-1	Sequence 1, Appl	c 224	23	1.0	1804	4	PCT-US93-06251-82	Sequence 82, Appl
c 152	24	1.0	2419	2	US-08-785-662-13	Sequence 13, Appl	c 225	23	1.0	1817	3	US-08-564-496C-14	Sequence 14, Appl
c 153	24	1.0	2419	5	PCT-US95-08745-13	Sequence 13, Appl	c 226	23	1.0	2255	4	US-08-871-572B-3	Sequence 3, Appl
154	24	1.0	2448	2	US-08-687-080-111	Sequence 111, App	c 227	23	1.0	2296	4	US-09-851-896-11	Sequence 11, Appl
c 155	24	1.0	2921	3	US-08-618-100B-4	Sequence 4, Appl	c 228	23	1.0	2329	4	US-08-927-219-80	Sequence 80, Appl
c 156	24	1.0	3507	1	US-08-832-883-67	Sequence 67, Appl	c 229	23	1.0	2426	4	US-09-605-785-470	Sequence 470, App
c 157	24	1.0	3507	2	US-08-832-877-67	Sequence 67, Appl	c 230	23	1.0	2426	4	US-09-439-313-470	Sequence 470, App
158	24	1.0	4183	4	US-08-460-145-1	Sequence 1, Appl	c 231	23	1.0	2426	4	US-09-352-616A-470	Sequence 470, App
c 159	24	1.0	4421	2	US-08-257-963B-9	Sequence 9, Appl	c 232	23	1.0	2886	2	US-08-687-080-55	Sequence 55, Appl
160	24	1.0	4421	4	US-08-367-841A-9	Sequence 9, Appl	c 233	23	1.0	4326	2	US-08-852-807-12	Sequence 12, Appl
161	24	1.0	4421	4	US-08-520-373D-6	Sequence 6, Appl	c 234	23	1.0	4326	2	US-08-852-807-12	Sequence 12, Appl
162	24	1.0	4421	5	PCT-US95-07201-9	Sequence 9, Appl	c 235	23	1.0	4421	2	US-08-257-963B-9	Sequence 9, Appl
c 163	24	1.0	4793	4	US-09-561-497-10	Sequence 10, Appl	c 236	23	1.0	4421	4	US-08-367-841A-9	Sequence 9, Appl
164	24	1.0	5375	3	US-08-757-223-7	Sequence 7, Appl	c 237	23	1.0	4421	4	US-08-520-373D-6	Sequence 6, Appl
c 165	24	1.0	6623	2	US-08-687-080-68	Sequence 68, Appl	c 238	23	1.0	4421	5	PCT-US95-07201-9	Sequence 9, Appl
166	24	1.0	7452	3	US-08-592-500-1	Sequence 1, Appl	c 239	23	1.0	4550	4	US-09-103-663-35	Sequence 35, Appl
167	24	1.0	7452	3	US-08-195-006-1	Sequence 1, Appl	c 240	23	1.0	5789	4	US-09-242-948-3	Sequence 3, Appl
168	24	1.0	7452	5	PCT-US94-07644A-1	Sequence 1, Appl	c 241	23	1.0	6340	1	US-08-187-785-3	Sequence 3, Appl
c 169	24	1.0	8453	4	US-09-167-681-45	Sequence 45, Appl	c 242	23	1.0	6709	4	US-09-285-601-3	Sequence 3, Appl
c 170	24	1.0	10504	4	US-09-423-744A-19	Sequence 19, Appl	c 243	23	1.0	7210	2	US-08-257-963B-10	Sequence 10, Appl
171	24	1.0	10684	3	US-08-618-100B-3	Sequence 3, Appl	c 244	23	1.0	7210	4	US-08-367-841A-10	Sequence 10, Appl
172	24	1.0	11298	1	US-07-869-933-31	Sequence 31, Appl	c 245	23	1.0	7210	4	PCT-US95-07201-10	Sequence 10, Appl
173	24	1.0	11298	1	US-08-201-879A-2	Sequence 2, Appl	c 246	23	1.0	9837	1	US-08-832-883-68	Sequence 68, Appl

247	23	1.0	9837	2	US-08-832-877-68	Sequence 68, Appl	c 320	22	0.9	619	4	US-09-385-982-358	Sequence 358, App
248	23	1.0	10380	4	US-09-077-354B-3	Sequence 3, Appl	321	22	0.9	764	4	US-09-288-143-57	Sequence 57, Appl
249	23	1.0	11298	1	US-07-869-933-31	Sequence 31, Appl	322	22	0.9	826	4	US-09-288-143-45	Sequence 45, Appl
250	23	1.0	11298	1	US-08-201-879A-2	Sequence 2, Appl	323	22	0.9	1045	5	US-08-599-252-92	Sequence 92, Appl
251	23	1.0	11298	1	US-03-103-663-31	Sequence 31, Appl	324	22	0.9	1045	5	PCT-US96-06352-92	Sequence 92, Appl
252	23	1.0	11613	1	US-08-484-044-10	Sequence 10, Appl	325	22	0.9	1045	5	PCT-US96-06352-92	Sequence 92, Appl
253	23	1.0	11811	4	US-09-078-294-7	Sequence 7, Appl	326	22	0.9	1182	4	US-09-469-242-1	Sequence 1, Appl
254	23	1.0	12394	4	US-09-488-856A-10	Sequence 10, Appl	327	22	0.9	1247	4	US-09-178-115-110	Sequence 110, App
255	23	1.0	12565	4	US-09-345-217-3	Sequence 3, Appl	328	22	0.9	1247	4	US-09-177-776-110	Sequence 110, App
256	23	1.0	12597	4	US-09-705-299-12	Sequence 12, Appl	329	22	0.9	1448	4	US-09-387-212-12	Sequence 12, Appl
257	23	1.0	13674	2	US-08-852-807-1	Sequence 1, Appl	330	22	0.9	1448	4	US-09-948-802-12	Sequence 12, Appl
258	23	1.0	13674	2	US-08-852-807-1	Sequence 1, Appl	331	22	0.9	1542	4	US-09-008-271A-13	Sequence 13, Appl
259	23	1.0	14581	4	US-08-520-373D-4	Sequence 4, Appl	332	22	0.9	2071	4	US-09-816-088-1	Sequence 1, Appl
260	23	1.0	15297	4	US-09-817-180-3	Sequence 3, Appl	333	22	0.9	2119	2	US-08-381-691-17	Sequence 17, Appl
261	23	1.0	17327	1	US-07-906-871-15	Sequence 15, Appl	334	22	0.9	2415	3	US-09-019-689-1	Sequence 1, Appl
262	23	1.0	18596	4	US-09-318-448-11	Sequence 11, Appl	335	22	0.9	2501	3	US-08-787-739-58	Sequence 58, Appl
263	23	1.0	20674	4	US-09-641-638-651	Sequence 651, App	336	22	0.9	2501	4	US-09-178-115-58	Sequence 58, Appl
264	23	1.0	20674	4	US-09-641-638-651	Sequence 651, App	337	22	0.9	2501	4	US-09-177-776-58	Sequence 58, Appl
265	23	1.0	22481	4	US-08-367-841A-43	Sequence 43, Appl	338	22	0.9	2721	3	US-08-921-195-1	Sequence 1, Appl
266	23	1.0	22481	5	PCT-US95-07201-43	Sequence 43, Appl	339	22	0.9	3095	1	US-08-119-773-1	Sequence 1, Appl
267	23	1.0	22484	4	US-09-875-223-2	Sequence 2, Appl	340	22	0.9	3214	1	US-08-484-105-17	Sequence 17, Appl
268	23	1.0	32042	4	US-09-245-281-44	Sequence 44, Appl	341	22	0.9	3214	1	US-08-484-105-17	Sequence 17, Appl
269	23	1.0	35100	1	US-08-306-691B-19	Sequence 19, Appl	342	22	0.9	3532	3	US-08-787-739-90	Sequence 90, Appl
270	23	1.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl	343	22	0.9	3532	4	US-09-178-115-90	Sequence 90, Appl
271	23	1.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl	344	22	0.9	3532	4	US-09-177-776-90	Sequence 90, Appl
272	23	1.0	45716	4	US-08-965-048-5	Sequence 5, Appl	345	22	0.9	3885	1	US-08-688-145-1	Sequence 1, Appl
273	23	1.0	45989	4	US-08-965-048-5	Sequence 5, Appl	346	22	0.9	4136	4	US-09-103-875-2	Sequence 2, Appl
274	23	1.0	50000	4	US-09-146-053-4	Sequence 4, Appl	347	22	0.9	4233	4	US-09-056-105-27	Sequence 27, Appl
275	23	1.0	80246	4	US-09-078-294-4	Sequence 4, Appl	348	22	0.9	4285	4	US-09-040-774-1	Sequence 1, Appl
276	23	1.0	80595	4	US-09-078-294-3	Sequence 3, Appl	349	22	0.9	5037	4	US-09-705-299-13	Sequence 13, Appl
277	23	1.0	81001	4	US-09-750-580-1	Sequence 1, Appl	350	22	0.9	5137	5	PCT-US96-01314-39	Sequence 39, Appl
278	23	1.0	98844	4	US-09-791-211-10	Sequence 10, Appl	351	22	0.9	5138	2	US-08-476-062A-39	Sequence 39, Appl
279	23	1.0	111282	4	US-09-754-250-3	Sequence 3, Appl	352	22	0.9	5143	1	US-08-574-043A-7	Sequence 7, Appl
280	23	1.0	111282	4	US-09-754-250-3	Sequence 3, Appl	353	22	0.9	5143	2	US-08-795-015-7	Sequence 7, Appl
281	23	1.0	112132	4	US-09-741-150-3	Sequence 3, Appl	354	22	0.9	6235	4	US-09-305-384-5	Sequence 5, Appl
282	23	1.0	168575	4	US-09-426-290-1	Sequence 1, Appl	355	22	0.9	6678	3	US-08-816-617A-1	Sequence 1, Appl
283	23	1.0	176733	3	US-09-128-155-17	Sequence 17, Appl	356	22	0.9	6679	4	US-09-305-384-1	Sequence 1, Appl
284	23	1.0	68	4	US-09-358-972-253	Sequence 253, App	357	22	0.9	6709	4	US-09-285-601-3	Sequence 3, Appl
285	22	0.9	68	4	US-09-383-316-93	Sequence 93, Appl	358	22	0.9	6769	1	US-08-784-20	Sequence 20, Appl
286	22	0.9	257	3	US-08-741-402-3	Sequence 3, Appl	359	22	0.9	6769	1	US-08-480-784-20	Sequence 20, Appl
287	22	0.9	257	3	US-08-024-476-3	Sequence 3, Appl	360	22	0.9	6769	1	US-08-483-553-20	Sequence 20, Appl
288	22	0.9	262	2	US-08-481-658B-57	Sequence 57, Appl	361	22	0.9	6769	1	US-08-483-553-20	Sequence 20, Appl
289	22	0.9	262	2	US-08-481-658B-60	Sequence 60, Appl	362	22	0.9	6769	1	US-08-487-002-20	Sequence 20, Appl
290	22	0.9	262	2	US-08-481-658B-60	Sequence 60, Appl	363	22	0.9	6769	1	US-08-487-002-20	Sequence 20, Appl
291	22	0.9	262	2	US-08-477-504A-57	Sequence 57, Appl	364	22	0.9	6769	1	US-08-483-554B-20	Sequence 20, Appl
292	22	0.9	262	2	US-08-477-504A-60	Sequence 60, Appl	365	22	0.9	6769	1	US-08-483-554B-20	Sequence 20, Appl
293	22	0.9	262	2	US-08-486-756A-57	Sequence 57, Appl	366	22	0.9	6769	1	US-08-488-011B-20	Sequence 20, Appl
294	22	0.9	262	2	US-08-486-756A-60	Sequence 60, Appl	367	22	0.9	6769	1	US-08-488-011B-20	Sequence 20, Appl
295	22	0.9	262	2	US-08-485-862B-57	Sequence 57, Appl	368	22	0.9	6769	4	US-08-850-727-20	Sequence 20, Appl
296	22	0.9	262	2	US-08-485-862B-60	Sequence 60, Appl	369	22	0.9	6769	4	US-08-850-727-20	Sequence 20, Appl
297	22	0.9	262	3	US-08-787-739-57	Sequence 57, Appl	370	22	0.9	6769	5	PCT-US95-10202-20	Sequence 20, Appl
298	22	0.9	262	3	US-08-787-739-60	Sequence 60, Appl	371	22	0.9	6769	5	PCT-US95-10202-20	Sequence 20, Appl
299	22	0.9	262	3	US-08-487-077A-57	Sequence 57, Appl	372	22	0.9	6769	5	PCT-US95-10203-20	Sequence 20, Appl
300	22	0.9	262	3	US-08-487-077A-60	Sequence 60, Appl	373	22	0.9	6769	5	PCT-US95-10203-20	Sequence 20, Appl
301	22	0.9	262	3	US-08-485-863A-57	Sequence 57, Appl	374	22	0.9	6769	5	PCT-US95-10220-20	Sequence 20, Appl
302	22	0.9	262	3	US-08-485-863A-60	Sequence 60, Appl	375	22	0.9	6769	5	PCT-US95-10220-20	Sequence 20, Appl
303	22	0.9	262	4	US-08-485-049D-60	Sequence 60, Appl	376	22	0.9	7228	2	US-08-850-049-128	Sequence 128, App
304	22	0.9	262	4	US-09-178-115-57	Sequence 57, Appl	377	22	0.9	7228	2	US-08-850-049-128	Sequence 128, App
305	22	0.9	262	4	US-08-178-115-60	Sequence 60, Appl	378	22	0.9	7228	2	US-08-050-478-128	Sequence 128, App
306	22	0.9	262	4	US-09-177-776-57	Sequence 57, Appl	379	22	0.9	7228	2	US-08-050-478-128	Sequence 128, App
307	22	0.9	262	4	US-09-177-776-60	Sequence 60, Appl	380	22	0.9	7228	4	US-09-414-117-128	Sequence 128, App
308	22	0.9	423	4	US-08-943-731-131	Sequence 131, App	381	22	0.9	7228	4	US-09-414-117-129	Sequence 129, App
309	22	0.9	489	4	US-09-370-838-109	Sequence 109, App	382	22	0.9	7228	4	US-09-678-437-128	Sequence 128, App
310	22	0.9	498	4	US-09-078-294-29	Sequence 29, Appl	383	22	0.9	7228	4	US-09-678-437-129	Sequence 129, App
311	22	0.9	517	1	US-08-480-784-33	Sequence 33, Appl	384	22	0.9	7301	4	US-09-816-088-3	Sequence 3, Appl
312	22	0.9	517	1	US-08-483-553-33	Sequence 33, Appl	385	22	0.9	7379	4	US-09-341-587-5	Sequence 5, Appl
313	22	0.9	517	1	US-08-487-002-33	Sequence 33, Appl	386	22	0.9	7676	1	US-08-451-778A-7	Sequence 7, Appl
314	22	0.9	517	1	US-08-483-554B-33	Sequence 33, Appl	387	22	0.9	7676	2	US-08-451-778A-7	Sequence 7, Appl
315	22	0.9	517	1	US-08-488-011B-33	Sequence 33, Appl	388	22	0.9	7676	2	US-08-998-208-7	Sequence 7, Appl
316	22	0.9	517	4	US-08-850-727-33	Sequence 33, Appl	389	22	0.9	7676	5	PCT-US95-05743-7	Sequence 7, Appl
317	22	0.9	517	5	PCT-US95-10202-33	Sequence 33, Appl	390	22	0.9	9365	4	US-09-608-285A-8	Sequence 8, Appl
318	22	0.9	517	5	PCT-US95-10203-33	Sequence 33, Appl	391	22	0.9	9365	4	US-09-350-836B-8	Sequence 8, Appl
319	22	0.9	517	5	PCT-US95-10220-33	Sequence 33, Appl	392	22	0.9	9365	4	US-09-370-265-8	Sequence 8, Appl

393	22	0.9	10898	2	US-08-481-658B-5	Sequence 5, Appli	c 466	21	0.9	5261	1	US-08-366-051B-3	Sequence 3, Appli
394	22	0.9	10898	2	US-08-477-504A-5	Sequence 5, Appli	c 467	21	0.9	5543	2	US-08-687-080-101	Sequence 101, App
395	22	0.9	10898	2	US-08-485-756A-1	Sequence 5, Appli	c 468	21	0.9	5581	4	US-08-973-544-1	Sequence 1, Appli
396	22	0.9	10898	2	US-08-485-862B-5	Sequence 5, Appli	c 469	21	0.9	5668	4	US-09-112-096-14	Sequence 14, Appli
397	22	0.9	10898	3	US-08-787-739-5	Sequence 5, Appli	c 470	21	0.9	5668	4	US-09-605-785-777	Sequence 777, App
398	22	0.9	10898	3	US-08-487-077A-5	Sequence 5, Appli	c 471	21	0.9	5668	4	US-08-195-744-4	Sequence 4, Appli
399	22	0.9	10898	3	US-08-485-863A-5	Sequence 5, Appli	c 472	21	0.9	6063	1	US-08-788-279-4	Sequence 4, Appli
400	22	0.9	10898	4	US-08-485-049D-5	Sequence 5, Appli	c 473	21	0.9	6063	2	US-09-305-639-1	Sequence 1, Appli
401	22	0.9	10898	4	US-09-178-115-5	Sequence 5, Appli	c 474	21	0.9	7622	3	US-08-611-587-1	Sequence 1, Appli
402	22	0.9	10898	4	US-09-177-776-5	Sequence 5, Appli	c 475	21	0.9	8353	3	US-08-080-255-6	Sequence 6, Appli
403	22	0.9	14747	4	US-09-608-285A-42	Sequence 42, Appli	c 476	21	0.9	8392	3	US-08-465-713-6	Sequence 6, Appli
404	22	0.9	15581	3	US-08-646-538-35	Sequence 35, Appli	c 477	21	0.9	8392	5	PCT-US93-05857-6	Sequence 6, Appli
405	22	0.9	15581	4	US-09-503-222-35	Sequence 35, Appli	c 478	21	0.9	9301	4	US-09-449-218D-18	Sequence 18, Appli
406	22	0.9	15977	4	US-08-608-285A-59	Sequence 59, Appli	c 479	21	0.9	10825	3	US-08-652-265-1	Sequence 1, Appli
407	22	0.9	16389	4	US-09-741-154-3	Sequence 3, Appli	c 480	21	0.9	10825	3	US-08-652-265-3	Sequence 3, Appli
408	22	0.9	16389	4	US-09-741-154-3	Sequence 3, Appli	c 481	21	0.9	10825	3	US-08-652-265-5	Sequence 5, Appli
409	22	0.9	18443	4	US-09-078-294-6	Sequence 6, Appli	c 482	21	0.9	10825	3	US-08-652-265-7	Sequence 7, Appli
410	22	0.9	18596	4	US-09-318-448-11	Sequence 11, Appli	c 483	21	0.9	10825	3	US-08-834-497A-1	Sequence 1, Appli
411	22	0.9	19736	4	US-09-740-035-3	Sequence 3, Appli	c 484	21	0.9	10825	3	US-08-834-497A-3	Sequence 3, Appli
412	22	0.9	19736	4	US-09-740-035-3	Sequence 3, Appli	c 485	21	0.9	10825	3	US-08-834-497A-5	Sequence 5, Appli
413	22	0.9	2183	4	US-08-943-731-3	Sequence 3, Appli	c 486	21	0.9	10825	3	US-08-834-497A-7	Sequence 7, Appli
414	22	0.9	32042	4	US-09-245-281-44	Sequence 44, Appli	c 487	21	0.9	10825	4	US-09-503-444A-1	Sequence 1, Appli
415	22	0.9	36741	4	US-09-301-665-3	Sequence 3, Appli	c 488	21	0.9	10825	4	US-09-503-444A-3	Sequence 3, Appli
416	22	0.9	40000	4	US-08-780-049-18	Sequence 18, Appli	c 489	21	0.9	10825	4	US-09-503-444A-5	Sequence 5, Appli
417	22	0.9	40352	3	US-08-846-111D-15	Sequence 15, Appli	c 490	21	0.9	10825	4	US-09-503-444A-7	Sequence 7, Appli
418	22	0.9	40352	4	US-09-443-077-15	Sequence 15, Appli	c 491	21	0.9	11288	4	US-08-646-301A-1	Sequence 1, Appli
419	22	0.9	42571	4	US-08-810-347-3	Sequence 3, Appli	c 492	21	0.9	11288	4	US-08-481-968A-4	Sequence 4, Appli
420	22	0.9	49136	4	US-09-422-869-1	Sequence 1, Appli	c 493	21	0.9	11288	4	US-08-154-712B-4	Sequence 4, Appli
421	22	0.9	169998	4	US-08-676-610B-24	Sequence 24, Appli	c 494	21	0.9	12146	4	US-09-277-457-27	Sequence 27, Appli
422	21	0.9	60	2	US-08-454-557C-66	Sequence 66, Appli	c 495	21	0.9	14796	4	US-08-975-080-35	Sequence 35, Appli
423	21	0.9	60	2	US-08-340-426D-66	Sequence 66, Appli	c 496	21	0.9	14796	4	US-09-630-706-10	Sequence 10, Appli
424	21	0.9	60	2	US-08-450-673C-66	Sequence 66, Appli	c 497	21	0.9	14796	4	US-09-496-694B-3	Sequence 3, Appli
425	21	0.9	60	5	PCT-US95-17111A-66	Sequence 66, Appli	c 498	21	0.9	26684	4	US-09-564-805-28	Sequence 28, Appli
426	21	0.9	377	2	US-08-454-557C-37	Sequence 37, Appli	c 499	21	0.9	31571	1	US-08-323-443B-1	Sequence 1, Appli
427	21	0.9	377	2	US-08-340-426D-37	Sequence 37, Appli	c 500	21	0.9	36159	4	US-09-749-588-3	Sequence 3, Appli
428	21	0.9	377	5	PCT-US95-17111A-37	Sequence 37, Appli	c 501	21	0.9	38564	4	US-09-734-673-3	Sequence 3, Appli
429	21	0.9	377	5	PCT-US95-17111A-37	Sequence 37, Appli	c 502	21	0.9	65042	4	US-09-784-316-3	Sequence 3, Appli
430	21	0.9	379	3	US-09-157-177-134	Sequence 134, App	c 503	21	0.9	152331	3	US-09-128-155-16	Sequence 16, Appli
431	21	0.9	542	4	US-09-305-639-5	Sequence 5, Appli	c 504	20	0.8	57	3	US-09-056-762-9	Sequence 9, Appli
432	21	0.9	561	4	US-09-404-879A-50	Sequence 50, Appli	c 505	20	0.8	75	3	US-09-056-762-7	Sequence 7, Appli
433	21	0.9	569	4	US-08-943-731-144	Sequence 144, App	c 506	20	0.8	674	4	US-09-328-111-76	Sequence 76, Appli
434	21	0.9	591	4	US-09-385-982-406	Sequence 406, App	c 507	20	0.8	788	4	US-09-288-143-27	Sequence 27, Appli
435	21	0.9	618	4	US-09-328-111-215	Sequence 215, App	c 508	20	0.8	1052	4	US-09-442-143A-9	Sequence 9, Appli
436	21	0.9	951	4	US-09-605-785-570	Sequence 570, App	c 509	20	0.8	1554	1	US-08-370-975B-10	Sequence 10, Appli
437	21	0.9	999	4	US-08-641-638-290	Sequence 290, App	c 510	20	0.8	1589	1	US-07-971-092-1	Sequence 1, Appli
438	21	0.9	1000	2	US-08-718-538-1	Sequence 1, Appli	c 511	20	0.8	1611	6	5198342-1	Patent No. 5198342
439	21	0.9	1381	2	US-08-454-557C-49	Sequence 49, Appli	c 512	20	0.8	1634	2	US-08-852-807-10	Sequence 10, Appli
440	21	0.9	1381	2	US-08-340-426D-49	Sequence 49, Appli	c 513	20	0.8	1773	4	US-08-943-731-215	Sequence 215, App
441	21	0.9	1381	2	US-08-450-673C-49	Sequence 49, Appli	c 514	20	0.8	2372	1	US-07-903-103-1	Sequence 1, Appli
442	21	0.9	1386	5	PCT-US95-17111A-49	Sequence 49, Appli	c 515	20	0.8	2372	1	US-08-044-619A-1	Sequence 1, Appli
443	21	0.9	1386	2	US-08-687-080-76	Sequence 76, Appli	c 516	20	0.8	2372	1	US-08-283-911-1	Sequence 1, Appli
444	21	0.9	1418	5	PCT-US95-17111A-120	Sequence 120, App	c 517	20	0.8	2372	1	US-08-245-500A-2	Sequence 2, Appli
445	21	0.9	1442	2	US-08-454-557C-120	Sequence 120, App	c 518	20	0.8	2372	1	US-08-390-546-2	Sequence 2, Appli
446	21	0.9	1442	2	US-08-340-426D-120	Sequence 120, App	c 519	20	0.8	2372	1	US-08-390-479A-2	Sequence 2, Appli
447	21	0.9	1442	2	US-08-450-673C-120	Sequence 120, App	c 520	20	0.8	2372	1	US-08-557-393-2	Sequence 2, Appli
448	21	0.9	1480	2	US-08-454-557C-38	Sequence 38, Appli	c 521	20	0.8	2372	1	US-08-390-516C-2	Sequence 2, Appli
449	21	0.9	1480	2	US-08-340-426D-38	Sequence 38, Appli	c 522	20	0.8	2372	1	US-08-390-517A-2	Sequence 2, Appli
450	21	0.9	1480	5	PCT-US95-17111A-38	Sequence 38, Appli	c 523	20	0.8	2372	1	US-08-390-515A-2	Sequence 2, Appli
451	21	0.9	1480	5	PCT-US95-17111A-38	Sequence 38, Appli	c 524	20	0.8	2372	2	US-08-801-718-2	Sequence 2, Appli
452	21	0.9	2127	1	US-08-832-883-54	Sequence 54, Appli	c 525	20	0.8	2372	4	US-09-073-567-1	Sequence 1, Appli
453	21	0.9	2127	2	US-08-832-883-54	Sequence 54, Appli	c 526	20	0.8	2372	4	US-09-280-805-1	Sequence 1, Appli
454	21	0.9	2542	1	US-08-441-370-1	Sequence 1, Appli	c 527	20	0.8	2372	4	US-09-048-810-1	Sequence 1, Appli
455	21	0.9	2559	2	US-08-886-152-4	Sequence 4, Appli	c 528	20	0.8	2372	4	US-09-170-159A-2	Sequence 2, Appli
456	21	0.9	2559	4	US-08-196-222-4	Sequence 4, Appli	c 529	20	0.8	2372	4	US-09-480-718-43	Sequence 43, Appli
457	21	0.9	3224	4	US-08-965-729A-2	Sequence 2, Appli	c 530	20	0.8	2950	5	PCT-US93-08386-7	Sequence 7, Appli
458	21	0.9	3431	4	US-09-632-098-1	Sequence 1, Appli	c 531	20	0.8	2957	2	US-08-394-152A-48	Sequence 48, Appli
459	21	0.9	3468	4	US-09-632-098-3	Sequence 3, Appli	c 532	20	0.8	2968	5	PCT-US93-08386-1	Sequence 1, Appli
460	21	0.9	3848	4	US-09-112-096-28	Sequence 28, Appli	c 533	20	0.8	3017	2	US-08-394-152A-39	Sequence 39, Appli
461	21	0.9	4576	1	US-08-832-883-49	Sequence 49, Appli	c 534	20	0.8	3441	4	US-09-026-033-17	Sequence 17, Appli
462	21	0.9	4576	2	US-08-832-883-49	Sequence 49, Appli	c 535	20	0.8	4630	4	US-09-442-143A-1	Sequence 1, Appli
463	21	0.9	4803	4	US-09-197-636-1	Sequence 1, Appli	c 536	20	0.8	5232	3	US-09-212-971-3	Sequence 3, Appli
464	21	0.9	4803	4	US-09-197-636-3	Sequence 3, Appli	c 537	20	0.8	5232	3	US-08-800-929A-3	Sequence 3, Appli
465	21	0.9	5261	1	US-08-045-806-3	Sequence 3, Appli	c 538	20	0.8	5232	4	US-09-617-053A-3	Sequence 3, Appli

539	20	0.8	6246	4	US-08-943-731-640	Sequence 640, App	612	19	0.8	18073	4	US-09-078-294-12	Sequence 12, Appl
540	20	0.8	6464	2	US-08-400-159-5	Sequence 5, Appl	c 613	19	0.8	35060	3	US-08-814-095-7	Sequence 7, Appl
541	20	0.8	6464	3	US-08-611-729A-5	Sequence 5, Appl	c 614	19	0.8	72928	3	US-09-009-913-1	Sequence 1, Appl
542	20	0.8	7610	4	US-09-659-975B-12	Sequence 12, Appl	c 615	18	0.7	20	4	US-09-280-805-245	Sequence 245, App
543	20	0.8	26764	1	US-08-370-975B-1	Sequence 1, Appl	c 616	18	0.7	149	2	US-08-454-557C-89	Sequence 89, Appl
544	20	0.8	29629	4	US-09-729-995-3	Sequence 3, Appl	c 617	18	0.7	149	2	US-08-340-426B-89	Sequence 89, Appl
545	20	0.8	44453	4	US-09-146-053-5	Sequence 5, Appl	c 618	18	0.7	149	2	US-08-450-673C-89	Sequence 89, Appl
546	20	0.8	49136	4	US-09-422-869-1	Sequence 1, Appl	c 619	18	0.7	149	5	PCT-US95-1711A-89	Sequence 89, Appl
547	20	0.8	51259	3	US-08-781-891-209	Sequence 209, App	620	18	0.7	165	1	US-08-209-747-9	Sequence 9, Appl
548	20	0.8	168575	4	US-09-426-290-1	Sequence 1, Appl	621	18	0.7	165	1	US-08-458-298-9	Sequence 9, Appl
549	19	0.8	320	3	US-09-157-177-131	Sequence 131, App	622	18	0.7	300	4	US-09-199-637A-198	Sequence 198, App
550	19	0.8	434	2	US-08-332-766A-10	Sequence 10, App	623	18	0.7	325	2	US-08-940-332-3	Sequence 3, Appl
551	19	0.8	462	4	US-09-328-111-79	Sequence 79, App	624	18	0.7	345	4	US-09-385-982-164	Sequence 164, App
552	19	0.8	523	4	US-09-286-132-8	Sequence 8, Appl	c 625	18	0.7	372	4	US-09-018-584A-13	Sequence 13, Appl
553	19	0.8	523	4	US-09-836-941-8	Sequence 8, Appl	626	18	0.7	378	4	US-09-199-637A-197	Sequence 197, App
554	19	0.8	542	4	US-09-461-697-136	Sequence 136, App	627	18	0.7	396	4	US-09-199-637A-262	Sequence 262, App
555	19	0.8	588	4	US-09-385-982-128	Sequence 128, App	628	18	0.7	411	4	US-09-385-982-5	Sequence 5, Appl
556	19	0.8	597	4	US-08-286-132-7	Sequence 7, Appl	629	18	0.7	423	4	US-09-199-637A-196	Sequence 196, App
557	19	0.8	597	4	US-09-836-941-7	Sequence 7, Appl	c 630	18	0.7	461	4	US-09-404-879A-1	Sequence 1, Appl
558	19	0.8	738	4	US-09-662-250A-23	Sequence 23, App	c 631	18	0.7	461	4	US-09-404-879A-3	Sequence 3, Appl
559	19	0.8	1000	4	US-09-018-584A-40	Sequence 40, App	c 632	18	0.7	489	4	US-09-199-637A-260	Sequence 260, App
560	19	0.8	1001	4	US-09-641-638-397	Sequence 397, App	c 633	18	0.7	624	1	US-08-776-088-7	Sequence 7, Appl
561	19	0.8	1320	1	US-08-599-252-84	Sequence 84, App	634	18	0.7	624	5	PCT-US95-09145A-7	Sequence 7, Appl
562	19	0.8	1320	1	US-08-436-074-57	Sequence 57, App	635	18	0.7	670	4	US-09-605-785-680	Sequence 680, App
563	19	0.8	1320	5	PCT-US96-06352-84	Sequence 84, App	636	18	0.7	687	4	US-09-199-637A-195	Sequence 195, App
564	19	0.8	1320	5	PCT-US96-06583-84	Sequence 84, App	637	18	0.7	690	4	US-09-199-637A-194	Sequence 194, App
565	19	0.8	1366	4	US-09-265-630-10	Sequence 10, App	c 638	18	0.7	690	4	US-09-199-637A-264	Sequence 264, App
566	19	0.8	1509	4	US-09-265-630-12	Sequence 12, App	c 639	18	0.7	957	4	US-09-199-637A-193	Sequence 193, App
567	19	0.8	1725	4	US-09-082-440-3	Sequence 3, Appl	640	18	0.7	1001	4	US-09-641-638-319	Sequence 319, App
568	19	0.8	1725	4	US-09-712-495-3	Sequence 3, Appl	c 641	18	0.7	1001	4	US-09-641-638-521	Sequence 521, App
569	19	0.8	1762	4	US-09-443-184-35	Sequence 35, App	c 642	18	0.7	1275	2	US-08-958-642-1	Sequence 1, Appl
570	19	0.8	1798	4	US-09-345-214-16	Sequence 16, App	c 643	18	0.7	1275	3	US-08-778-394-3	Sequence 3, Appl
571	19	0.8	2019	4	US-09-345-214-15	Sequence 15, App	c 644	18	0.7	1275	3	US-08-778-423A-1	Sequence 1, Appl
572	19	0.8	2053	4	US-09-227-357-45	Sequence 45, App	c 645	18	0.7	1288	4	US-08-047-041A-24	Sequence 24, Appl
573	19	0.8	2248	4	US-09-345-214-20	Sequence 20, App	c 646	18	0.7	1288	4	US-09-417-278A-1	Sequence 1, Appl
574	19	0.8	2262	4	US-09-286-132-1	Sequence 1, Appl	c 647	18	0.7	1316	1	US-08-047-041A-11	Sequence 11, Appl
575	19	0.8	2262	4	US-09-836-941-1	Sequence 1, Appl	c 648	18	0.7	1316	2	US-08-795-006A-31	Sequence 31, Appl
576	19	0.8	2387	4	US-09-375-318-38	Sequence 38, App	c 649	18	0.7	1316	4	US-09-184-073-31	Sequence 31, Appl
577	19	0.8	2589	2	US-08-482-728A-3	Sequence 3, Appl	c 650	18	0.7	1558	4	US-09-123-030-7	Sequence 7, Appl
578	19	0.8	2743	1	US-08-317-707-1	Sequence 1, Appl	651	18	0.7	1624	4	US-08-430-225A-19	Sequence 19, Appl
579	19	0.8	3760	2	US-08-724-354D-1	Sequence 1, Appl	652	18	0.7	1643	2	US-08-933-750C-68	Sequence 68, Appl
580	19	0.8	3760	3	US-09-270-984A-1	Sequence 1, Appl	653	18	0.7	1643	3	US-09-234-613-68	Sequence 68, Appl
581	19	0.8	4041	1	US-08-147-812-4	Sequence 4, Appl	654	18	0.7	1653	4	US-09-199-637A-192	Sequence 192, App
582	19	0.8	4110	3	US-09-123-708-1	Sequence 1, Appl	655	18	0.7	1827	4	US-09-199-637A-191	Sequence 191, App
583	19	0.8	4110	3	US-09-123-624-1	Sequence 1, Appl	656	18	0.7	1844	1	US-07-872-644-26	Sequence 26, Appl
584	19	0.8	4165	1	US-08-147-812-6	Sequence 6, Appl	657	18	0.7	1844	1	US-08-297-494-26	Sequence 26, Appl
585	19	0.8	4265	4	US-09-651-011A-3	Sequence 3, Appl	658	18	0.7	1844	1	US-08-297-510-26	Sequence 26, Appl
586	19	0.8	4441	4	US-09-641-999-2	Sequence 2, Appl	659	18	0.7	1844	1	US-08-479-532-26	Sequence 26, Appl
587	19	0.8	4543	2	US-08-519-547A-5	Sequence 5, Appl	660	18	0.7	1844	1	US-08-455-526-26	Sequence 26, Appl
588	19	0.8	5037	4	US-09-705-299-13	Sequence 13, App	661	18	0.7	1844	1	US-08-455-525-26	Sequence 26, Appl
589	19	0.8	6038	4	US-09-305-639-4	Sequence 4, Appl	662	18	0.7	1844	1	US-09-139-491-26	Sequence 26, Appl
590	19	0.8	7152	4	US-09-167-681-29	Sequence 29, App	663	18	0.7	1844	5	PCT-US92-03222-26	Sequence 26, Appl
591	19	0.8	7210	2	US-08-257-963B-10	Sequence 10, App	664	18	0.7	1920	4	US-09-199-637A-190	Sequence 190, App
592	19	0.8	7210	4	US-08-367-841A-10	Sequence 10, App	665	18	0.7	1932	4	US-09-199-637A-189	Sequence 189, App
593	19	0.8	7210	5	PCT-US95-07201-10	Sequence 10, App	666	18	0.7	1938	4	US-09-199-637A-252	Sequence 252, App
594	19	0.8	7622	4	US-09-305-639-1	Sequence 1, Appl	667	18	0.7	1999	4	US-09-167-109-4	Sequence 4, Appl
595	19	0.8	8367	2	US-08-583-562B-7	Sequence 7, Appl	668	18	0.7	2004	2	US-08-691-814B-1	Sequence 1, Appl
596	19	0.8	8367	2	US-08-779-113-7	Sequence 7, Appl	669	18	0.7	2101	4	US-09-199-637A-102	Sequence 102, App
597	19	0.8	8396	4	US-09-328-174A-1	Sequence 1, Appl	670	18	0.7	2265	2	US-08-940-332-1	Sequence 1, Appl
598	19	0.8	8409	1	US-09-167-681-37	Sequence 37, App	c 671	18	0.7	2336	1	US-08-247-946A-1	Sequence 1, Appl
599	19	0.8	9103	1	US-08-466-033-182	Sequence 182, App	c 672	18	0.7	2336	5	PCT-US95-06420-1	Sequence 1, Appl
600	19	0.8	9103	1	US-08-444-733-182	Sequence 182, App	673	18	0.7	2373	4	US-08-975-762-45	Sequence 45, Appl
601	19	0.8	9103	2	US-08-464-134-182	Sequence 182, App	674	18	0.7	2373	4	US-09-295-028-45	Sequence 45, Appl
602	19	0.8	9103	2	US-08-461-361-182	Sequence 182, App	675	18	0.7	2373	4	US-09-106-582-45	Sequence 45, Appl
603	19	0.8	9103	2	US-08-485-910-182	Sequence 182, App	676	18	0.7	2539	3	US-09-000-016-3	Sequence 3, Appl
604	19	0.8	9103	5	PCT-US95-06266-156	Sequence 156, App	677	18	0.7	2539	4	US-09-514-340-3	Sequence 3, Appl
605	19	0.8	9388	4	US-08-991-789A-141	Sequence 141, App	678	18	0.7	2679	1	US-08-479-328-1	Sequence 1, Appl
606	19	0.8	9388	4	US-09-062-451-141	Sequence 141, App	679	18	0.7	2679	1	US-08-761-119-1	Sequence 1, Appl
607	19	0.8	9388	4	US-09-598-326-141	Sequence 141, App	680	18	0.7	2679	2	US-08-668-128B-1	Sequence 1, Appl
608	19	0.8	12394	4	US-09-488-856A-10	Sequence 10, App	681	18	0.7	2679	2	US-08-805-445-1	Sequence 1, Appl
609	19	0.8	13875	2	US-08-734-344-1	Sequence 1, Appl	682	18	0.7	2679	3	US-08-959-625-1	Sequence 1, Appl
610	19	0.8	14747	4	US-09-608-285A-42	Sequence 42, App	683	18	0.7	2679	3	US-09-008-466-1	Sequence 1, Appl
611	19	0.8	15977	4	US-09-608-285A-59	Sequence 59, App	684	18	0.7	2679	3	US-08-580-980A-1	Sequence 1, Appl

685	18	0.7	2679	3	US-09-053-453-1	Sequence 1, Appli	758	17	0.7	841	5	PCT-US93-06251-80	Sequence 80, Appli
686	18	0.7	2679	3	US-08-644-116A-1	Sequence 1, Appli	759	17	0.7	841	5	PCT-US93-06251-81	Sequence 81, Appli
687	18	0.7	2793	1	US-08-209-747-1	Sequence 1, Appli	760	17	0.7	882	4	US-09-134-001C-1530	Sequence 530, Appli
688	18	0.7	2793	1	US-08-458-298-1	Sequence 1, Appli	761	17	0.7	882	4	US-09-288-143-55	Sequence 55, Appli
689	18	0.7	2809	3	US-09-000-016-1	Sequence 1, Appli	762	17	0.7	885	4	US-09-247-155-141	Sequence 141, Appli
690	18	0.7	2809	3	US-09-514-340-1	Sequence 1, Appli	763	17	0.7	891	4	US-08-961-083-23	Sequence 23, Appli
691	18	0.7	2885	3	US-08-948-705-2	Sequence 2, Appli	764	17	0.7	895	3	US-09-641-638-636	Sequence 636, Appli
692	18	0.7	2884	4	US-08-605-785-335	Sequence 335, App	765	17	0.7	1000	4	US-09-641-638-637	Sequence 637, App
693	18	0.7	2984	4	US-08-439-313-335	Sequence 335, App	766	17	0.7	1000	4	US-09-641-638-86	Sequence 86, Appli
694	18	0.7	2984	4	US-09-352-616A-335	Sequence 335, App	767	17	0.7	1001	4	US-09-641-638-121	Sequence 121, App
695	18	0.7	2984	4	US-09-232-149A-335	Sequence 335, App	768	17	0.7	1002	4	US-09-641-638-578	Sequence 578, App
696	18	0.7	3011	1	US-07-821-716-1	Sequence 1, Appli	769	17	0.7	1082	2	US-08-909-965C-12	Sequence 12, Appli
697	18	0.7	3047	1	US-08-280-690-1	Sequence 1, Appli	770	17	0.7	1082	2	US-09-195-666A-11	Sequence 11, Appli
698	18	0.7	3568	4	US-08-218-363-3	Sequence 3, Appli	771	17	0.7	1095	3	US-09-195-666A-12	Sequence 12, Appli
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700	18	0.7	3590	5	PCT-US96-09193-1	Sequence 1, Appli	773	17	0.7	1095	3	US-09-195-666A-14	Sequence 14, Appli
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702	18	0.7	4517	4	US-09-140-804-9	Sequence 9, Appli	775	17	0.7	1095	4	US-09-635-705-12	Sequence 12, Appli
703	18	0.7	4704	2	US-08-476-062A-52	Sequence 52, Appli	776	17	0.7	1095	4	US-09-635-705-13	Sequence 13, Appli
704	18	0.7	5035	2	US-08-616-392C-3	Sequence 3, Appli	777	17	0.7	1095	4	US-09-635-705-14	Sequence 14, Appli
705	18	0.7	5044	4	US-09-735-335-3	Sequence 3, Appli	778	17	0.7	1095	4	US-09-634-858A-11	Sequence 11, Appli
706	18	0.7	5095	1	US-08-092-817-3	Sequence 3, Appli	779	17	0.7	1095	4	US-09-634-858A-12	Sequence 12, Appli
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709	18	0.7	15202	3	US-08-922-635-21	Sequence 21, Appli	782	17	0.7	1174	2	US-08-481-658B-39	Sequence 39, Appli
710	18	0.7	15602	4	US-08-844-634-17	Sequence 17, Appli	783	17	0.7	1174	2	US-08-477-504A-39	Sequence 39, Appli
711	18	0.7	17949	4	US-08-087-465-3	Sequence 3, Appli	784	17	0.7	1174	2	US-08-486-756A-39	Sequence 39, Appli
712	18	0.7	21234	4	US-09-810-671-3	Sequence 3, Appli	785	17	0.7	1174	2	US-08-485-862B-39	Sequence 39, Appli
713	18	0.7	29598	4	US-09-341-587-6	Sequence 6, Appli	786	17	0.7	1174	3	US-08-787-739-39	Sequence 39, Appli
714	18	0.7	40328	3	US-08-742-185-102	Sequence 102, App	787	17	0.7	1174	3	US-08-487-077A-39	Sequence 39, Appli
715	18	0.7	42235	4	US-09-199-637A-1	Sequence 1, Appli	788	17	0.7	1174	3	US-08-485-863A-39	Sequence 39, Appli
716	18	0.7	43795	3	US-08-742-185-101	Sequence 101, App	789	17	0.7	1174	4	US-08-485-049D-39	Sequence 39, Appli
717	17	0.7	20	1	US-07-922-723A-35	Sequence 35, App	790	17	0.7	1174	4	US-09-178-115-39	Sequence 39, Appli
718	17	0.7	20	1	US-07-799-828C-35	Sequence 35, App	791	17	0.7	1174	4	US-09-177-776-39	Sequence 39, Appli
719	17	0.7	20	2	US-07-952-277A-35	Sequence 35, App	792	17	0.7	1200	4	US-09-018-584A-37	Sequence 37, Appli
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726	17	0.7	239	2	US-08-687-080-93	Sequence 93, Appli	799	17	0.7	1255	3	US-08-474-410-3	Sequence 3, Appli
727	17	0.7	260	4	US-09-030-607-216	Sequence 216, App	800	17	0.7	1255	4	US-08-486-673B-3	Sequence 3, Appli
728	17	0.7	260	4	US-09-605-785-216	Sequence 216, App	801	17	0.7	1276	4	US-09-177-325-2	Sequence 2, Appli
729	17	0.7	260	4	US-09-439-313-216	Sequence 216, App	802	17	0.7	1276	4	US-09-611-812A-2	Sequence 2, Appli
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740	17	0.7	294	4	US-08-485-049D-61	Sequence 61, Appli	813	17	0.7	1401	3	US-08-485-863A-49	Sequence 49, Appli
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742	17	0.7	294	4	US-09-177-776-61	Sequence 61, Appli	815	17	0.7	1401	4	US-09-178-115-49	Sequence 49, Appli
743	17	0.7	410	4	US-09-221-298-63	Sequence 63, App	816	17	0.7	1401	4	US-09-177-776-49	Sequence 49, Appli
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745	17	0.7	592	4	US-09-276-531-115	Sequence 115, App	818	17	0.7	1441	4	US-09-122-1710-4	Sequence 4, Appli
746	17	0.7	614	4	US-09-844-525A-12	Sequence 12, App	819	17	0.7	1491	2	US-08-941-647A-4	Sequence 1, Appli
747	17	0.7	618	4	US-09-385-982-218	Sequence 218, App	820	17	0.7	1505	4	US-09-142-481-1	Sequence 1, Appli
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750	17	0.7	653	4	US-09-328-111-614	Sequence 614, App	823	17	0.7	1719	3	US-09-008-481A-4	Sequence 4, Appli
751	17	0.7	665	4	US-08-896-164-43	Sequence 43, App	824	17	0.7	1719	3	US-09-195-666A-18	Sequence 18, Appli
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753	17	0.7	696	4	US-09-740-235-16	Sequence 16, App	826	17	0.7	1719	4	US-09-635-705-18	Sequence 18, Appli
754	17	0.7	789	1	US-08-039-778B-14	Sequence 14, App	827	17	0.7	1776	2	US-08-531-927B-1	Sequence 1, Appli
755	17	0.7	789	2	US-08-394-152A-42	Sequence 42, App	828	17	0.7	1776	2	US-08-531-927B-1	Sequence 1, Appli
756	17	0.7	807	2	US-08-531-927B-9	Sequence 9, Appli	829	17	0.7	1776	4	US-09-041-886-12	Sequence 12, Appli
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832	17	0.7	1853	4	US-09-605-785-369	Sequence 369, App	905	17	0.7	3500	4	US-09-197-636-7	Sequence 7, Appl
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844	17	0.7	1988	4	US-08-367-841A-11	Sequence 11, Appl	c 917	17	0.7	4460	4	US-09-103-875-4	Sequence 4, Appl
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853	17	0.7	2096	4	US-09-635-705-16	Sequence 16, Appl	926	17	0.7	5381	4	US-09-750-580-4	Sequence 4, Appl
854	17	0.7	2096	4	US-09-634-858A-16	Sequence 16, Appl	927	17	0.7	5408	1	US-08-471-058-20	Sequence 20, Appl
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858	17	0.7	2140	4	US-09-611-781-6	Sequence 6, Appl	c 931	17	0.7	5843	1	US-08-554-612C-2	Sequence 2, Appl
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861	17	0.7	2184	4	US-09-062-451-296	Sequence 296, App	c 934	17	0.7	7886	2	US-09-060-836-2	Sequence 2, Appl
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865	17	0.7	2461	2	US-08-832-877-113	Sequence 113, App	c 938	17	0.7	8342	5	PCT-US94-04496-63	Sequence 63, Appl
866	17	0.7	2504	2	US-09-218-363-7	Sequence 7, Appl	939	17	0.7	8342	5	PCT-US94-04496-63	Sequence 63, Appl
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871	17	0.7	2531	4	US-09-844-525A-3	Sequence 3, Appl	944	17	0.7	8722	4	US-09-221-017B-263	Sequence 263, App
872	17	0.7	2562	2	US-08-436-771-8	Sequence 8, Appl	945	17	0.7	8835	3	US-08-884-324-10	Sequence 10, Appl
873	17	0.7	2562	2	US-08-434-998-8	Sequence 8, Appl	c 946	17	0.7	9306	4	US-09-453-702B-231	Sequence 231, App
874	17	0.7	2562	2	US-08-487-797-8	Sequence 8, Appl	947	17	0.7	9620	4	US-08-952-127-11	Sequence 11, Appl
875	17	0.7	2562	5	PCT-US95-02058-8	Sequence 8, Appl	c 948	17	0.7	9707	4	US-08-961-527-164	Sequence 164, App
876	17	0.7	2628	1	US-08-143-219-1	Sequence 1, Appl	949	17	0.7	10079	2	US-08-476-866-20	Sequence 20, Appl
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878	17	0.7	2630	4	US-08-469-233-6	Sequence 6, Appl	c 951	17	0.7	10898	2	US-08-481-558B-5	Sequence 5, Appl
879	17	0.7	2630	4	US-08-642-146-6	Sequence 6, Appl	c 952	17	0.7	10898	2	US-08-477-504A-5	Sequence 5, Appl
880	17	0.7	2680	2	US-08-533-306A-5	Sequence 5, Appl	c 953	17	0.7	10898	2	US-08-486-756A-5	Sequence 5, Appl
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882	17	0.7	2682	4	US-09-020-465-1	Sequence 1, Appl	c 955	17	0.7	10898	3	US-08-787-739-5	Sequence 5, Appl
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884	17	0.7	2768	1	US-08-321-478-1	Sequence 1, Appl	c 957	17	0.7	10898	3	US-08-485-863A-5	Sequence 5, Appl
885	17	0.7	2768	1	US-08-321-478-3	Sequence 3, Appl	c 958	17	0.7	10898	4	US-08-485-049D-5	Sequence 5, Appl
886	17	0.7	2768	1	US-08-321-478-5	Sequence 5, Appl	c 959	17	0.7	10898	4	US-09-178-115-5	Sequence 5, Appl
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889	17	0.7	2784	2	US-08-466-974-1	Sequence 1, Appl	962	17	0.7	11531	1	US-08-068-945A-1	Sequence 1, Appl
890	17	0.7	2813	4	US-08-471-453-1	Sequence 3, Appl	963	17	0.7	11531	1	US-08-442-806-1	Sequence 1, Appl
891	17	0.7	2813	4	US-09-689-255C-3	Sequence 3, Appl	964	17	0.7	12565	4	US-09-345-217-3	Sequence 3, Appl
892	17	0.7	2887	2	US-08-533-306A-3	Sequence 3, Appl	c 965	17	0.7	12847	1	US-08-550-715-1	Sequence 1, Appl
893	17	0.7	2887	2	US-08-742-923A-3	Sequence 3, Appl	966	17	0.7	14753	4	US-09-821-736-3	Sequence 3, Appl
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895	17	0.7	3090	4	US-09-276-531-78	Sequence 78, Appl	968	17	0.7	16595	4	US-09-146-053-7	Sequence 7, Appl
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897	17	0.7	3158	2	US-08-246-361A-36	Sequence 36, Appl	970	17	0.7	20598	4	US-09-593-995-10	Sequence 10, Appl
898	17	0.7	3158	3	US-08-463-772-36	Sequence 36, Appl	c 971	17	0.7	22846	3	US-08-469-461-3	Sequence 3, Appl
899	17	0.7	3195	2	US-08-951-648-5	Sequence 5, Appl	c 972	17	0.7	22846	3	US-07-890-609-3	Sequence 3, Appl
900	17	0.7	3195	3	US-09-174-437-5	Sequence 5, Appl	973	17	0.7	28994	3	US-08-884-324-14	Sequence 14, Appl
901	17	0.7	3267	2	US-08-257-963B-12	Sequence 12, Appl	c 974	17	0.7	36651	4	US-09-738-894A-3	Sequence 3, Appl
902	17	0.7	3267	4	US-08-367-841A-12	Sequence 12, Appl	c 975	17	0.7	36778	4	US-09-105-537-5	Sequence 5, Appl
903	17	0.7	3267	5	PCT-US95-07201-12	Sequence 12, Appl	c 976	17	0.7	38506	3	US-09-320-878-19	Sequence 19, Appl

c 977 17 0.7 38844 4 US-09-734-675-3
c 978 17 0.7 51259 3 US-08-781-891-209
c 979 17 0.7 55827 4 US-09-813-133A-3
980 17 0.7 65042 4 US-09-784-316-3
981 17 0.7 80161 3 US-09-036-987A-1
982 17 0.7 80161 4 US-09-370-700-1
983 17 0.7 98844 4 US-09-791-211-10
c 984 17 0.7 4403765 4 US-09-103-840A-2
c 985 17 0.7 4411529 4 US-09-103-840A-1
986 16 0.7 19 1 US-08-487-759-1
987 16 0.7 19 2 US-08-807-104-1
988 16 0.7 19 2 US-08-807-104-4
989 16 0.7 19 2 US-08-807-104-6
990 16 0.7 19 2 US-08-807-104-7
991 16 0.7 19 2 US-08-807-104-8
992 16 0.7 19 2 US-08-807-104-9
993 16 0.7 19 2 US-08-807-104-10
994 16 0.7 19 2 US-08-807-104-13
995 16 0.7 19 2 US-08-807-104-14
996 16 0.7 19 2 US-08-807-104-15
997 16 0.7 19 2 US-08-807-104-16
998 16 0.7 19 3 US-08-973-139-1
999 16 0.7 19 3 US-08-480-068-1
1000 16 0.7 19 3 US-08-480-068-4

ALIGNMENTS

RESULT 1
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-79

Query Match 1.5%; Score 37; DB 3; Length 87350;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGAGGGGAGGTTGCAGTGCAGCAAGATCAGCCACT 42
Db 77833 GGAGGGGAGGTTGCAGTGCAGCAAGATCAGCCACT 77797
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RESULT 2
US-09-791-211-3/c
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791.211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 3
; LENGTH: 87543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 7421
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7427
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 11609
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12605
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31206
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31592
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33095


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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33160
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34066
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34072
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 36816
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 39020
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42164
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59215
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59235
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59242
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 63290
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 66614
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68660
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68657
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68718
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68733
; OTHER INFORMATION: unknown

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; NAME/KEY: unsure
; LOCATION: 68739
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 69785
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79134
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79198
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 86336
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-3

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Query Match 1.5%; Score 37; DB 4; Length 87543;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 42
Db 78026 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 77990

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RESULT 3
US-09-798-096-10
; Sequence 10, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

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Query Match 1.5%; Score 37; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 42
Db 55180 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 55216

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RESULT 4
US-09-729-995-3/c
; Sequence 3, Application US/09729995
; Patent No. 6428206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904
; CURRENT APPLICATION NUMBER: US/09/729,995
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human

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US-09-729-995-3

Query Match 1.5%; Score 35; DB 4; Length 29629;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGAGGTTGCAGTGAGCCAAAGATCAGCCACTACAC 46
Db 2123 GGAGGTTGCAGTGAGCCAAAGATCAGCCACTACAC 2089

RESULT 5

US-09-345-982-1
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345.882
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 8073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99117
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103806
; OTHER INFORMATION: 5-131-395 : polymorphic base A or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106940
; OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
; FEATURE:

; NAME/KEY: allele
; LOCATION: 108106
; OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108149
; OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108308
; OTHER INFORMATION: 5-135-357 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108471
; OTHER INFORMATION: 5-136-174 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134134
; OTHER INFORMATION: 5-140-120 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134362
; OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134374
; OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
; FEATURE:
; NAME/KEY: allele
; LOCATION: 146328
; OTHER INFORMATION: 5-143-84 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 146345
; OTHER INFORMATION: 5-143-101 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 150329
; OTHER INFORMATION: 5-145-24 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 160031
; OTHER INFORMATION: 5-148-352 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72771..72817
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72771..72817
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
; FEATURE:
; NAME/KEY: allele
; LOCATION: 8050...8096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
; FEATURE:
; NAME/KEY: allele
; LOCATION: 8050...8096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90819...90865
; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90819...90865
; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93690...93736
; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
; FEATURE:
; NAME/KEY: allele

LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

Query Match 1.5%; Score 35; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GGAGCGGAGGTTGCTGAGTGAAGATCAGCGCA 40

Db 29125 GGAGCGGAGGTTGCTGAGTGAAGATCAGCGCA 29159
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RESULT 6
US-08-827-208-1/c
; Sequence 1, Application US/09827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chlou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Striffler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1611..2063
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5315..6045
; FEATURE:
; NAME/KEY: exon
; LOCATION: 6143..6758
; FEATURE:
; NAME/KEY: exon
; LOCATION: 7075..7317
; FEATURE:
; NAME/KEY: exon
; LOCATION: 7473..8499
US-08-827-208-1

Query Match 1.4%; Score 34; DB 3; Length 8517;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCATION: 7473..8499
US-09-498-809-1
Query Match 1.4%; Score 34; DB 4; Length 8517;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GAGCGGAGGTTGTCAGTGAGCCCAAGATCACGCCA 40
Db 6091 GAGCGGAGGTTGTCAGTGAGCCCAAGATCACGCCA 6058
RESULT 9
US-09-800-960-3/c
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/800,960
; EARLIER FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3
Query Match 1.3%; Score 32; DB 4; Length 62804;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 36
Db 43316 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 43285
RESULT 10
US-09-211-417-2/c
; Sequence 2, Application US/09211417A
; Patent No. 6177254
; GENERAL INFORMATION:
; APPLICANT: Rattner, Jerome B
; APPLICANT: Whitehead, Clark M
; TITLE OF INVENTION: NUCLEOLUS AUTOANTIGENIC MARKER FOR SYSTEMIC LUPUS
; TITLE OF INVENTION: ERHYMATOSUS
; TITLE OF INVENTION: GenBank
; FILE REFERENCE: UCC1
; CURRENT APPLICATION NUMBER: US/09/211,417A
; EARLIER FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 2
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Sequence of ASE-1
; Patent No. 6177254
US-09-211-417-2
Query Match 1.3%; Score 31; DB 4; Length 3286;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 36
Db 2795 GGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 2765
RESULT 11
US-09-166-350-32
; Sequence 32, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: Uses Therefor
; CURRENT APPLICATION NUMBER: US/09/166,350A
; EARLIER FILING DATE: 1998-10-05
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 4169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-32
Query Match 1.3%; Score 31; DB 4; Length 4169;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCA 35
Db 3831 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCA 3861
RESULT 12
US-09-422-936-60/c
; Sequence 60, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-02-19
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 15652
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(15652)
; OTHER INFORMATION: n = A, T, G, or C
; NAME/KEY: misc_feature
; LOCATION: (1)...(15652)


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; NAME/KEY: misc_feature
; LOCATION: (1)...(38564)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-673-3

Query Match      1.3%; Score 31; DB 4; Length 38564;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGGGCGGAGTTGCAGTGAGCCCAAGATCA 35
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Db      32975 GGGAGGGCGGAGTTGCAGTGAGCCCAAGATCA 32945
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Search completed: June 17, 2003, 06:28:56
Job time : 119.105 secs

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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 254.144 Seconds
(without alignments)

Sequence: 1 agagggaggagggttgc.....gacagggtctgtctgttc 2404
13697.491 Million cell updates/sec

Title: US-09-513-888c-1_COPY_4514_6917

Perfect score: 2404

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

1029858 seqs, 724030393 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:

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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	8.0	475	9	US-09-918-995-29121
2	39	1.6	30350	9	US-10-118-328-3
3	39	1.6	397658	10	US-09-813-320-3
4	38	1.6	438	10	US-09-867-701-8927
5	38	1.6	449	10	US-09-867-701-4634
6	38	1.6	455	9	US-09-918-995-24949
7	38	1.6	9883	9	US-10-016-1574-71
8	38	1.6	15857	10	US-09-764-864-1704
9	38	1.6	16225	9	US-10-079-854-370
10	38	1.6	16225	9	US-09-764-891-9432
11	38	1.6	16225	10	US-09-764-878-370
12	38	1.6	18657	9	US-10-074-045-70
13	38	1.6	32195	9	US-09-764-891-8668
14	38	1.6	45839	12	US-10-025-187-3
15	38	1.6	62944	10	US-09-954-456-2257
16	38	1.6	175561	9	US-10-017-721-3
17	38	1.6	397658	10	US-09-813-320-3
18	37	1.5	89	9	US-09-764-891-9583
19	37	1.5	245	9	US-10-040-719-1286

20	37	1.5	248	9	US-10-092-154-1741	Sequence 1741, Ap
21	37	1.5	248	10	US-09-764-847-1741	Sequence 1741, Ap
22	37	1.5	563	9	US-09-918-995-11202	Sequence 11202, A
23	37	1.5	2147	9	US-10-092-154-1738	Sequence 1738, Ap
24	37	1.5	2147	10	US-09-764-847-1738	Sequence 1738, Ap
25	37	1.5	2854	9	US-09-764-891-8205	Sequence 8205, Ap
26	37	1.5	3271	9	US-09-764-891-8206	Sequence 8206, Ap
27	37	1.5	11991	9	US-09-764-891-9893	Sequence 9893, Ap
28	37	1.5	11991	10	US-09-764-877-2942	Sequence 2942, Ap
29	37	1.5	15366	9	US-10-074-095-1057	Sequence 1057, Ap
30	37	1.5	15366	10	US-09-764-860-1057	Sequence 1057, Ap
31	37	1.5	28690	9	US-10-010-802-1	Sequence 1, Appli
32	37	1.5	30350	9	US-10-118-328-3	Sequence 3, Appli
33	36	1.5	493	9	US-09-764-891-1697	Sequence 1697, Ap
34	36	1.5	506	9	US-10-092-154-1626	Sequence 1626, Ap
35	36	1.5	506	10	US-09-764-847-1626	Sequence 1626, Ap
36	36	1.5	692	9	US-09-764-891-2627	Sequence 2627, Ap
37	36	1.5	1351	9	US-09-764-891-8391	Sequence 8391, Ap
38	36	1.5	1430	9	US-09-764-891-10178	Sequence 10178, A
39	36	1.5	1655	10	US-09-764-877-2361	Sequence 2361, Ap
40	35	1.5	318	10	US-09-867-701-3011	Sequence 3011, Ap
41	35	1.5	477	9	US-09-918-995-11218	Sequence 11218, A
42	35	1.5	488	9	US-09-918-995-11210	Sequence 11210, A
43	35	1.5	620	9	US-10-198-846-5084	Sequence 5084, Ap
44	35	1.5	5257	9	US-10-171-581-63	Sequence 63, Appli
45	35	1.5	8911	10	US-09-764-853-895	Sequence 895, Appli
46	35	1.5	29629	12	US-10-135-689-3	Sequence 3, Appli
47	35	1.5	32082	9	US-09-764-891-9679	Sequence 9679, Ap
48	35	1.5	32184	9	US-09-764-891-8538	Sequence 8538, Ap
49	35	1.5	32204	9	US-09-764-891-8537	Sequence 8537, Ap
50	35	1.5	106344	9	US-09-910-185-10	Sequence 10, Appli
51	34	1.4	5629	9	US-10-092-154-1162	Sequence 1162, Ap
52	34	1.4	6265	9	US-10-092-154-1161	Sequence 1161, Ap
53	34	1.4	6265	10	US-09-764-847-1161	Sequence 1161, Ap
54	34	1.4	48841	9	US-09-844-653-32	Sequence 32, Appli
55	34	1.4	170834	10	US-09-835-232-7	Sequence 7, Appli
56	34	1.4	302250	10	US-09-962-832-154	Sequence 154, App
57	34	1.4	15295	10	US-09-764-877-3404	Sequence 3404, Ap
58	33	1.4	174424	10	US-09-967-768A-314	Sequence 314, App
59	33	1.4	338	10	US-09-867-701-9905	Sequence 9905, Ap
60	32	1.3	414	10	US-09-867-701-8173	Sequence 8173, Ap
61	32	1.3	449	10	US-09-867-701-8942	Sequence 8942, Ap
62	32	1.3	455	10	US-09-867-701-6589	Sequence 6589, Ap
63	32	1.3	485	9	US-09-918-995-2090	Sequence 2090, Ap
64	32	1.3	1659	9	US-09-892-877-24	Sequence 24, Appli
65	32	1.3	1659	9	US-09-948-783-25	Sequence 25, Appli
66	32	1.3	2571	10	US-09-764-877-2215	Sequence 2215, Ap
67	32	1.3	2571	10	US-09-764-877-2216	Sequence 2216, Ap
68	32	1.3	2571	10	US-09-764-877-2217	Sequence 2217, Ap
69	32	1.3	2892	9	US-10-079-854-197	Sequence 197, App
70	32	1.3	2892	9	US-09-764-878-197	Sequence 197, App
71	32	1.3	3351	9	US-10-092-154-1138	Sequence 1138, Ap
72	32	1.3	3351	10	US-09-764-847-1138	Sequence 1138, Ap
73	32	1.3	5632	9	US-09-764-891-7395	Sequence 7395, Ap
74	32	1.3	6295	9	US-10-163-866-9	Sequence 8, Appli
75	32	1.3	6296	9	US-10-163-866-9	Sequence 9, Appli
76	32	1.3	13315	9	US-10-079-854-328	Sequence 328, App
77	32	1.3	13315	10	US-09-764-878-328	Sequence 328, App
78	32	1.3	13409	9	US-09-764-891-9601	Sequence 9601, App
79	32	1.3	14718	9	US-09-764-891-5981	Sequence 5981, Ap
80	32	1.3	16062	9	US-09-764-891-8047	Sequence 8047, Ap
81	32	1.3	19696	9	US-10-091-572-874	Sequence 874, App
82	32	1.3	19696	9	US-09-764-891-9327	Sequence 9327, App
83	32	1.3	20261	9	US-10-079-854-325	Sequence 325, App
84	32	1.3	20261	10	US-09-764-878-325	Sequence 325, App
85	32	1.3	27154	9	US-09-764-891-8396	Sequence 8396, Ap
86	32	1.3	31168	9	US-09-764-868-1464	Sequence 1464, Ap
87	32	1.3	31813	9	US-09-764-891-9685	Sequence 9685, Ap
88	32	1.3	53000	9	US-09-953-611-10	Sequence 10, Appli
89	32	1.3	60153	9	US-10-222-334-7	Sequence 7, Appli
90	32	1.3	62804	12	US-10-096-960-3	Sequence 3, Appli
91	32	1.3	143306	10	US-09-729-920-3	Sequence 3, Appli
92	32	1.3				

c 93	32	1.3	167343	10	US-09-962-436-281	Sequence 281, App	c 166	31	1.3	46718	10	US-09-816-093-3	Sequence 3, Appli
c 94	32	1.3	167343	10	US-09-964-824A-273	Sequence 273, App	c 167	31	1.3	53542	10	US-09-801-574-61	Sequence 61, Appl
c 95	32	1.3	174566	9	US-10-020-141-1	Sequence 1, Appli	c 168	31	1.3	62944	10	US-09-954-456-2257	Sequence 2257, Ap
c 96	32	1.3	368004	10	US-09-949-654-3	Sequence 3, Appli	c 169	31	1.3	75270	9	US-09-790-852-1	Sequence 1, Appli
c 97	32	1.3	402850	9	US-09-844-653-5	Sequence 5, Appli	c 170	31	1.3	81001	9	US-09-842-364-1	Sequence 1, Appli
c 98	31	1.3	114	9	US-10-125-540-610	Sequence 610, App	c 171	31	1.3	81001	10	US-09-751-877-1	Sequence 1542, Ap
c 99	31	1.3	114	10	US-09-764-870-610	Sequence 610, App	c 172	31	1.3	110096	10	US-09-880-107-1542	Sequence 3, Appli
c 100	31	1.3	146	9	US-10-091-504-1389	Sequence 1389, App	c 173	31	1.3	116592	10	US-09-818-512-3	Sequence 3, Appli
c 101	31	1.3	146	10	US-09-764-869-1389	Sequence 1389, App	c 174	31	1.3	116840	9	US-10-020-141-3	Sequence 11, Appl
c 102	31	1.3	159	9	US-09-764-872-544	Sequence 544, App	c 175	31	1.3	139257	9	US-09-920-671-11	Sequence 79, Appl
c 103	31	1.3	410	9	US-09-918-995-13769	Sequence 13769, A	c 176	31	1.3	145831	10	US-09-969-708-79	Sequence 2116, Ap
c 104	31	1.3	436	10	US-09-867-701-429	Sequence 429, App	c 177	31	1.3	145831	10	US-09-954-456-2116	Sequence 16, Appl
c 105	31	1.3	456	9	US-09-918-995-28012	Sequence 28012, A	c 178	31	1.3	152331	9	US-10-095-407-16	Sequence 7, Appli
c 106	31	1.3	510	9	US-10-198-846-13421	Sequence 13421, A	c 179	31	1.3	170834	10	US-09-835-232-7	Sequence 3, Appli
c 107	31	1.3	525	9	US-09-918-995-31520	Sequence 31520, A	c 180	31	1.3	174493	9	US-10-238-709-3	Sequence 3, Appli
c 108	31	1.3	528	9	US-09-918-995-31523	Sequence 31523, A	c 181	31	1.3	174493	10	US-09-804-471A-3	Sequence 3, Appli
c 109	31	1.3	860	9	US-10-198-846-6751	Sequence 6751, App	c 182	31	1.3	176373	9	US-10-095-407-17	Sequence 17, Appl
c 110	31	1.3	2194	9	US-09-764-891-7481	Sequence 7481, App	c 183	31	1.3	203654	10	US-09-820-905-3	Sequence 3, Appli
c 111	31	1.3	2195	9	US-09-764-891-7482	Sequence 7482, App	c 184	31	1.3	235033	9	US-10-301-844-1	Sequence 1, Appli
c 112	31	1.3	2197	9	US-09-764-891-7483	Sequence 7483, App	c 185	31	1.3	235033	9	US-10-301-844-2	Sequence 2, Appli
c 113	31	1.3	3045	10	US-09-354-456-218	Sequence 218, App	c 186	31	1.3	237236	10	US-09-933-267A-1	Sequence 1, Appli
c 114	31	1.3	3045	10	US-09-880-107-2319	Sequence 2319, App	c 187	31	1.3	465237	9	US-09-946-807-1	Sequence 1, Appli
c 115	31	1.3	3593	9	US-09-764-891-10220	Sequence 10220, A	c 188	31	1.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
c 116	31	1.3	4025	10	US-09-764-877-2340	Sequence 2340, App	c 189	31	1.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
c 117	31	1.3	4025	10	US-09-764-877-2343	Sequence 2343, App	c 190	30	1.2	107	9	US-09-764-891-7423	Sequence 7423, Ap
c 118	31	1.3	4025	10	US-09-764-877-2345	Sequence 2345, App	c 191	30	1.2	107	9	US-09-764-891-7426	Sequence 7426, Ap
c 119	31	1.3	4090	10	US-09-764-877-2256	Sequence 2256, App	c 192	30	1.2	114	9	US-10-091-504-1717	Sequence 1717, Ap
c 120	31	1.3	4223	9	US-10-125-237-50	Sequence 50, Appl	c 193	30	1.2	114	10	US-09-764-869-1717	Sequence 1717, Ap
c 121	31	1.3	4223	9	US-10-105-891-50	Sequence 50, Appl	c 194	30	1.2	127	10	US-09-764-877-3290	Sequence 3290, App
c 122	31	1.3	5352	9	US-09-984-827-22	Sequence 22, Appl	c 195	30	1.2	127	10	US-09-764-877-742	Sequence 742, App
c 123	31	1.3	9615	10	US-09-764-877-2955	Sequence 2955, App	c 196	30	1.2	308	10	US-09-867-701-3479	Sequence 3479, App
c 124	31	1.3	9732	10	US-09-764-877-2804	Sequence 2804, App	c 197	30	1.2	312	10	US-09-867-701-3820	Sequence 7820, App
c 125	31	1.3	11977	10	US-09-764-864-1726	Sequence 1726, App	c 198	30	1.2	313	10	US-09-867-701-7820	Sequence 1003, Ap
c 126	31	1.3	12149	9	US-10-091-504-2258	Sequence 2258, App	c 199	30	1.2	323	10	US-09-920-300A-1003	Sequence 1003, Ap
c 127	31	1.3	12149	9	US-09-764-869-2258	Sequence 2258, App	c 200	30	1.2	323	12	US-10-033-528-1003	Sequence 715, App
c 128	31	1.3	12409	9	US-09-989-442-156	Sequence 156, App	c 201	30	1.2	369	9	US-09-918-995-16631	Sequence 16631, A
c 129	31	1.3	13058	9	US-10-091-483-303	Sequence 303, App	c 202	30	1.2	380	10	US-09-867-701-7481	Sequence 7481, Ap
c 130	31	1.3	13058	10	US-09-764-846-303	Sequence 303, App	c 203	30	1.2	401	9	US-09-946-807-808	Sequence 808, App
c 131	31	1.3	13216	9	US-09-764-891-7810	Sequence 7810, App	c 204	30	1.2	401	10	US-09-795-668-808	Sequence 808, App
c 132	31	1.3	14012	9	US-09-819-994-3	Sequence 3, Appli	c 205	30	1.2	401	10	US-09-795-668-808	Sequence 808, App
c 133	31	1.3	14874	9	US-09-764-891-7672	Sequence 7672, App	c 206	30	1.2	412	10	US-09-867-701-6651	Sequence 6651, App
c 134	31	1.3	15531	9	US-10-125-540-600	Sequence 600, App	c 207	30	1.2	482	10	US-09-867-701-8803	Sequence 8803, Ap
c 135	31	1.3	15531	10	US-09-764-870-600	Sequence 600, App	c 208	30	1.2	487	9	US-10-060-036-820	Sequence 820, Ap
c 136	31	1.3	17138	12	US-10-014-501-3	Sequence 3, Appli	c 209	30	1.2	507	9	US-09-918-995-21355	Sequence 21355, A
c 137	31	1.3	17200	10	US-09-764-877-3390	Sequence 3390, App	c 210	30	1.2	546	10	US-09-867-701-8700	Sequence 8700, Ap
c 138	31	1.3	19125	10	US-09-764-877-2805	Sequence 2805, App	c 211	30	1.2	574	10	US-09-954-456-1482	Sequence 1482, Ap
c 139	31	1.3	19740	9	US-10-142-356-3	Sequence 3, Appli	c 212	30	1.2	586	9	US-10-091-504-2281	Sequence 2281, Ap
c 140	31	1.3	20869	10	US-09-91-504-2427	Sequence 2427, App	c 213	30	1.2	586	10	US-09-764-869-2281	Sequence 2281, Ap
c 141	31	1.3	20869	10	US-09-764-869-2427	Sequence 2427, App	c 214	30	1.2	593	9	US-10-091-504-2278	Sequence 2278, Ap
c 142	31	1.3	21358	9	US-09-764-872-816	Sequence 816, App	c 215	30	1.2	593	9	US-10-091-504-2280	Sequence 2280, Ap
c 143	31	1.3	21358	9	US-09-764-891-9107	Sequence 9107, App	c 216	30	1.2	593	10	US-09-764-869-2278	Sequence 2278, Ap
c 144	31	1.3	21676	9	US-09-764-872-815	Sequence 815, App	c 217	30	1.2	606	9	US-10-066-543-684	Sequence 2280, Ap
c 145	31	1.3	22645	9	US-09-764-891-9106	Sequence 9106, App	c 218	30	1.2	606	10	US-09-764-869-2280	Sequence 684, App
c 146	31	1.3	22645	9	US-09-764-891-9106	Sequence 9106, App	c 219	30	1.2	1000	10	US-09-784-423-33	Sequence 33, Appl
c 147	31	1.3	22645	9	US-09-764-891-9106	Sequence 9106, App	c 220	30	1.2	1002	9	US-09-764-891-9626	Sequence 9626, Ap
c 148	31	1.3	23603	9	US-09-860-670-264	Sequence 264, App	c 221	30	1.2	1083	9	US-09-764-891-7194	Sequence 7194, Ap
c 149	31	1.3	23613	9	US-09-860-670-258	Sequence 258, App	c 222	30	1.2	1432	9	US-10-125-540-164	Sequence 164, App
c 150	31	1.3	24218	9	US-09-860-670-263	Sequence 263, App	c 223	30	1.2	1432	10	US-09-764-870-164	Sequence 164, App
c 151	31	1.3	26995	9	US-10-079-854-227	Sequence 227, App	c 224	30	1.2	1494	9	US-09-764-891-9623	Sequence 9623, Ap
c 152	31	1.3	26995	10	US-09-764-878-227	Sequence 227, App	c 225	30	1.2	1496	9	US-09-764-891-5888	Sequence 5888, Ap
c 153	31	1.3	29163	9	US-09-764-891-7809	Sequence 7809, App	c 226	30	1.2	1496	9	US-09-764-891-9622	Sequence 9622, Ap
c 154	31	1.3	29449	9	US-09-989-442-161	Sequence 161, App	c 227	30	1.2	1496	9	US-09-764-891-9629	Sequence 9629, Ap
c 155	31	1.3	29449	9	US-10-074-045-73	Sequence 73, Appl	c 228	30	1.2	1849	10	US-09-822-830A-298	Sequence 298, App
c 156	31	1.3	31871	9	US-10-092-154-1403	Sequence 1403, App	c 229	30	1.2	1946	9	US-10-097-065-112	Sequence 112, App
c 157	31	1.3	31871	10	US-09-764-847-1403	Sequence 1403, App	c 230	30	1.2	1946	9	US-10-037-270-462	Sequence 462, App
c 158	31	1.3	32190	9	US-09-860-670-255	Sequence 255, App	c 231	30	1.2	1965	10	US-09-822-849A-118	Sequence 118, App
c 159	31	1.3	32195	9	US-10-091-504-2017	Sequence 2017, App	c 232	30	1.2	2109	9	US-10-072-349-325	Sequence 325, App
c 160	31	1.3	32195	10	US-09-764-869-2017	Sequence 2017, App	c 233	30	1.2	2109	9	US-09-764-855-325	Sequence 325, App
c 161	31	1.3	32219	9	US-10-091-504-2016	Sequence 2016, App	c 234	30	1.2	2290	10	US-09-822-849A-152	Sequence 152, App
c 162	31	1.3	32219	10	US-09-764-869-2016	Sequence 2016, App	c 235	30	1.2	2972	10	US-09-779-239-1	Sequence 1, Appli
c 163	31	1.3	32249	9	US-09-860-670-260	Sequence 260, App	c 236	30	1.2	3270	10	US-09-764-864-1681	Sequence 1681, Ap
c 164	31	1.3	33795	10	US-09-880-107-2184	Sequence 2184, App	c 237	30	1.2	4301	9	US-09-989-919-69	Sequence 69, Appl
c 165	31	1.3	46718	9	US-10-274-873-3	Sequence 3, Appli	c 238	30	1.2	4837	10	US-09-764-877-2839	Sequence 2839, Ap

239	30	1.2	4963	9	US-10-135-540-606	Sequence 606, App	312	30	1.2	32193	10	US-09-764-878-200	Sequence 200, App
c 240	30	1.2	4963	9	US-10-074-095-694	Sequence 694, App	313	30	1.2	32249	9	US-10-079-854-202	Sequence 202, App
241	30	1.2	4963	10	US-09-764-870-606	Sequence 606, App	314	30	1.2	32249	9	US-09-764-878-202	Sequence 202, App
c 242	30	1.2	4963	10	US-09-764-860-694	Sequence 694, App	315	30	1.2	36303	9	US-10-152-7248-24	Sequence 24, Appl
243	30	1.2	5096	9	US-10-102-627-94	Sequence 94, Appl	316	30	1.2	38059	10	US-09-880-107-2125	Sequence 125, Ap
c 244	30	1.2	5150	9	US-09-764-891-5560	Sequence 5560, Ap	317	30	1.2	38186	9	US-09-373-658-38	Sequence 38, Appl
245	30	1.2	5151	9	US-09-764-891-6561	Sequence 6561, Ap	318	30	1.2	38844	12	US-10-060-333-3	Sequence 3, Appli
c 246	30	1.2	6040	9	US-10-074-095-1029	Sequence 1029, Ap	319	30	1.2	43950	12	US-10-060-332-3	Sequence 3, Appli
247	30	1.2	6040	10	US-09-764-860-1029	Sequence 1029, Ap	320	30	1.2	52216	10	US-09-747-810-1	Sequence 1, Appli
c 248	30	1.2	6284	10	US-09-764-877-3643	Sequence 3643, Ap	321	30	1.2	64467	9	US-10-274-409-3	Sequence 3, Appli
249	30	1.2	6461	9	US-10-125-540-546	Sequence 546, App	322	30	1.2	65608	9	US-09-954-531-180	Sequence 180, App
c 250	30	1.2	6461	10	US-09-764-870-546	Sequence 546, App	323	30	1.2	65608	10	US-09-962-436-292	Sequence 292, App
c 251	30	1.2	6708	9	US-09-764-891-6566	Sequence 6566, Ap	324	30	1.2	65608	10	US-09-962-832-119	Sequence 119, App
c 252	30	1.2	7023	10	US-09-764-877-2802	Sequence 2802, Ap	325	30	1.2	76738	10	US-09-880-107-3949	Sequence 3949, Ap
c 253	30	1.2	7062	10	US-09-764-877-3889	Sequence 3889, Ap	326	30	1.2	84539	10	US-09-962-436-36	Sequence 36, Appl
c 254	30	1.2	7588	9	US-09-764-891-9724	Sequence 9724, Ap	327	30	1.2	98865	10	US-09-770-689A-3	Sequence 3, Appli
c 255	30	1.2	8082	9	US-10-074-095-1106	Sequence 1106, Ap	328	30	1.2	98014	10	US-09-880-107-3428	Sequence 1428, Ap
c 256	30	1.2	8082	10	US-09-764-860-1106	Sequence 1106, Ap	329	30	1.2	110056	10	US-09-880-107-1542	Sequence 1542, Ap
c 257	30	1.2	8821	9	US-09-764-868-1497	Sequence 1497, Ap	330	30	1.2	116592	10	US-09-818-512-3	Sequence 3, Appli
c 258	30	1.2	8821	9	US-10-000-639-7	Sequence 7, Appli	331	30	1.2	126512	10	US-09-804-474A-3	Sequence 3, Appli
c 259	30	1.2	10283	9	US-09-938-795A-3	Sequence 3, Appli	332	30	1.2	174424	10	US-09-967-769A-314	Sequence 314, App
c 260	30	1.2	10445	9	US-09-764-891-6380	Sequence 6380, Ap	333	30	1.2	180216	10	US-09-835-232-6	Sequence 6, Appli
c 261	30	1.2	10563	10	US-09-764-864-1680	Sequence 1680, Ap	334	30	1.2	185695	9	US-10-020-141-11	Sequence 11, Appl
c 262	30	1.2	11079	9	US-10-073-961-465	Sequence 465, App	335	30	1.2	185695	9	US-10-017-721-1	Sequence 1, Appli
c 263	30	1.2	11079	9	US-09-764-887-465	Sequence 465, App	336	30	1.2	1503841	10	US-09-946-807-1	Sequence 1, Appli
c 264	30	1.2	11337	10	US-09-764-877-2651	Sequence 2651, Ap	337	30	1.2	1503841	9	US-09-795-668-1	Sequence 1, Appli
c 265	30	1.2	11618	9	US-09-764-891-9890	Sequence 9890, Ap	338	30	1.2	1503841	10	US-09-795-668-1	Sequence 1, Appli
c 266	30	1.2	11870	9	US-09-764-891-10016	Sequence 10016, A	339	29	1.2	101	9	US-10-091-572-578	Sequence 578, App
c 267	30	1.2	11870	9	US-09-764-891-10017	Sequence 10017, A	340	29	1.2	101	9	US-09-764-891-6722	Sequence 6722, Ap
c 268	30	1.2	12232	9	US-09-764-891-9634	Sequence 9634, Ap	341	29	1.2	143	9	US-10-092-154-1676	Sequence 1676, Ap
c 269	30	1.2	12452	10	US-09-764-877-2399	Sequence 2399, Ap	342	29	1.2	143	10	US-09-764-847-1676	Sequence 1676, Ap
c 270	30	1.2	12562	10	US-09-764-877-2460	Sequence 2460, Ap	343	29	1.2	145	9	US-10-074-095-713	Sequence 713, App
c 271	30	1.2	13467	9	US-09-764-868-1330	Sequence 1330, Ap	344	29	1.2	145	10	US-09-764-860-713	Sequence 713, App
c 272	30	1.2	13467	9	US-09-764-868-1498	Sequence 1498, Ap	345	29	1.2	145	9	US-10-116-016-42	Sequence 42, Appl
c 273	30	1.2	13467	9	US-09-764-891-8632	Sequence 8632, Ap	346	29	1.2	147	10	US-09-764-848-42	Sequence 42, Appl
c 274	30	1.2	13824	10	US-09-764-877-3492	Sequence 3492, Ap	347	29	1.2	167	9	US-09-764-891-6593	Sequence 6593, Ap
c 275	30	1.2	14040	9	US-09-764-891-5478	Sequence 5478, Ap	348	29	1.2	167	9	US-09-764-891-6594	Sequence 6594, Ap
c 276	30	1.2	14040	9	US-09-764-891-10205	Sequence 10205, A	349	29	1.2	201	12	US-10-033-528-1856	Sequence 1856, Ap
c 277	30	1.2	14175	9	US-09-764-868-1474	Sequence 1474, Ap	350	29	1.2	221	9	US-10-073-961-574	Sequence 574, App
c 278	30	1.2	14299	9	US-10-073-961-466	Sequence 466, App	351	29	1.2	221	10	US-09-764-887-574	Sequence 574, App
c 279	30	1.2	14299	10	US-09-764-887-466	Sequence 466, App	352	29	1.2	284	9	US-10-074-095-1111	Sequence 1111, Ap
c 280	30	1.2	14403	9	US-09-764-891-9834	Sequence 9834, Ap	353	29	1.2	284	10	US-09-764-860-1111	Sequence 1111, Ap
c 281	30	1.2	15610	9	US-09-764-891-9760	Sequence 9760, Ap	354	29	1.2	337	9	US-10-091-504-1528	Sequence 1528, Ap
c 282	30	1.2	15734	9	US-10-091-504-1922	Sequence 1922, Ap	355	29	1.2	337	10	US-09-764-869-1528	Sequence 1528, Ap
c 283	30	1.2	15734	10	US-09-764-869-1922	Sequence 1922, Ap	356	29	1.2	352	10	US-09-764-869-1528	Sequence 1528, Ap
c 284	30	1.2	15843	9	US-10-091-504-2396	Sequence 2396, Ap	357	29	1.2	378	10	US-09-867-701-8905	Sequence 8905, Ap
c 285	30	1.2	15843	10	US-09-764-869-2396	Sequence 2396, Ap	358	29	1.2	388	10	US-09-925-302-360	Sequence 360, App
c 286	30	1.2	16057	9	US-10-091-504-1435	Sequence 1435, Ap	359	29	1.2	401	9	US-09-946-807-121	Sequence 121, App
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c 288	30	1.2	16086	10	US-09-764-877-2385	Sequence 2385, Ap	361	29	1.2	401	10	US-09-795-668-121	Sequence 121, App
c 289	30	1.2	16181	9	US-10-092-154-1426	Sequence 1426, Ap	362	29	1.2	401	10	US-09-795-668-1471	Sequence 1471, Ap
c 290	30	1.2	16181	9	US-09-764-891-6956	Sequence 6956, Ap	363	29	1.2	401	10	US-09-795-668-1471	Sequence 1471, Ap
c 291	30	1.2	16181	10	US-09-764-847-1426	Sequence 1426, Ap	364	29	1.2	403	9	US-09-946-807-1470	Sequence 1470, Ap
c 292	30	1.2	16774	9	US-10-091-504-2395	Sequence 2395, Ap	365	29	1.2	403	9	US-09-946-807-1472	Sequence 1472, Ap
c 293	30	1.2	16774	10	US-10-091-504-2398	Sequence 2398, Ap	366	29	1.2	403	10	US-09-795-668-1470	Sequence 1470, Ap
c 294	30	1.2	16774	10	US-09-764-869-2395	Sequence 2395, Ap	367	29	1.2	403	10	US-09-795-668-1472	Sequence 1472, Ap
c 295	30	1.2	16774	10	US-09-764-869-2398	Sequence 2398, Ap	368	29	1.2	403	10	US-09-795-668-1470	Sequence 1470, Ap
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c 297	30	1.2	17000	10	US-09-764-887-467	Sequence 467, App	370	29	1.2	438	9	US-10-198-846-2733	Sequence 2733, Ap
c 298	30	1.2	17286	10	US-09-764-877-3234	Sequence 3234, Ap	371	29	1.2	442	9	US-09-764-891-8331	Sequence 8331, Ap
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c 301	30	1.2	22786	10	US-09-764-877-3727	Sequence 3727, Ap	374	29	1.2	463	9	US-09-764-891-8942	Sequence 8942, Ap
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c 305	30	1.2	32188	9	US-10-074-095-799	Sequence 799, App	378	29	1.2	683	9	US-10-232-803-19	Sequence 19, Appl
c 306	30	1.2	32188	10	US-09-764-860-799	Sequence 799, App	379	29	1.2	761	9	US-09-986-480-101	Sequence 101, App
c 307	30	1.2	32190	9	US-10-079-854-201	Sequence 201, App	380	29	1.2	818	9	US-10-198-846-6587	Sequence 6587, Ap
c 308	30	1.2	32190	10	US-09-764-878-201	Sequence 201, App	381	29	1.2	830	9	US-10-198-846-4206	Sequence 4206, Ap
c 309	30	1.2	32192	9	US-09-764-891-9791	Sequence 9791, Ap	382	29	1.2	837	9	US-10-198-846-6650	Sequence 6650, Ap
c 310	30	1.2	32192	10	US-09-764-877-3657	Sequence 3657, Ap	383	29	1.2	879	10	US-09-764-853-13	Sequence 13, Appl
c 311	30	1.2	32193	9	US-10-079-854-200	Sequence 200, App	384	29	1.2	884	9	US-10-198-846-4038	Sequence 4038, Ap

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c 391	29	1.2	1180	10	US-09-764-860-809	Sequence 809, App	464	29	1.2	2336	9	US-10-125-924-383	Sequence 383, App
c 392	29	1.2	1257	9	US-10-074-095-996	Sequence 996, App	465	29	1.2	2336	9	US-10-127-825A-383	Sequence 383, App
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c 445	29	1.2	2336	9	US-10-123-292-383	Sequence 383, App	518	29	1.2	2336	9	US-10-147-484-383	Sequence 383, App
c 446	29	1.2	2336	9	US-10-123-903-383	Sequence 383, App	519	29	1.2	2336	9	US-10-147-492-383	Sequence 383, App
c 447	29	1.2	2336	9	US-10-124-819-383	Sequence 383, App	520	29	1.2	2336	9	US-10-147-508-383	Sequence 383, App
c 448	29	1.2	2336	9	US-10-124-822-383	Sequence 383, App	521	29	1.2	2336	9	US-10-147-512-383	Sequence 383, App
c 449	29	1.2	2336	9	US-10-140-925-383	Sequence 383, App	522	29	1.2	2336	9	US-10-158-782-383	Sequence 383, App
c 450	29	1.2	2336	9	US-10-160-498-383	Sequence 383, App	523	29	1.2	2336	9	US-10-175-735-383	Sequence 383, App
c 451	29	1.2	2336	9	US-09-999-830A-144	Sequence 144, App	524	29	1.2	2336	9	US-10-123-905-383	Sequence 383, App
c 452	29	1.2	2336	9	US-10-121-041-383	Sequence 383, App	525	29	1.2	2336	9	US-10-123-907-383	Sequence 383, App
c 453	29	1.2	2336	9	US-10-121-043-383	Sequence 383, App	526	29	1.2	2336	9	US-10-124-815-383	Sequence 383, App
c 454	29	1.2	2336	9	US-10-121-047-383	Sequence 383, App	527	29	1.2	2336	9	US-10-125-921A-383	Sequence 383, App
c 455	29	1.2	2336	9	US-10-123-215-383	Sequence 383, App	528	29	1.2	2336	9	US-10-125-928A-383	Sequence 383, App
c 456	29	1.2	2336	9	US-10-123-902-383	Sequence 383, App	529	29	1.2	2336	9	US-10-127-821A-383	Sequence 383, App
c 457	29	1.2	2336	9	US-10-123-908-383	Sequence 383, App	530	29	1.2	2336	9	US-10-127-822A-383	Sequence 383, App

531	29	1.2	2336	9	US-10-127-824A-383	Sequence 383, App	604	29	1.2	10248	10	US-09-764-847-1238	Sequence 1238, Ap
532	29	1.2	2336	9	US-10-127-826A-383	Sequence 383, App	c 605	29	1.2	10377	9	US-09-764-891-6453	Sequence 6453, Ap
533	29	1.2	2336	9	US-10-127-827A-383	Sequence 383, App	c 606	29	1.2	11185	9	US-10-074-095-1096	Sequence 1096, Ap
534	29	1.2	2336	9	US-10-127-828A-383	Sequence 383, App	c 607	29	1.2	11185	9	US-09-764-860-1096	Sequence 1096, Ap
535	29	1.2	2336	9	US-10-127-829A-383	Sequence 383, App	c 608	29	1.2	11294	9	US-09-764-891-7594	Sequence 7594, Ap
536	29	1.2	2336	9	US-10-127-830A-383	Sequence 383, App	c 609	29	1.2	12452	10	US-09-764-877-3989	Sequence 3989, Ap
537	29	1.2	2336	9	US-10-127-831A-383	Sequence 383, App	c 610	29	1.2	12542	9	US-09-764-864-1774	Sequence 1774, Ap
538	29	1.2	2336	9	US-10-127-832A-383	Sequence 383, App	c 611	29	1.2	12542	9	US-10-092-154-1489	Sequence 1489, Ap
539	29	1.2	2336	9	US-10-127-833A-383	Sequence 383, App	c 612	29	1.2	12989	9	US-09-764-847-1489	Sequence 1489, Ap
540	29	1.2	2336	9	US-10-127-834A-383	Sequence 383, App	c 613	29	1.2	13046	9	US-10-125-540-595	Sequence 595, App
541	29	1.2	2336	9	US-10-127-835A-383	Sequence 383, App	c 614	29	1.2	13046	9	US-09-764-891-5938	Sequence 5938, Ap
542	29	1.2	2336	9	US-10-128-687A-383	Sequence 383, App	c 615	29	1.2	13046	9	US-09-764-870-595	Sequence 595, App
543	29	1.2	2336	9	US-10-128-688A-383	Sequence 383, App	c 616	29	1.2	13953	9	US-10-096-961-3	Sequence 3, Appli
544	29	1.2	2336	9	US-10-128-689A-383	Sequence 383, App	c 617	29	1.2	13996	9	US-10-125-540-602	Sequence 602, App
545	29	1.2	2336	9	US-10-128-690A-383	Sequence 383, App	c 618	29	1.2	13996	9	US-09-764-870-602	Sequence 602, App
546	29	1.2	2336	9	US-10-131-825A-383	Sequence 383, App	c 619	29	1.2	14001	9	US-10-125-540-601	Sequence 601, App
547	29	1.2	2336	9	US-10-230-417-383	Sequence 383, App	c 620	29	1.2	14001	9	US-09-764-870-601	Sequence 601, App
548	29	1.2	2336	9	US-10-121-051-383	Sequence 383, App	c 621	29	1.2	14152	9	US-10-091-504-1573	Sequence 1573, Ap
549	29	1.2	2336	9	US-10-131-815A-383	Sequence 383, App	c 622	29	1.2	14152	9	US-09-764-869-1573	Sequence 1573, Ap
550	29	1.2	2336	9	US-10-131-817A-383	Sequence 383, App	c 623	29	1.2	14485	10	US-09-764-876-216-3	Sequence 3, Appli
551	29	1.2	2336	9	US-10-131-821A-383	Sequence 383, App	c 624	29	1.2	14581	9	US-10-216-373-4	Sequence 4, Appli
552	29	1.2	2336	9	US-10-131-822A-383	Sequence 383, App	c 625	29	1.2	14874	9	US-09-764-891-7672	Sequence 7672, Ap
553	29	1.2	2336	9	US-10-131-828A-383	Sequence 383, App	c 626	29	1.2	15123	9	US-09-764-891-7595	Sequence 7595, Ap
554	29	1.2	2336	9	US-10-131-835A-383	Sequence 383, App	c 627	29	1.2	15772	9	US-10-091-391-66	Sequence 66, Appl
555	29	1.2	2336	9	US-10-137-864A-383	Sequence 383, App	c 628	29	1.2	15772	9	US-09-764-903-66	Sequence 66, Appl
556	29	1.2	2336	9	US-10-137-869A-383	Sequence 383, App	c 629	29	1.2	15980	9	US-09-764-864-1714	Sequence 1714, Ap
557	29	1.2	2336	9	US-10-147-523-383	Sequence 383, App	c 630	29	1.2	16062	9	US-09-764-891-8047	Sequence 8047, Ap
558	29	1.2	2336	9	US-10-158-785-383	Sequence 383, App	c 631	29	1.2	16100	9	US-09-764-877-3698	Sequence 3698, Ap
559	29	1.2	2336	9	US-09-978-187B-144	Sequence 144, App	c 632	29	1.2	16825	9	US-10-092-154-1495	Sequence 1495, Ap
560	29	1.2	2336	9	US-10-121-042-383	Sequence 383, App	c 633	29	1.2	16825	10	US-09-764-847-1495	Sequence 1495, Ap
561	29	1.2	2336	9	US-10-123-312-383	Sequence 383, App	c 634	29	1.2	17431	9	US-10-072-349-247	Sequence 247, App
562	29	1.2	2336	9	US-09-978-643A-144	Sequence 144, App	c 635	29	1.2	17431	9	US-09-764-855-247	Sequence 247, App
563	29	1.2	2336	9	US-10-166-709A-144	Sequence 144, App	c 636	29	1.2	17538	10	US-09-893-348-9	Sequence 9, Appli
564	29	1.2	2336	9	US-10-192-007-383	Sequence 383, App	c 637	29	1.2	17601	9	US-09-764-891-7111	Sequence 7111, Ap
565	29	1.2	2336	9	US-10-194-359-383	Sequence 383, App	c 638	29	1.2	17787	9	US-09-764-868-1285	Sequence 1285, Ap
566	29	1.2	2336	9	US-10-037-270-411	Sequence 411, App	c 639	29	1.2	17787	9	US-09-764-891-5648	Sequence 5648, Ap
567	29	1.2	2584	9	US-10-198-846-13670	Sequence 13670, A	c 640	29	1.2	17787	9	US-09-764-891-5648	Sequence 5648, Ap
568	29	1.2	2916	9	US-09-822-846-249	Sequence 249, App	c 641	29	1.2	17787	9	US-09-764-891-6051	Sequence 6051, Ap
569	29	1.2	3144	9	US-10-163-866-31	Sequence 31, Appl	c 642	29	1.2	17787	9	US-09-764-891-6051	Sequence 6051, Ap
570	29	1.2	3895	9	US-10-011-585A-76	Sequence 76, Appl	c 643	29	1.2	17787	9	US-09-764-891-6051	Sequence 6051, Ap
571	29	1.2	4108	10	US-09-883-096-1	Sequence 1, Appli	c 644	29	1.2	17792	9	US-10-091-504-1599	Sequence 1599, Ap
572	29	1.2	4242	12	US-10-044-090-190	Sequence 190, App	c 645	29	1.2	17792	10	US-09-764-869-1599	Sequence 1599, Ap
573	29	1.2	4440	9	US-09-981-503-132	Sequence 132, App	c 646	29	1.2	18820	9	US-09-764-891-6452	Sequence 6452, Ap
574	29	1.2	4660	9	US-10-091-504-1572	Sequence 1572, App	c 647	29	1.2	18981	9	US-09-764-891-7649	Sequence 7649, Ap
575	29	1.2	4660	10	US-09-764-869-1572	Sequence 1572, Ap	c 648	29	1.2	19553	9	US-10-092-154-1425	Sequence 1425, Ap
576	29	1.2	4963	10	US-09-764-877-2903	Sequence 2903, Ap	c 649	29	1.2	19553	9	US-09-764-847-1425	Sequence 1425, Ap
577	29	1.2	5156	10	US-09-764-877-3945	Sequence 3945, Ap	c 650	29	1.2	21724	10	US-09-764-864-1604	Sequence 1604, Ap
578	29	1.2	5881	9	US-09-764-891-9918	Sequence 9918, Ap	c 651	29	1.2	21724	10	US-09-764-864-1604	Sequence 1604, Ap
579	29	1.2	6153	9	US-09-764-891-5720	Sequence 5720, App	c 652	29	1.2	21727	10	US-09-764-877-2275	Sequence 2275, Ap
580	29	1.2	6153	10	US-09-764-877-3077	Sequence 3077, App	c 653	29	1.2	22073	9	US-09-764-891-7351	Sequence 7351, Ap
581	29	1.2	6465	10	US-09-954-456-193	Sequence 193, App	c 654	29	1.2	22484	10	US-09-875-114-2	Sequence 2, Appli
582	29	1.2	6719	9	US-10-232-803-36	Sequence 36, Appl	c 655	29	1.2	22484	9	US-09-880-107-3341	Sequence 3341, Ap
583	29	1.2	6834	9	US-09-764-891-8002	Sequence 8002, App	c 656	29	1.2	22645	9	US-09-764-891-7673	Sequence 7673, Ap
584	29	1.2	8021	9	US-10-091-438-263	Sequence 263, App	c 657	29	1.2	22645	9	US-09-764-891-8163	Sequence 8163, Ap
585	29	1.2	8021	9	US-10-232-803-2	Sequence 2, Appli	c 658	29	1.2	23309	10	US-09-764-877-2455	Sequence 2455, Ap
586	29	1.2	8095	9	US-09-989-920-73	Sequence 73, Appl	c 659	29	1.2	23309	10	US-10-291-737-3	Sequence 3, Appli
587	29	1.2	8194	9	US-09-789-629-15	Sequence 15, Appl	c 660	29	1.2	26591	10	US-09-764-877-2678	Sequence 2678, Ap
588	29	1.2	8194	9	US-10-035-045-15	Sequence 15, Appl	c 661	29	1.2	26664	9	US-09-988-626-28	Sequence 28, Appl
589	29	1.2	8746	9	US-10-074-095-1022	Sequence 1022, App	c 662	29	1.2	26664	9	US-09-988-687-28	Sequence 28, Appl
590	29	1.2	8746	10	US-09-764-860-1022	Sequence 1022, App	c 663	29	1.2	27332	10	US-10-092-154-1555	Sequence 1555, Ap
591	29	1.2	8835	9	US-09-764-891-5494	Sequence 5494, App	c 664	29	1.2	27332	10	US-09-764-847-1555	Sequence 1555, Ap
592	29	1.2	8894	10	US-09-764-864-1692	Sequence 1692, Ap	c 665	29	1.2	27681	9	US-10-091-504-1997	Sequence 1997, Ap
593	29	1.2	8894	10	US-09-764-877-3063	Sequence 3063, Ap	c 666	29	1.2	27681	9	US-10-091-504-1998	Sequence 1998, Ap
594	29	1.2	9519	9	US-10-092-154-1056	Sequence 1056, Ap	c 667	29	1.2	27681	10	US-09-764-869-1997	Sequence 1997, Ap
595	29	1.2	9519	10	US-09-764-847-1056	Sequence 1056, Ap	c 668	29	1.2	27681	10	US-09-764-869-1998	Sequence 1998, Ap
596	29	1.2	9519	10	US-09-764-877-3534	Sequence 3534, App	c 669	29	1.2	28818	10	US-09-764-877-2266	Sequence 2266, Ap
597	29	1.2	9620	9	US-09-764-891-8895	Sequence 8895, App	c 670	29	1.2	29695	10	US-09-752-820A-3	Sequence 3, Appli
598	29	1.2	9877	10	US-09-764-877-3944	Sequence 3944, App	c 671	29	1.2	29695	10	US-09-813-319A-3	Sequence 3, Appli
599	29	1.2	9970	10	US-09-764-877-2277	Sequence 2277, App	c 672	29	1.2	31132	10	US-09-764-864-1690	Sequence 1690, Ap
600	29	1.2	10195	10	US-09-764-864-1600	Sequence 1600, App	c 673	29	1.2	31132	10	US-09-764-877-3062	Sequence 3062, Ap
601	29	1.2	10198	9	US-09-764-891-8743	Sequence 8743, App	c 674	29	1.2	31766	9	US-10-288-478-5	Sequence 5, Appli
602	29	1.2	10198	9	US-09-764-891-8744	Sequence 8744, App	c 675	29	1.2	31766	9	US-09-765-344-5	Sequence 5, Appli
603	29	1.2	10248	9	US-10-092-154-1238	Sequence 1238, App	c 676	29	1.2	32170	9	US-10-074-095-1108	Sequence 1108, Ap

677	29	1.2	32170	10	US-09-764-860-1108	Sequence 1108, Ap	750	28	1.2	2275	9	US-09-764-891-9061	Sequence 9061, Ap
678	29	1.2	32184	9	US-09-764-891-7300	Sequence 7300, Ap	751	28	1.2	2275	9	US-09-764-891-9062	Sequence 9062, Ap
679	29	1.2	32190	9	US-10-091-504-2209	Sequence 2209, Ap	752	28	1.2	2517	9	US-10-198-846-11008	Sequence 11008, A
680	29	1.2	32190	10	US-09-764-869-2209	Sequence 2209, Ap	c 753	28	1.2	2903	10	US-09-822-830A-221	Sequence 221, App
681	29	1.2	32191	9	US-09-764-891-6454	Sequence 6454, Ap	754	28	1.2	3088	10	US-09-954-456-45	Sequence 45, Appl
682	29	1.2	32194	9	US-09-764-891-7028	Sequence 7028, Ap	755	28	1.2	3088	10	US-09-954-456-1621	Sequence 1621, Ap
683	29	1.2	32195	9	US-10-102-672-92	Sequence 92, Appl	756	28	1.2	3088	10	US-09-969-347-234	Sequence 234, App
684	29	1.2	32203	9	US-10-091-504-1849	Sequence 1849, Ap	c 757	28	1.2	3805	9	US-09-764-891-7518	Sequence 7518, Ap
685	29	1.2	32203	10	US-09-764-869-1849	Sequence 1849, Ap	c 758	28	1.2	3846	9	US-10-245-103-55	Sequence 55, Appl
686	29	1.2	32249	9	US-09-764-891-7364	Sequence 7364, Ap	c 759	28	1.2	3846	9	US-10-245-107-55	Sequence 55, Appl
687	29	1.2	32249	9	US-09-764-891-7619	Sequence 7619, Ap	c 760	28	1.2	3846	9	US-10-245-143-55	Sequence 55, Appl
688	29	1.2	33795	10	US-09-880-107-2184	Sequence 2184, Ap	c 761	28	1.2	3846	9	US-10-245-771-55	Sequence 55, Appl
689	29	1.2	35465	9	US-10-161-572-6	Sequence 6, Appli	c 762	28	1.2	3846	9	US-10-245-851-55	Sequence 55, Appl
690	29	1.2	36991	9	US-10-161-572-8	Sequence 8, Appli	c 763	28	1.2	3846	9	US-10-245-883-55	Sequence 55, Appl
691	29	1.2	38374	10	US-09-880-107-3463	Sequence 3463, Ap	c 764	28	1.2	3846	9	US-10-237-535-55	Sequence 55, Appl
692	29	1.2	42999	10	US-09-740-029-3	Sequence 3, Appli	c 765	28	1.2	3846	9	US-10-238-183-55	Sequence 55, Appl
693	29	1.2	43058	10	US-09-954-456-292	Sequence 292, App	c 766	28	1.2	3846	9	US-10-238-283-55	Sequence 55, Appl
694	29	1.2	43058	10	US-09-954-456-292	Sequence 292, App	c 767	28	1.2	3846	9	US-10-238-370-55	Sequence 55, Appl
695	29	1.2	43058	10	US-09-954-456-529	Sequence 529, App	c 768	28	1.2	3846	9	US-10-245-055-55	Sequence 55, Appl
696	29	1.2	43058	10	US-09-954-456-529	Sequence 529, App	c 769	28	1.2	3846	9	US-10-245-147-55	Sequence 55, Appl
697	29	1.2	43058	10	US-09-880-107-3950	Sequence 3950, App	c 770	28	1.2	3846	9	US-10-245-730-55	Sequence 55, Appl
698	29	1.2	43058	10	US-09-880-107-3950	Sequence 3950, App	c 771	28	1.2	3846	9	US-10-245-739-55	Sequence 55, Appl
699	29	1.2	43950	12	US-10-060-332-3	Sequence 3, Appli	c 772	28	1.2	3846	9	US-10-246-210-55	Sequence 55, Appl
700	29	1.2	49984	10	US-09-739-457-5	Sequence 5, Appli	c 773	28	1.2	3846	9	US-10-239-196-55	Sequence 55, Appl
701	29	1.2	53522	9	US-09-904-968A-1	Sequence 1, Appli	c 774	28	1.2	3846	9	US-10-243-024-55	Sequence 55, Appl
702	29	1.2	56516	9	US-09-853-526-1	Sequence 1, Appli	c 775	28	1.2	3846	9	US-10-243-409-55	Sequence 55, Appl
703	29	1.2	56516	9	US-09-901-484A-1	Sequence 1, Appli	c 776	28	1.2	3846	9	US-10-245-033-55	Sequence 55, Appl
704	29	1.2	56520	9	US-09-853-526-179	Sequence 179, App	c 777	28	1.2	3846	9	US-10-245-621-55	Sequence 55, Appl
705	29	1.2	56520	10	US-09-901-484A-179	Sequence 179, App	c 778	28	1.2	3846	9	US-10-245-880-55	Sequence 55, Appl
706	29	1.2	57130	10	US-09-835-081-3	Sequence 3, Appli	c 779	28	1.2	3846	9	US-10-243-095-55	Sequence 55, Appl
707	29	1.2	58837	10	US-09-982-091A-5	Sequence 5, Appli	c 780	28	1.2	3846	9	US-10-245-185-55	Sequence 55, Appl
708	29	1.2	62804	12	US-10-096-960-3	Sequence 3, Appli	c 781	28	1.2	3846	9	US-10-245-427-55	Sequence 55, Appl
709	29	1.2	65359	10	US-09-804-472-3	Sequence 3, Appli	c 782	28	1.2	3846	9	US-10-245-473-55	Sequence 55, Appl
710	29	1.2	65464	9	US-09-859-888-3	Sequence 3, Appli	c 783	28	1.2	3846	9	US-10-245-770-55	Sequence 55, Appl
711	29	1.2	73308	10	US-09-954-456-2276	Sequence 2276, Ap	c 784	28	1.2	3846	9	US-10-245-877-55	Sequence 55, Appl
712	29	1.2	90541	10	US-09-759-359A-3	Sequence 3, Appli	c 785	28	1.2	3846	9	US-10-246-976-55	Sequence 55, Appl
713	29	1.2	96649	9	US-09-956-712-10	Sequence 10, Appli	c 786	28	1.2	3846	9	US-10-243-320-55	Sequence 55, Appl
714	29	1.2	118951	9	US-10-161-572-11	Sequence 11, Appli	c 787	28	1.2	3846	9	US-10-242-743-55	Sequence 55, Appl
715	29	1.2	128762	9	US-09-954-556-17	Sequence 17, Appli	c 788	28	1.2	3846	9	US-10-242-845-55	Sequence 55, Appl
716	29	1.2	145831	10	US-09-969-708-79	Sequence 79, Appli	c 789	28	1.2	3846	9	US-10-237-636-55	Sequence 55, Appl
717	29	1.2	145831	10	US-09-954-456-2116	Sequence 2116, Ap	c 790	28	1.2	3846	9	US-10-238-325-55	Sequence 55, Appl
718	29	1.2	180216	10	US-09-835-232-6	Sequence 6, Appli	c 791	28	1.2	3846	9	US-10-238-346-55	Sequence 55, Appl
719	29	1.2	402850	9	US-09-844-653-5	Sequence 5, Appli	c 792	28	1.2	3846	9	US-10-238-411-55	Sequence 55, Appl
720	29	1.2	1691139	9	US-10-067-514-1	Sequence 1, Appli	c 793	28	1.2	3846	9	US-10-243-124-55	Sequence 55, Appl
721	28	1.2	198	9	US-10-066-543-2824	Sequence 2824, Ap	c 794	28	1.2	3846	9	US-10-243-425-55	Sequence 55, Appl
722	28	1.2	290	9	US-10-091-504-1466	Sequence 1466, Ap	c 795	28	1.2	3846	9	US-10-243-446-55	Sequence 55, Appl
723	28	1.2	290	10	US-09-764-869-1466	Sequence 1466, Ap	c 796	28	1.2	3846	9	US-10-245-874-55	Sequence 55, Appl
724	28	1.2	315	10	US-09-964-824A-523	Sequence 523, Ap	c 797	28	1.2	3900	10	US-09-764-864-1703	Sequence 1703, Ap
725	28	1.2	315	10	US-09-964-824A-523	Sequence 523, Ap	c 798	28	1.2	3901	10	US-09-764-891-6949	Sequence 6949, Ap
726	28	1.2	347	9	US-09-918-995-18604	Sequence 1469, Ap	c 799	28	1.2	5281	9	US-10-079-854-409	Sequence 409, App
727	28	1.2	371	10	US-09-867-701-4466	Sequence 1466, Ap	c 800	28	1.2	5299	10	US-09-764-878-409	Sequence 409, App
728	28	1.2	391	10	US-09-867-701-4466	Sequence 1466, Ap	c 801	28	1.2	5299	10	US-09-764-878-409	Sequence 409, App
729	28	1.2	418	9	US-10-165-835-5	Sequence 5, Appli	c 802	28	1.2	5530	9	US-09-764-904-112	Sequence 112, App
730	28	1.2	451	9	US-09-918-995-8988	Sequence 8988, Ap	c 803	28	1.2	5530	9	US-10-091-548-112	Sequence 112, App
731	28	1.2	451	10	US-09-764-877-3554	Sequence 3554, Ap	c 804	28	1.2	5530	10	US-10-074-095-1167	Sequence 1167, Ap
732	28	1.2	455	9	US-10-198-846-1579	Sequence 1579, Ap	c 805	28	1.2	5530	10	US-09-764-860-1167	Sequence 1167, Ap
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737	28	1.2	543	10	US-09-867-701-2460	Sequence 2460, Ap	c 810	28	1.2	8210	10	US-09-764-878-406	Sequence 406, App
738	28	1.2	549	10	US-09-998-598-1277	Sequence 1277, Ap	c 811	28	1.2	8553	9	US-09-764-891-7456	Sequence 7456, Ap
739	28	1.2	558	9	US-10-198-846-11656	Sequence 11656, Ap	c 812	28	1.2	8895	9	US-10-091-438-250	Sequence 250, App
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741	28	1.2	633	9	US-10-198-846-3496	Sequence 3496, Ap	c 814	28	1.2	8895	10	US-09-764-853-887	Sequence 887, App
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744	28	1.2	1452	9	US-10-091-572-856	Sequence 856, App	c 817	28	1.2	9656	9	US-10-091-438-255	Sequence 255, App
745	28	1.2	1452	9	US-09-764-891-9295	Sequence 9295, Ap	c 818	28	1.2	9656	10	US-09-764-853-886	Sequence 886, App
746	28	1.2	1647	10	US-09-764-877-2360	Sequence 2360, Ap	c 819	28	1.2	9656	10	US-09-764-853-933	Sequence 933, App
747	28	1.2	1742	9	US-10-097-065-100	Sequence 100, App	c 820	28	1.2	10680	9	US-09-764-891-8367	Sequence 8367, Ap
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826	28	1.2	12988	10	US-09-764-869-2285	Sequence 2285, Ap	899	27	1.1	89	10	US-09-764-847-1924	Sequence 1924, Ap
827	28	1.2	13026	9	US-09-764-891-10217	Sequence 10217, A	900	27	1.1	104	10	US-09-764-877-2686	Sequence 2686, Ap
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832	28	1.2	19206	10	US-09-764-869-1258	Sequence 1258, Ap	905	27	1.1	406	9	US-09-918-995-17792	Sequence 17792, A
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842	28	1.2	20966	10	US-09-909-547-7	Sequence 7, Appli	c 915	27	1.1	2290	10	US-09-822-849A-152	Sequence 152, App
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c 846	28	1.2	21608	9	US-10-091-504-1733	Sequence 1733, Ap	c 919	27	1.1	3566	9	US-10-074-095-1105	Sequence 1105, Ap
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c 856	28	1.2	24268	9	US-10-073-961-602	Sequence 602, App	c 929	27	1.1	8191	9	US-10-092-154-1920	Sequence 1920, Ap
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c 861	28	1.2	31140	9	US-09-764-891-9479	Sequence 9479, Ap	c 934	27	1.1	12324	10	US-09-764-853-897	Sequence 897, App
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c 867	28	1.2	32189	10	US-09-764-891-8604	Sequence 8604, Ap	c 940	27	1.1	16774	10	US-09-764-869-2398	Sequence 2398, Ap
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c 873	28	1.2	32195	9	US-10-125-540-611	Sequence 611, App	c 946	27	1.1	32152	9	US-10-072-349-328	Sequence 328, App
c 874	28	1.2	32195	9	US-10-125-540-617	Sequence 617, App	c 947	27	1.1	32152	10	US-09-764-853-328	Sequence 328, App
c 875	28	1.2	32195	10	US-09-764-870-611	Sequence 611, App	c 948	27	1.1	32152	9	US-10-092-154-1963	Sequence 1963, Ap
c 876	28	1.2	32195	10	US-09-764-870-617	Sequence 617, App	c 949	27	1.1	32152	10	US-09-764-847-1963	Sequence 1963, Ap
c 877	28	1.2	32195	9	US-09-764-869-1605	Sequence 1605, Ap	c 950	27	1.1	32170	9	US-10-074-095-1108	Sequence 1108, Ap
c 878	28	1.2	32199	9	US-10-072-349-210	Sequence 210, App	c 951	27	1.1	32170	10	US-09-764-860-1108	Sequence 1108, Ap
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c 888	28	1.2	68804	10	US-09-740-041-3	Sequence 3, Appli	c 961	27	1.1	48841	9	US-09-844-653-32	Sequence 30, Appl
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c 891	28	1.2	98829	9	US-10-017-724-3	Sequence 1, Appli	c 964	27	1.1	132762	9	US-09-954-556-17	Sequence 1662, Ap
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969 26 1.1 273 9 US-09-764-891-7564 Sequence 7564, Ap
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971 26 1.1 307 9 US-09-764-891-6081 Sequence 6081, Ap
c 972 26 1.1 362 9 US-09-918-995-18419 Sequence 18419, A
973 26 1.1 402 9 US-10-198-846-1750 Sequence 1750, Ap
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975 26 1.1 460 9 US-10-046-935-394 Sequence 394, App
976 26 1.1 460 9 US-09-878-178-394 Sequence 394, App
977 26 1.1 460 9 US-10-146-502-394 Sequence 394, App
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981 26 1.1 848 9 US-10-198-846-10677 Sequence 10677, A
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c 983 26 1.1 875 9 US-10-074-095-171 Sequence 171, App
984 26 1.1 875 10 US-09-764-860-171 Sequence 171, App
985 26 1.1 964 9 US-09-984-130-91 Sequence 91, App1
986 26 1.1 1035 9 US-09-764-891-2666 Sequence 2666, Ap
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990 26 1.1 1766 9 US-09-764-891-1793 Sequence 7393, Ap
991 26 1.1 1901 9 US-09-853-526-181 Sequence 181, App
992 26 1.1 1901 10 US-09-901-484A-181 Sequence 181, App
993 26 1.1 2764 9 US-09-978-295A-258 Sequence 258, App
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995 26 1.1 2764 9 US-09-978-192A-258 Sequence 258, App
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ALIGNMENTS

RESULT 1
US-09-918-995-29121
; Sequence 29121, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29121
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(475)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29121
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Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 42 GCCAGGTTACGGCAACCTTTCCCTTAGCAGCTTACGAGTCTAGTCTGGTTCT 101
Qy 2084 AGAGTTCAGGACGGTCTCTCAGAGCGCCAGAGCCAGAGCCCAAGCAGACGAAAG 2143
Db 102 AGAGTTCAGGACGGTCTCTCAGAGCGCCAGAGCCAGAGCCCAAGCAGACGAAAG 161

Qy 2144 AGGCATACACAGCAGTGTGAATAGCTGGCCACGAGCATCTCCCTCCACTCAAGA 2203
Db 162 AGGCATACACAGCAGTGTGAATAGCTGGCCACGAGCATCTCCCTCCACTCAAGA 221
Qy 2204 CCCCATTGTGTC 2216
Db 222 CCCCATTGTGTC 234

RESULT 2

US-10-118-328-3/c
; Sequence 3, Application US/10118328
; Patent No. US20020169289A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001220
; CURRENT APPLICATION NUMBER: US/10/118,328
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,460
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30350
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-328-3
Query Match 1.6%; Score 39; DB 9; Length 30350;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGAGGGGAGGTTGCAGTGAGCCAGCAAGATCAGCCACTAC 44
Db 11147 GGAGGGGAGGTTGCAGTGAGCCAGCAAGATCAGCCACTAC 11109

RESULT 3

US-09-813-320-3/c
; Sequence 3, Application US/09813320
; Patent No. US20020142378A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Hongyu et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001172
; CURRENT APPLICATION NUMBER: US/09/813,320
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 397658
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(397658)
; OTHER INFORMATION: n = A,T,C or G
US-09-813-320-3
Query Match 1.6%; Score 39; DB 10; Length 397658;
Best Local Similarity 100.0%; Pred. No. 9.8e-10;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAGGGGAGGTTGCAGTGAGCCAGCAAGATCAGCCACTA 43
Db 138900 GGAGGGGAGGTTGCAGTGAGCCAGCAAGATCAGCCACTA 138862

RESULT 4

US-09-867-701-8927/c
; Sequence 8927, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8927
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(438)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-8927

Query Match 1.6%; Score 38; DB 10; Length 438;

Best Local Similarity 100.0%; Pred. No. 3.6e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 42

Db 88 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 51

RESULT 5

US-09-867-701-4634/c
; Sequence 4634, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4634
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4634

Query Match 1.6%; Score 38; DB 10; Length 449;

Best Local Similarity 100.0%; Pred. No. 3.5e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 42

Db 91 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 54

RESULT 6

US-09-918-995-24949
; Sequence 24949, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24949
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(456)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24949

Query Match 1.6%; Score 38; DB 9; Length 456;

Best Local Similarity 100.0%; Pred. No. 3.5e-09; Mismatches 38; Conservative 0; Indels 0; Gaps 0;

Qy 5 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 42

Db 99 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 136

RESULT 7

US-10-016-157A-71
; Sequence 71, Application US/10016157A
; Publication No. US20020192220A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Ghosh, Malavika
; APPLICANT: Liu, Chenchua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro
; FILE REFERENCE: DEX-0253
; CURRENT APPLICATION NUMBER: US/10/016,157A
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/244,717
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 250
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 9883
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7153)..(7153)
; OTHER INFORMATION: n=a, c, g or t
US-10-016-157A-71

Query Match 1.6%; Score 38; DB 9; Length 9883;

Best Local Similarity 100.0%; Pred. No. 3.4e-09; Mismatches 38; Conservative 0; Indels 0; Gaps 0;

Qy 5 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 42

Db 6724 GGGAGGCGGAGTTGTCAGTGAGCCCAAGATCAGGCCACT 6761

RESULT 8

US-09-764-864-1704/c
; Sequence 1704, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper

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; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 15857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1704

Query Match          1.6%; Score 38; DB 10; Length 15857;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
      |||||||
Db      14952 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 14915

RESULT 9
US-10-079-854-370/c
; Sequence 370, Application US/10079854
; Publication No. US20030054368A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121C1
; CURRENT APPLICATION NUMBER: US/10/079,854
; CURRENT FILING DATE: 2002-02-22
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 370
; LENGTH: 16225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-854-370

Query Match          1.6%; Score 38; DB 9; Length 16225;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
      |||||||
Db      5049 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 5012

RESULT 10
US-09-764-891-9432/c
; Sequence 9432, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9432
; LENGTH: 16225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9432

Query Match          1.6%; Score 38; DB 9; Length 16225;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
      |||||||
Db      5049 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 5012

RESULT 11
US-09-764-878-370/c
; Sequence 370, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 370
; LENGTH: 16225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-370

Query Match          1.6%; Score 38; DB 10; Length 16225;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
      |||||||
Db      5049 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 5012

RESULT 12
US-10-074-045-70
; Sequence 70, Application US/10074045
; Publication No. US20030092102A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ21C1
; CURRENT APPLICATION NUMBER: US/10/074,045
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 18657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-045-70

Query Match          1.6%; Score 38; DB 9; Length 18657;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
      |||||||
Db      10882 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 10919

RESULT 13
US-09-764-891-6868/c
; Sequence 6868, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6868
; LENGTH: 32195
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-764-891-6868

Query Match 1.6%; Score 38; DB 9; Length 32195;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACT 42
Db 1983 GGGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACT 1946

RESULT 14

US-10-025-187-3/c
; Sequence 3, Application US/10025187
; Patent No. US20020150931A1
; GENERAL INFORMATION:
; APPLICANT: SHEFFIELD, VAL
; APPLICANT: NISHIMURA, DARRYL
; APPLICANT: STONE, EDWARD
; TITLE OF INVENTION: A BARDET-BIEDL SUSCEPTIBILITY GENE AND USES THEREOF
; FILE REFERENCE: IOWA:034US
; CURRENT APPLICATION NUMBER: US/10/025,187
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,900
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 45839
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-187-3

Query Match 1.6%; Score 38; DB 12; Length 45839;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACT 42
Db 19401 GGGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACT 19364

RESULT 15

US-09-954-456-2257/c
; Sequence 2257, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2257
; LENGTH: 62944
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2257

Query Match 1.6%; Score 38; DB 10; Length 62944;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACT 42
Db 31008 GGGAGCGGAGGTTGCAGTGAGCCAGATCAGCCACT 30971

Search completed: June 17, 2003, 09:59:13
Job time : 273.144 secs

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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 2731.82 Seconds

(without alignments)

14252.028 Million cell updates/sec

Title: US-09-513-888c-1_COPY_4514_6917

Perfect score: 2404

Sequence: 1 agagggagcgagggttc.....gacagggctctgtctgtcc 2404

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database :

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10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: gb_gss:**

18: em_gss_hum:**

19: em_gss_inv:**

20: em_gss_pln:**

21: em_gss_vrt:**

22: em_gss_fun:**

23: em_gss_nam:**

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25: em_gss_other:**

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27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	603	25.1	705	9	AL118597
2	570	23.7	922	9	AL536293
3	456	19.0	929	13	BM560284
4	383	15.9	1020	12	BF689781
5	296	12.3	296	9	AL134288
6	292	12.1	751	10	BE312985

BF313433	601900020	12	BF313433	432	10.0	240	7
BG765063	602737675	12	BG765063	939	9.7	233	8
BF317160	601901286	12	BF317160	901	8.8	212	9
BI034804	RC4-NN117	446	13	BI034804	7.4	177	10
AA020852	ze64b08.r	463	9	AA020852	6.4	153	11
N35845	yx89f10.r1	643	14	N35845	5.6	134	12
BE384676	601276954	558	10	BE384676	4.3	104	13
BE540725	601065002	797	10	BE540725	4.1	98	14
BG769644	602744561	1120	12	BG769644	3.7	89	15
AL135213	DKFZp762E	247	9	AL135213	3.5	84	16
BE279166	601156630	796	10	BE279166	2.5	60	17
AW47817	UI-M-BH3-	326	10	AW47817	2.2	52	18
BM663827	UI-E-CL1-	700	13	BM663827	1.8	43	19
AA081323	zn33c09.s	214	9	AA081323	1.7	42	20
T06967	EST04856.Fe	370	14	T06967	1.7	42	21
AA641057	nr29a09.s	406	9	AA641057	1.7	42	22
AV720296	AV720296	589	10	AV720296	1.7	42	23
AV718428	AV718428	605	10	AV718428	1.7	42	24
AW855437	CM2-CT027	594	10	AW855437	1.7	41	25
AG009193	Homo sapi	754	17	AG009193	1.6	39	26
AI832003	wj98h07.x	165	9	AI832003	1.6	38	27
BF959498	OV2-NN004	168	12	BF959498	1.6	38	28
AI290407	qm59e03.x	217	9	AI290407	1.6	38	29
BE041322	hr80g04.x	217	10	BE041322	1.6	38	30
AW856084	RC1-CT028	218	10	AW856084	1.6	38	31
AA179433	zp45a09.r	240	9	AA179433	1.6	38	32
AA258134	zb32g05.s	261	9	AA258134	1.6	38	33
F03493	HSC12B042.n	262	14	F03493	1.6	38	34
BF815113	MR2-CT012	282	12	BF815113	1.6	38	35
AI251576	qv45b02.x	314	9	AI251576	1.6	38	36
AI306232	qw80b05.x	320	9	AI306232	1.6	38	37
AI583466	tt69h09.x	326	9	AI583466	1.6	38	38
AW504297	UI-HF-BN0	338	10	AW504297	1.6	38	39
AI085814	ox47b05.s	386	9	AI085814	1.6	38	40
H75720	yu07d05.r1	393	14	H75720	1.6	38	41
AA457655	aas1h02.s	396	9	AA457655	1.6	38	42
AQ349633	RFC111-11	417	17	AQ349633	1.6	38	43
AI054354	qi64b03.x	438	9	AI054354	1.6	38	44
AQ205159	HS 3231.A	441	17	AQ205159	1.6	38	45
AA676875	ae28b04.s	443	9	AA676875	1.6	38	46
AI291961	qm81d06.x	444	9	AI291961	1.6	38	47
BF725595	bxi8d01.x	444	12	BF725595	1.6	38	48
AA430514	zw21a08.s	449	9	AA430514	1.6	38	49
AQ877853	HS 2152.B	457	17	AQ877853	1.6	38	50
AL035971	DKFZp564G	471	9	AL035971	1.6	38	51
BE147645	RC1-HT022	475	10	BE147645	1.6	38	52
AI831171	wj81g12.x	477	9	AI831171	1.6	38	53
BE263346	601190845	479	10	BE263346	1.6	38	54
AQ472136	CITBI-E1-	490	17	AQ472136	1.6	38	55
AQ542657	RPCI-11-3	492	17	AQ542657	1.6	38	56
BQ082221	K-EST0073	500	14	BQ082221	1.6	38	57
AQ479637	RPCI-11-2	502	17	AQ479637	1.6	38	58
W40469	zb74g05.r1	506	14	W40469	1.6	38	59
AW504686	UI-HF-BN0	527	10	AW504686	1.6	38	60
AQ784229	HS 3087.B	535	17	AQ784229	1.6	38	61
AI734279	zb74g05.y	582	9	AI734279	1.6	38	62
AG038593	Pan trogl	649	17	AG038593	1.6	38	63
BF212791	601814055	667	12	BF212791	1.6	38	64
AG138366	Pan trogl	676	17	AG138366	1.6	38	65
AG03264	Pan trogl	680	17	AG03264	1.6	38	66
AF010903	AF010903	697	17	AF010903	1.6	38	67
AG009226	Homo sapi	698	17	AG009226	1.6	38	68
AQ782298	HS 3184.B	700	17	AQ782298	1.6	38	69
AQ311647	RFC111-10	701	17	AQ311647	1.6	38	70
AG117882	Pan trogl	706	17	AG117882	1.6	38	71
AG117952	Pan trogl	706	17	AG117952	1.6	38	72
AG009228	Homo sapi	711	17	AG009228	1.6	38	73
BG678435	602625085	732	12	BG678435	1.6	38	74
AG009195	Homo sapi	748	17	AG009195	1.6	38	75
BG614932	602644147	790	12	BG614932	1.6	38	76
AA522500	n138a03.s	823	9	AA522500	1.6	38	77
BG778845	602667518	831	12	BG778845	1.6	38	78

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C 81	38	1.6	858	14	BQ221178	BQ221178 AGENCOURT	C 154	36	1.5	607	17	B01406	B01406 CSRL-131C10
C 82	38	1.6	869	17	AQ741610	AQ741610 HS_5572_B	C 155	36	1.5	620	9	AL042635	AL042635 DKEZP434M
C 83	38	1.6	888	14	BQ898813	BQ898813 AGENCOURT	C 156	36	1.5	632	17	AG149791	AG149791 Pan trogl
C 84	38	1.6	933	14	BQ706641	BQ706641 AGENCOURT	C 157	36	1.5	662	17	AQ379438	AQ379438 RHC111-16
C 85	38	1.6	943	14	BQ058053	BQ058053 AGENCOURT	C 158	36	1.5	736	17	AQ748064	AQ748064 HS_5538_A
C 86	38	1.6	950	14	BQ062719	BQ062719 AGENCOURT	C 159	36	1.5	750	12	BG566041	BG566041 602582640
C 87	38	1.6	979	13	BM469390	BM469390 AGENCOURT	C 160	36	1.5	770	12	BG212347	BG212347 601813621
C 88	38	1.6	1002	14	BQ081858	BQ081858 AGENCOURT	C 161	36	1.5	778	12	BG563240	BG563240 602144358
C 89	38	1.6	1005	14	BQ056123	BQ056123 AGENCOURT	C 162	36	1.5	799	17	BQ751118	BQ751118 HS_5575_B
C 90	38	1.6	1012	13	BM469629	BM469629 AGENCOURT	C 163	36	1.5	821	12	BF974661	BF974661 602243396
C 91	38	1.6	1026	14	BQ056173	BQ056173 AGENCOURT	C 164	36	1.5	941	14	BQ711583	BQ711583 AGENCOURT
C 92	38	1.6	1026	14	BQ063043	BQ063043 AGENCOURT	C 165	35	1.5	156	17	AQ266335	AQ266335 RHC111-72
C 93	38	1.6	1041	14	BQ058749	BQ058749 AGENCOURT	C 166	35	1.5	157	13	BM142414	BM142414 if32403.X
C 94	38	1.6	1043	14	BQ085255	BQ085255 AGENCOURT	C 167	35	1.5	211	17	AQ541195	AQ541195 RHC1-11-3
C 95	38	1.6	1063	14	BM800338	BM800338 AGENCOURT	C 168	35	1.5	230	9	AA287872	AA287872 zslsh04.s
C 96	38	1.6	1085	14	BQ059031	BQ059031 AGENCOURT	C 169	35	1.5	302	9	AA303988	AA303988 EST16700
C 97	38	1.6	1124	10	AV762309	AV762309 AV762309	C 170	35	1.5	309	12	BF812434	BF812434 MR2-C1018
C 98	38	1.6	1842	11	BC011119	BC011119 Homo sapi	C 171	35	1.5	318	9	AA292387	AA292387 zt39C05.X
C 99	37	1.5	176	14	N53518	N53518 YZ26d04.s1	C 172	35	1.5	333	17	AQ066918	AQ066918 HS_2227_B
C 100	37	1.5	228	12	BF928074	BF928074 IL5-NT022	C 173	35	1.5	335	9	AA829564	AA829564 od37a10.s
C 101	37	1.5	382	10	AW814730	AW814730 MR1-ST020	C 174	35	1.5	338	9	AA828045	AA828045 od70g02.s
C 102	37	1.5	385	14	H93735	H93735 Ys77a09.s1	C 175	35	1.5	365	12	BF477384	BF477384 nacs59g01.
C 103	37	1.5	389	10	BE206039	BE206039 bb55g07.X	C 176	35	1.5	367	17	AQ041782	AQ041782 CIT-HSP-2
C 104	37	1.5	393	9	AA931162	AA931162 oo70e03.s	C 177	35	1.5	383	9	AA570255	AA570255 nf39e07.s
C 105	37	1.5	398	17	AQ035831	AQ035831 CIT-HSP-2	C 178	35	1.5	397	9	AA490908	AA490908 aa52c01.s
C 106	37	1.5	412	14	T47889	T47889 Yb18a09.s1	C 179	35	1.5	412	10	AW519290	AW519290 XE80C02.X
C 107	37	1.5	421	9	AA593375	AA593375 nm08h10.s	C 180	35	1.5	416	14	TS1572	TS1572 Yb25g07.s1
C 108	37	1.5	426	10	AV760528	AV760528 AV760528	C 181	35	1.5	419	14	T65989	T65989 ycl12d04.s1
C 109	37	1.5	459	13	BI493089	BI493089 df97e07.Y	C 182	35	1.5	431	17	AQ176276	AQ176276 HS_3209_A
C 110	37	1.5	464	17	B89523	B89523 RHC111-27K1	C 183	35	1.5	432	17	AQ482806	AQ482806 RHC1-11-2
C 111	37	1.5	490	12	BF953490	BF953490 RC3-NN118	C 184	35	1.5	441	9	AA838227	AA838227 oe37d03.s
C 112	37	1.5	513	17	AQ190314	AQ190314 HS_3223_A	C 185	35	1.5	457	17	AQ197732	AQ197732 CIT-HSP-2
C 113	37	1.5	521	12	BF953646	BF953646 RC3-NN118	C 186	35	1.5	459	10	AW963966	AW963966 EST376039
C 114	37	1.5	548	17	AQ485704	AQ485704 RHC1-11-2	C 187	35	1.5	461	13	BM141828	BM141828 if27a02.X
C 115	37	1.5	593	17	AQ351689	AQ351689 CITBI-E1-	C 188	35	1.5	466	17	AQ229478	AQ229478 HS_2021_A
C 116	37	1.5	664	17	AG185369	AG185369 Pan trogl	C 189	35	1.5	489	14	T65778	T65778 ycl11f03.s1
C 117	37	1.5	670	17	AG067776	AG067776 Pan trogl	C 190	35	1.5	501	17	B92576	B92576 CIT-HSP-217
C 118	37	1.5	691	9	AU141371	AU141371 AU141371	C 191	35	1.5	501	17	AQ482803	AQ482803 RHC1-11-2
C 119	37	1.5	751	13	BM007824	BM007824 603617296	C 192	35	1.5	542	9	AL120867	AL120867 DKEZP762K
C 120	37	1.5	769	17	AQ900076	AQ900076 HS_3034_B	C 193	35	1.5	566	17	AQ454593	AQ454593 HS_5217_A
C 121	37	1.5	908	10	BE256728	BE256728 601115545	C 194	35	1.5	570	9	AU148264	AU148264 AU148264
C 122	37	1.5	1005	13	BM480128	BM480128 AGENCOURT	C 195	35	1.5	616	17	AQ423170	AQ423170 CITBI-E1-
C 123	37	1.5	1040	14	BQ221982	BQ221982 AGENCOURT	C 196	35	1.5	623	17	AQ036239	AQ036239 Pan trogl
C 124	36	1.5	1051	11	BC022296	BC022296 Homo sapi	C 197	35	1.5	629	14	BM969453	BM969453 UI-CF-DU1
C 125	36	1.5	152	14	N85987	N85987 J5881F Huma	C 198	35	1.5	672	12	BG501601	BG501601 602548640
C 126	36	1.5	209	12	BF860674	BF860674 QV3-ET019	C 199	35	1.5	697	10	AV723135	AV723135 AV723135
C 127	36	1.5	226	12	BF879580	BF879580 PM4-ET015	C 200	35	1.5	706	14	BM975460	BM975460 UI-CF-EN1
C 128	36	1.5	231	12	BF920688	BF920688 RC5-NT018	C 201	35	1.5	777	12	BF219427	BF219427 601884218
C 129	36	1.5	253	9	AA377544	AA377544 EST90150	C 202	35	1.5	842	17	AQ878507	AQ878507 HS_3081_A
C 130	36	1.5	287	9	AA808843	AA808843 nv21b12.X	C 203	35	1.5	870	14	BQ711919	BQ711919 AGENCOURT
C 131	36	1.5	288	9	AA808847	AA808847 nv21d12.X	C 204	34	1.4	219	14	N78609	N78609 za94f09.s1
C 132	36	1.5	288	9	AA569474	AA569474 nm38f11.s	C 205	34	1.4	239	9	AA180815	AA180815 zp44f11.s
C 133	36	1.5	303	9	AA492269	AA492269 ng80a03.s	C 206	34	1.4	261	14	T61163	T61163 Yb75h08.r1
C 134	36	1.5	308	9	AA299129	AA299129 EST11596	C 207	34	1.4	265	9	A1264879	A1264879 qg89c04.X
C 135	36	1.5	322	9	AA532700	AA532700 nj59a11.s	C 208	34	1.4	315	14	T61595	T61595 Yb74h05.s1
C 136	36	1.5	378	14	R12765	R12765 Yf44a11.s1	C 209	34	1.4	324	10	AW274191	AW274191 x573b09.X
C 137	36	1.5	385	9	AA995373	AA995373 or74c07.s	C 210	34	1.4	374	9	AA642088	AA642088 nr30f11.s
C 138	36	1.5	389	9	A1560063	A1560063 tp21a12.X	C 211	34	1.4	384	9	AA847343	AA847343 oe18d10.s
C 139	36	1.5	407	12	BF680068	BF680068 602154792	C 212	34	1.4	400	9	A1167193	A1167193 ok28f05.X
C 140	36	1.5	411	12	BF851368	BF851368 IL5-EN008	C 213	34	1.4	434	17	AQ683459	AQ683459 HS_5432_B
C 141	36	1.5	422	10	AW974135	AW974135 EST3766238	C 214	34	1.4	467	9	A1961228	A1961228 wt15c05.X
C 142	36	1.5	433	17	AQ180272	AQ180272 HS_3209_B	C 215	34	1.4	501	17	B02391	B02391 CSRL-152G10
C 143	36	1.5	457	9	AA640314	AA640314 nu01g01.s	C 216	34	1.4	527	12	BG431625	BG431625 602499217
C 144	36	1.5	493	17	AQ351342	AQ351342 RHC111-11	C 217	34	1.4	552	17	AQ0706984	AQ0706984 HS_5551_B
C 145	36	1.5	501	10	BE019467	BE019467 db56c01.Y	C 218	34	1.4	590	9	AA209188	AA209188 zq95d06.r
C 146	36	1.5	509	10	BE294700	BE294700 601173920	C 219	34	1.4	592	10	AW833324	AW833324 QV4-TT000
C 147	36	1.5	518	17	AQ514908	AQ514908 HS_5208_B	C 220	34	1.4	642	17	AQ309769	AQ309769 CITBI-E1-
C 148	36	1.5	522	17	AQ155672	AQ155672 HS_3125_A	C 221	34	1.4	668	17	AG163782	AG163782 Pan trogl
C 149	36	1.5	530	17	AQ124065	AQ124065 HS_3121_A	C 222	34	1.4	671	10	AW833742	AW833742 QV4-TT000
C 150	36	1.5	536	17	AQ139263	AQ139263 HS_3079_A	C 223	34	1.4	715	17	AG163684	AG163684 Pan trogl
C 151	36	1.5	550	9	AU148708	AU148708 AU148708	C 224	34	1.4	748	17	AG181959	AG181959 Pan trogl
C 152	36	1.5	572	17	AQ122460	AQ122460 HS_3080_A	C 225	34	1.4	1107	12	BF340713	BF340713 602035470

C 372	32	1:3	753	17	AG029154	Pan trogl	C 445	31	1:3	368	14	H70737	H70737 yu59f10.s1
C 373	32	1:3	758	17	AG029792	Pan trogl	C 446	31	1:3	369	10	AM275498	AM275498 xn07f02.x
C 374	32	1:3	770	12	BF675504	602138482	C 447	31	1:3	377	9	AA602529	AA602529 n90a05.s
C 375	32	1:3	796	13	BI835431	603087540	C 448	31	1:3	379	10	AV693021	AV693021 av693021
C 376	32	1:3	832	12	BF673957	602137339	C 449	31	1:3	379	17	AA083206	AA083206 RPI11-54
C 377	32	1:3	846	17	AQ749752	HS 5573.A	C 450	31	1:3	384	9	AA174016	AA174016 zpl8h06.r
C 378	32	1:3	869	13	BI598769	603245578	C 451	31	1:3	384	10	AW090392	AW090392 xc81f02.x
C 379	32	1:3	898	13	BM453640	AGENCOURT	C 452	31	1:3	389	13	BI793141	BI793141 ie48d10.y
C 380	32	1:3	910	14	BQ681678	AGENCOURT	C 453	31	1:3	389	17	AQ503369	AQ503369 RPI1-11-3
C 381	32	1:3	913	12	BF677812	602085323	C 454	31	1:3	390	13	BI793172	BI793172 ie48h05.y
C 382	32	1:3	917	12	BE732904	601567847	C 455	31	1:3	393	10	BE143560	BE143560 MR0-HT016
C 383	32	1:3	944	14	BQ709478	AGENCOURT	C 456	31	1:3	393	17	AQ136323	AQ136323 HS 3056.B
C 384	32	1:3	948	17	AQ744098	HS 5501.A	C 457	31	1:3	395	9	AI289050	AI289050 QW32a01.x
C 385	32	1:3	956	13	BI756385	603030284	C 458	31	1:3	395	9	AA174017	AA174017 zpl8h06.s
C 386	32	1:3	1100	13	BM554817	AGENCOURT	C 459	31	1:3	395	14	N71033	N71033 za55e02.s1
C 387	32	1:3	1485	17	AF101893	AF101893	C 460	31	1:3	396	17	AQ027194	AQ027194 CIT-HSP-2
C 388	32	1:3	2084	11	BC025705	Homo sapi	C 461	31	1:3	398	14	F24745	F24745 HSPD11276.H
C 389	32	1:3	2638	11	AF318344	Homo sapi	C 462	31	1:3	399	9	AL700720	AL700720 DKFZP686B
C 390	32	1:3	3352	11	BC013681	Homo sapi	C 463	31	1:3	404	14	H63496	H63496 y54a06.s1
C 391	31	1:3	87	14	N85990	J5884F.Huma	C 464	31	1:3	404	17	AQ347410	AQ347410 RPI11-11
C 392	31	1:3	122	9	AI003655	AI003655 zg01a01.s	C 465	31	1:3	405	10	BE065718	BE065718 RC2-BT031
C 393	31	1:3	173	12	BF900510	PM1-MT019	C 466	31	1:3	407	9	AI858889	AI858889 w45b03.x
C 394	31	1:3	187	10	AW080185	xe49f06.x	C 467	31	1:3	408	9	AI362442	AI362442 q196a03.x
C 395	31	1:3	202	12	BF811008	BM456815	C 468	31	1:3	409	17	AQ1818485	AQ1818485 HS 5250.A
C 396	31	1:3	206	13	BM456815	AGENCOURT	C 469	31	1:3	410	9	AI911839	AI911839 wc79a04.x
C 397	31	1:3	206	17	AQ279397	CITB1-E1	C 470	31	1:3	411	9	AA564359	AA564359 nk45e04.s
C 398	31	1:3	216	17	AQ034502	CIT-HSP-2	C 471	31	1:3	411	17	AQ319503	AQ319503 RPI11-97
C 399	31	1:3	231	14	H68240	yu69f08.s1	C 472	31	1:3	411	17	AQ532648	AQ532648 RPI1-11-3
C 400	31	1:3	239	12	BF876573	QV0-ET014	C 473	31	1:3	412	9	AI055924	AI055924 ox44b06.s
C 401	31	1:3	244	12	BF857321	QV3-FT020	C 474	31	1:3	412	14	T83505	T83505 ye03e07.r1
C 402	31	1:3	245	9	AA525288	ni53a10.s	C 475	31	1:3	413	9	AI284092	AI284092 q67b11.x
C 403	31	1:3	248	10	AW945453	PM0-EN000	C 476	31	1:3	413	17	AQ512389	AQ512389 HS 5114.A
C 404	31	1:3	249	12	BF838584	IL5-HT099	C 477	31	1:3	413	17	AQ512408	AQ512408 HS-5114.A
C 405	31	1:3	249	14	BQ632526	il28c08.x	C 478	31	1:3	415	10	BE151738	BE151738 PM1-HT030
C 406	31	1:3	266	9	AA063139	zf68a03.s	C 479	31	1:3	417	17	AQ566115	AQ566115 HS-5374.A
C 407	31	1:3	270	10	AW936354	QV4-DT002	C 480	31	1:3	418	17	AQ443330	AQ443330 HS 2231.B
C 408	31	1:3	271	17	AQ561438	HS 5357.A	C 481	31	1:3	424	9	AI561041	AI561041 tq29d11.x
C 409	31	1:3	277	9	AA613761	no95g05.s	C 482	31	1:3	424	17	AQ038204	AQ038204 CIT-HSP-2
C 410	31	1:3	281	17	B51151	CIT978SK-76	C 483	31	1:3	425	9	AA856904	AA856904 oh93e02.s
C 411	31	1:3	283	9	AA610344	np90h11.s	C 484	31	1:3	425	10	AW513946	AW513946 xc83a12.x
C 412	31	1:3	283	12	BF927768	IL2-NT020	C 485	31	1:3	426	14	R62571	R62571 zal3b12.s1
C 413	31	1:3	286	9	AA082588	zn23f12.r	C 486	31	1:3	427	14	R64204	R64204 y118d06.r1
C 414	31	1:3	299	17	AQ040045	CIT-HSP-2	C 487	31	1:3	428	10	AW833161	AW833161 RC3-TT000
C 415	31	1:3	301	10	AW663162	hh75d08.y	C 488	31	1:3	430	14	H96479	H96479 vt98e03.r1
C 416	31	1:3	302	10	AW886085	RC6-OT007	C 489	31	1:3	430	17	AQ507157	AQ507157 RPI1-11-2
C 417	31	1:3	303	9	AA483126	ne93a11.s	C 490	31	1:3	432	17	AQ789970	AQ789970 HS-3177.B
C 418	31	1:3	304	17	B50766	CIT-HSP-698	C 491	31	1:3	433	9	AI160144	AI160144 qb63b09.x
C 419	31	1:3	305	10	AW993388	RC2-BN003	C 492	31	1:3	435	9	AA112791	AA112791 zn54d08.r
C 420	31	1:3	308	9	AA862184	oe13b04.s	C 493	31	1:3	436	14	T51832	T51832 yb54c08.s1
C 421	31	1:3	317	9	AI637960	tt26h08.x	C 494	31	1:3	438	10	AW303888	AW303888 xt24h07.x
C 422	31	1:3	317	17	AQ093667	HS 3022.A	C 495	31	1:3	441	17	AQ179780	AQ179780 HS 3185.B
C 423	31	1:3	318	10	AW022704	df42e11.y	C 496	31	1:3	443	14	BM690267	BM690267 UT-E-CL0-
C 424	31	1:3	322	17	AQ504293	RPC1-11-2	C 497	31	1:3	444	10	AW150111	AW150111 xg48d10.x
C 425	31	1:3	327	14	W45283	zc80c08.s1	C 498	31	1:3	444	17	AQ207583	AQ207583 HS 2243.B
C 426	31	1:3	329	14	W45298	zc80d07.s1	C 499	31	1:3	446	9	AA584241	AA584241 nn71g12.s
C 427	31	1:3	331	12	BG222405	naj74b12.	C 500	31	1:3	447	9	AI570805	AI570805 tr67d08.x
C 428	31	1:3	333	17	B63128	CIT978SK-A-	C 501	31	1:3	447	9	AI953764	AI953764 wx69b01.x
C 429	31	1:3	335	9	AL711619	DKFZP686C	C 502	31	1:3	447	10	AW250029	AW250029 z819251-3
C 430	31	1:3	337	17	AQ067790	HS 2239.B	C 503	31	1:3	447	17	B33682	B33682 HS-1023-A1-
C 431	31	1:3	342	9	AA053253	zl72e09.s	C 504	31	1:3	449	9	AA205399	AA205399 zq79g01.s
C 432	31	1:3	345	12	BG232550	naj52h02.	C 505	31	1:3	449	9	AA504996	AA504996 ab04f03.r
C 433	31	1:3	347	17	AQ097220	HS 3038.B	C 506	31	1:3	450	17	AQ064450	AQ064450 HS 2198.B
C 434	31	1:3	347	10	AW804963	OY4-UM009	C 507	31	1:3	451	17	B65846	B65846 CIT-HSP-202
C 435	31	1:3	350	17	AQ695996	HS 5486.B	C 508	31	1:3	452	10	AW235522	AW235522 xnl9b11.x
C 436	31	1:3	351	12	BF906827	RC3-ST019	C 509	31	1:3	453	17	AQ793843	AQ793843 HS 5252.B
C 437	31	1:3	356	17	AQ603968	HS 2136.A	C 510	31	1:3	454	17	B56476	B56476 CIT-HSP-200
C 438	31	1:3	357	9	AI433131	th41g10.x	C 511	31	1:3	456	14	T08075	T08075 EST05966.In
C 439	31	1:3	357	9	AA493464	AA493464 ng75d06.s	C 512	31	1:3	457	9	AI954248	AI954248 wx95a02.x
C 440	31	1:3	357	17	AQ151129	HS 2186.A	C 513	31	1:3	457	17	AQ222028	AQ222028 HS 2006.B
C 441	31	1:3	359	9	AA569089	nm36g04.s	C 514	31	1:3	459	9	AI598003	AI598003 ts05d01.x
C 442	31	1:3	361	9	AI366993	tb80d10.x	C 515	31	1:3	460	17	BI5692	BI5692 345N8.TP.CI
C 443	31	1:3	363	10	AV762979	AV762979	C 516	31	1:3	464	9	AI342622	AI342622 qt33e08.x
C 444	31	1:3	367	9	AI453476	tj28d07.x	C 517	31	1:3	465	10	AA972801	AA972801 EST384896

C 518	31	1.3	466	14	BQ575431	UI-H-EZ1-	BQ575431	UI-H-EZ1-	C 591	31	1.3	585	9	AUI45035	AUI45035
C 519	31	1.3	472	12	BF874974	MRI-ET014	BF874974	MRI-ET014	C 592	31	1.3	592	10	AV716255	AV716255
C 520	31	1.3	472	14	T78512	YD68C01.X1	T78512	YD68C01.X1	C 593	31	1.3	592	10	AQ008952	AQ008952
C 521	31	1.3	473	9	AA494452	ne38A09.S	AA494452	ne38A09.S	C 594	31	1.3	595	17	AQ344454	AQ344454
C 522	31	1.3	475	17	AQ123045	HS 3095.B	AQ123045	HS 3095.B	C 595	31	1.3	595	17	AQ424714	AQ424714
C 523	31	1.3	476	13	BI496628	df126G08.	BI496628	df126G08.	C 596	31	1.3	596	17	AQ210963	AQ210963
C 524	31	1.3	477	9	AI591174	tw86A01.X	AI591174	tw86A01.X	C 597	31	1.3	600	12	BF678990	BF678990
C 525	31	1.3	478	9	AA526099	n158F04.S	AA526099	n158F04.S	C 598	31	1.3	601	12	EG5688568	EG5688568
C 526	31	1.3	480	10	BE143258	MR0-HT016	BE143258	MR0-HT016	C 599	31	1.3	602	17	AQ554076	AQ554076
C 527	31	1.3	481	9	AI986165	w263C02.X	AI986165	w263C02.X	C 600	31	1.3	613	17	AQ144472	AQ144472
C 528	31	1.3	482	12	BF845248	MR1-HT106	BF845248	MR1-HT106	C 601	31	1.3	616	17	AQ732982	AQ732982
C 529	31	1.3	483	10	AV719884	AV719884	AV719884	AV719884	C 602	31	1.3	616	17	AQ039682	AQ039682
C 530	31	1.3	483	17	B47837	RPCI11-2M7.	B47837	RPCI11-2M7.	C 603	31	1.3	617	17	AQ560211	AQ560211
C 531	31	1.3	486	17	B87844	RPCI11-30J2	B87844	RPCI11-30J2	C 604	31	1.3	623	17	AG058831	AG058831
C 532	31	1.3	487	9	AA634095	ac74F05.S	AA634095	ac74F05.S	C 605	31	1.3	624	17	AG058831	AG058831
C 533	31	1.3	492	12	BF889156	PM2-TN011	BF889156	PM2-TN011	C 606	31	1.3	624	17	AG058831	AG058831
C 534	31	1.3	493	17	AQ142111	RPCI-11-1	AQ142111	RPCI-11-1	C 607	31	1.3	626	17	AG0480840	AG0480840
C 535	31	1.3	495	17	AQ342662	RPCI11-11	AQ342662	RPCI11-11	C 608	31	1.3	628	17	AG0480840	AG0480840
C 536	31	1.3	497	9	AA037725	r	AA037725	r	C 609	31	1.3	631	14	BM9933786	BM9933786
C 537	31	1.3	497	12	BE968744	601649912	BE968744	601649912	C 610	31	1.3	631	17	AQ061135	AQ061135
C 538	31	1.3	503	14	BQ015442	UI-1-BC0-	BQ015442	UI-1-BC0-	C 611	31	1.3	631	17	AQ061135	AQ061135
C 539	31	1.3	503	17	AQ732529	HS 5543.B	AQ732529	HS 5543.B	C 612	31	1.3	636	10	AV761707	AV761707
C 540	31	1.3	506	17	AZ755833	ev09g12.X	AZ755833	ev09g12.X	C 613	31	1.3	637	10	AV761729	AV761729
C 541	31	1.3	506	9	AI126238	QC55B04.X	AI126238	QC55B04.X	C 614	31	1.3	638	17	AG101075	AG101075
C 542	31	1.3	506	9	AI640367	w617d10.X	AI640367	w617d10.X	C 615	31	1.3	645	17	AQ315803	AQ315803
C 543	31	1.3	507	9	AI885488	wm24F08.X	AI885488	wm24F08.X	C 616	31	1.3	646	17	AQ315803	AQ315803
C 544	31	1.3	511	9	AI887716	wm17F01.X	AI887716	wm17F01.X	C 617	31	1.3	648	10	BE072376	BE072376
C 545	31	1.3	514	17	AQ0884228	HS 5504.B	AQ0884228	HS 5504.B	C 618	31	1.3	648	10	BE072376	BE072376
C 546	31	1.3	515	9	AA577706	nm23A03.S	AA577706	nm23A03.S	C 619	31	1.3	648	14	BQ015399	BQ015399
C 547	31	1.3	515	12	BF878961	RC1-ET013	BF878961	RC1-ET013	C 620	31	1.3	650	17	AG180765	AG180765
C 548	31	1.3	516	17	AQ347616	RPCI11-12	AQ347616	RPCI11-12	C 621	31	1.3	651	10	AV733239	AV733239
C 549	31	1.3	517	17	AQ155788	HS 3185.B	AQ155788	HS 3185.B	C 622	31	1.3	651	10	AV762002	AV762002
C 550	31	1.3	518	17	AZ757035	ew07f11.X	AZ757035	ew07f11.X	C 623	31	1.3	653	17	AG052307	AG052307
C 551	31	1.3	518	17	AQ252529	CITBI-E1-	AQ252529	CITBI-E1-	C 624	31	1.3	657	13	BI492664	BI492664
C 552	31	1.3	519	9	AI814721	wk66G04.X	AI814721	wk66G04.X	C 625	31	1.3	657	17	AQ782480	AQ782480
C 553	31	1.3	519	9	AI702651	DKF2P6860	AI702651	DKF2P6860	C 626	31	1.3	659	17	AG155371	AG155371
C 554	31	1.3	519	14	BM997623	UI-H-DH0-	BM997623	UI-H-DH0-	C 627	31	1.3	660	17	AG0590627	AG0590627
C 555	31	1.3	520	10	BE066487	RC3-BT033	BE066487	RC3-BT033	C 628	31	1.3	668	17	AG045483	AG045483
C 556	31	1.3	521	9	AA134472	z013C01.S	AA134472	z013C01.S	C 629	31	1.3	668	17	AG066149	AG066149
C 557	31	1.3	521	17	AQ462183	HS 5146.A	AQ462183	HS 5146.A	C 630	31	1.3	668	17	AG168977	AG168977
C 558	31	1.3	523	9	AI054414	q175h03.X	AI054414	q175h03.X	C 631	31	1.3	669	17	AG067062	AG067062
C 559	31	1.3	527	10	AA966677	EST378851	AA966677	EST378851	C 632	31	1.3	669	17	AG107057	AG107057
C 560	31	1.3	528	9	AA707137	z133G09.S	AA707137	z133G09.S	C 633	31	1.3	669	17	AG148458	AG148458
C 561	31	1.3	529	12	EG402924	602418727	EG402924	602418727	C 634	31	1.3	673	9	AI525037	AI525037
C 562	31	1.3	529	17	AQ464785	HS 5105.B	AQ464785	HS 5105.B	C 635	31	1.3	674	10	BE158682	BE158682
C 563	31	1.3	531	17	AQ452366	HS 5154.A	AQ452366	HS 5154.A	C 636	31	1.3	674	17	AG073055	AG073055
C 564	31	1.3	535	12	BF851643	QV1-EN013	BF851643	QV1-EN013	C 637	31	1.3	674	17	AG075454	AG075454
C 565	31	1.3	536	17	AZ254536	HSC 00128	AZ254536	HSC 00128	C 638	31	1.3	675	17	AG174756	AG174756
C 566	31	1.3	536	17	AQ236378	HS 2041.A	AQ236378	HS 2041.A	C 639	31	1.3	679	17	AG111125	AG111125
C 567	31	1.3	539	14	R76565	Y172H04.B1	R76565	Y172H04.B1	C 640	31	1.3	682	17	AQ138279	AQ138279
C 568	31	1.3	539	17	AQ450654	HS 5157.A	AQ450654	HS 5157.A	C 641	31	1.3	682	17	AQ384309	AQ384309
C 569	31	1.3	542	9	AI871103	w179B07.X	AI871103	w179B07.X	C 642	31	1.3	683	17	AG083056	AG083056
C 570	31	1.3	542	17	AQ635546	RPCI-11-4	AQ635546	RPCI-11-4	C 643	31	1.3	684	17	AQ896165	AQ896165
C 571	31	1.3	545	17	AQ712209	HS 2114.A	AQ712209	HS 2114.A	C 644	31	1.3	686	17	AG051181	AG051181
C 572	31	1.3	546	10	AW836779	QV1-LT003	AW836779	QV1-LT003	C 645	31	1.3	686	17	AG103219	AG103219
C 573	31	1.3	546	12	EG422108	602448824	EG422108	602448824	C 646	31	1.3	693	17	AG107570	AG107570
C 574	31	1.3	547	17	AQ800801	HS 5299.A	AQ800801	HS 5299.A	C 647	31	1.3	693	17	AG145808	AG145808
C 575	31	1.3	547	17	AQ344772	RPCI11-11	AQ344772	RPCI11-11	C 648	31	1.3	696	12	BF239048	BF239048
C 576	31	1.3	548	17	AQ318090	RPCI11-10	AQ318090	RPCI11-10	C 649	31	1.3	700	17	AQ240547	AQ240547
C 577	31	1.3	551	9	AL698703	DKF2P686A	AL698703	DKF2P686A	C 650	31	1.3	704	17	AG013798	AG013798
C 578	31	1.3	552	12	EG189142	RST8182.A	EG189142	RST8182.A	C 651	31	1.3	705	10	AV760497	AV760497
C 579	31	1.3	558	17	AQ630383	HS 2136.A	AQ630383	HS 2136.A	C 652	31	1.3	705	12	EG109247	EG109247
C 580	31	1.3	559	14	BM874128	laa01c10.	BM874128	laa01c10.	C 653	31	1.3	706	17	AG013348	AG013348
C 581	31	1.3	560	13	BM505425	ig94f05.X	BM505425	ig94f05.X	C 654	31	1.3	707	17	AG122572	AG122572
C 582	31	1.3	571	17	AQ802982	HS 3160.A	AQ802982	HS 3160.A	C 655	31	1.3	708	17	AG013797	AG013797
C 583	31	1.3	572	14	BQ020816	UI-H-DH1-	BQ020816	UI-H-DH1-	C 656	31	1.3	709	12	EG422281	EG422281
C 584	31	1.3	575	17	AQ563986	HS 5334.B	AQ563986	HS 5334.B	C 657	31	1.3	711	14	BQ009439	BQ009439
C 585	31	1.3	576	10	AV714986	AV714986	AV714986	AV714986	C 658	31	1.3	712	17	AQ038353	AQ038353
C 586	31	1.3	578	9	AL047793	DKF2P586D	AL047793	DKF2P586D	C 659	31	1.3	717	17	AQ381909	AQ381909
C 587	31	1.3	578	13	BM509841	ig94f05.Y	BM509841	ig94f05.Y	C 660	31	1.3	717	17	AQ392510	AQ392510
C 588	31	1.3	578	17	B93700	CIT-HSP-216	B93700	CIT-HSP-216	C 661	31	1.3	724	17	AG186364	AG186364
C 589	31	1.3	581	10	AV761497	AV761497	AV761497	AV761497	C 662	31	1.3	725	17	AG010801	AG010801
C 590	31	1.3	581	12	EG623941	602649105	EG623941	602649105	C 663	31	1.3	725	17	AG010802	AG010802

c 664	31	1.3	726	17	AZ254557	HSC 00177	737	30	1.2	219	17	AQ538879	RPIC-11-3
c 665	31	1.3	734	17	AG166338	Pan trogl	c 738	30	1.2	221	9	AI886056	w08h04.x
c 666	31	1.3	737	14	BM975105	UT-CF-ECL	c 739	30	1.2	223	9	AA812287	nr82f08.s
c 667	31	1.3	739	17	AG000964	Homo sapi	c 740	30	1.2	234	9	AA610803	np92e03.s
c 668	31	1.3	741	17	AG088253	Pan trogl	c 741	30	1.2	237	17	AQ274956	RPIC-4-72
c 669	31	1.3	748	17	AG000963	Homo sapi	c 742	30	1.2	241	9	AA773424	ab58b02.s
c 670	31	1.3	748	17	AG000970	Homo sapi	c 743	30	1.2	244	14	BQ360810	RC1-OT008
c 671	31	1.3	751	17	AG000944	Homo sapi	c 744	30	1.2	246	10	AA834473	MR2-TT001
c 672	31	1.3	753	14	BQ053071	AGENCOURT	c 745	30	1.2	247	9	AA715201	nv74g12.x
c 673	31	1.3	754	17	AG000969	Homo sapi	c 746	30	1.2	250	10	BE062239	RC1-ET025
c 674	31	1.3	755	17	AG000945	Homo sapi	c 747	30	1.2	251	12	BE783829	601471056
c 675	31	1.3	761	17	AQ745261	HS 5503.A	c 748	30	1.2	252	10	AA834369	MR2-TT001
c 676	31	1.3	766	17	AQ788194	HS 3135.A	c 749	30	1.2	255	9	AI886434	w094g04.x
c 677	31	1.3	776	17	AG000971	Homo sapi	c 750	30	1.2	255	10	BE063646	IL5-ET028
c 678	31	1.3	779	12	BF675202	602138131	c 751	30	1.2	256	9	AI926240	w041g01.x
c 679	31	1.3	779	12	BG197390	RST16633	c 752	30	1.2	256	14	FI3808	HSFIM1008.S
c 680	31	1.3	804	12	BG179552	602328163	c 753	30	1.2	258	17	AQ373299	RPIC11-14
c 681	31	1.3	804	12	BG179552	602328163	c 754	30	1.2	259	10	BE081332	QV1-BT063
c 682	31	1.3	809	12	BG207230	RST26698	c 755	30	1.2	259	14	T07414	EST05303.Fe
c 683	31	1.3	810	12	BG214593	RST34236	c 756	30	1.2	267	9	AI872513	w09b04.x
c 684	31	1.3	819	17	AQ741638	HS 5572.B	c 757	30	1.2	271	9	AA370455	EST82092
c 685	31	1.3	831	13	BI818348	603032973	c 758	30	1.2	272	10	AA834419	MR2-TT001
c 686	31	1.3	838	17	AQ782284	HS 3184.B	c 759	30	1.2	272	10	BE153150	PMO-HT033
c 687	31	1.3	839	17	AQ781535	HS 3174.A	c 760	30	1.2	274	9	AA054055	zf48e07.r
c 688	31	1.3	853	17	AQ739924	HS 5506.A	c 761	30	1.2	275	9	AA578925	nf30c01.s
c 689	31	1.3	861	12	BG752933	602732584	c 762	30	1.2	275	9	AA581238	nd38b01.s
c 690	31	1.3	886	17	AQ787966	HS 3100.A	c 763	30	1.2	275	10	AA131272	xf60h05.x
c 691	31	1.3	896	17	AQ738735	HS 5382.B	c 764	30	1.2	279	9	AA570136	ns46h08.s
c 692	31	1.3	898	12	BF215757	601881252	c 765	30	1.2	280	9	AA050502	nh96d11.s
c 693	31	1.3	911	14	BQ719276	AGENCOURT	c 766	30	1.2	282	9	AA078084	7P01D01.C
c 694	31	1.3	927	9	AL536593	AL536593	c 767	30	1.2	283	14	F02611	HSC14C112.n
c 695	31	1.3	952	14	BQ711992	AGENCOURT	c 768	30	1.2	288	14	FI2053	HSC35B071.n
c 696	31	1.3	964	12	BG483309	602504172	c 769	30	1.2	290	9	AI241851	qu69b01.x
c 697	31	1.3	967	13	BM466372	AGENCOURT	c 770	30	1.2	292	17	AZ757648	ew10f08.r
c 698	31	1.3	1001	14	BQ070984	AGENCOURT	c 771	30	1.2	293	17	AQ093533	HS 3026.B
c 699	31	1.3	1040	13	BM559264	AGENCOURT	c 772	30	1.2	293	17	AQ489212	RPIC-11-2
c 700	31	1.3	1072	14	BQ071445	AGENCOURT	c 773	30	1.2	294	10	AA886953	RC1-OT008
c 701	31	1.3	1103	13	BM479678	AGENCOURT	c 774	30	1.2	294	17	AQ067336	HS 2237.A
c 702	31	1.3	2435	11	AF289560	Homo sapi	c 775	30	1.2	300	9	AI824740	ws57f02.x
c 703	31	1.2	95	9	AA669571	ac18d10.s	c 776	30	1.2	300	9	AA381675	EST94781
c 704	30	1.2	104	9	AA129957	zn86h04.r	c 777	30	1.2	301	9	AA742818	nv34g04.r
c 705	30	1.2	112	10	AA589602	x013a01.x	c 778	30	1.2	302	9	AA853397	NHTBCae05
c 706	30	1.2	126	9	AA228768	nc14b07.s	c 779	30	1.2	305	9	AA747607	wx73g09.s
c 707	30	1.2	128	14	BQ353357	IL3-HT061	c 780	30	1.2	305	9	AI932902	no39d10.x
c 708	30	1.2	131	9	AI251360	qv56e03.x	c 781	30	1.2	306	9	AA728812	nx57g08.s
c 709	30	1.2	132	9	AA873660	oe02g11.s	c 782	30	1.2	306	9	AA985243	ng80e02.s
c 710	30	1.2	137	10	AA878190	MR3-OT000	c 783	30	1.2	306	9	AA494145	ng98b08.s
c 711	30	1.2	139	9	AF137025	AF137025	c 784	30	1.2	306	9	AA581183	nd38b01.r
c 712	30	1.2	141	9	AA582889	nm72d01.s	c 785	30	1.2	306	12	BF941940	nac37f05.
c 713	30	1.2	151	12	BF920430	QV2-NT014	c 786	30	1.2	309	10	AA841318	RC6-CN001
c 714	30	1.2	155	9	AI254980	qv48a11.x	c 787	30	1.2	309	10	AA841370	RC6-CN001
c 715	30	1.2	156	14	N52227	yv46c12.s1	c 788	30	1.2	312	9	AA363152	EST72963
c 716	30	1.2	162	9	AA354535	EST62814	c 789	30	1.2	313	9	AA834851	oe02a08.s
c 717	30	1.2	165	17	AQ045666	RPIC11-34	c 790	30	1.2	314	17	BE7600	CIT-HSP-201
c 718	30	1.2	170	9	AA775154	ac78e02.s	c 791	30	1.2	315	10	AA339296	hb72b01.x
c 719	30	1.2	174	9	AI555803	to31c10.x	c 792	30	1.2	316	14	F09946	z683c05.s
c 720	30	1.2	180	12	BG272027	na161g12.	c 793	30	1.2	316	14	F09946	HSC38E072.n
c 721	30	1.2	187	9	AA504921	ab03b09.r	c 794	30	1.2	316	17	AQ061991	CIT-HSP-2
c 722	30	1.2	188	14	BQ360836	RC1-OT008	c 795	30	1.2	317	10	AA875173	RCO-PT000
c 723	30	1.2	196	9	AI611736	tu79g09.x	c 796	30	1.2	318	14	FI1080	HSC3FC112.n
c 724	30	1.2	197	10	BE158883	RC5-HT040	c 797	30	1.2	319	14	F27738	HSPD15869.H
c 725	30	1.2	200	9	AA484901	ne81h11.s	c 798	30	1.2	320	14	HS1061	YP84g09.r1
c 726	30	1.2	201	9	AA877303	nr08d05.s	c 799	30	1.2	322	10	BE155708	PM4-HT035
c 727	30	1.2	202	9	AF202336	AF202336	c 800	30	1.2	324	14	R76682	Yi61d07.s1
c 728	30	1.2	202	14	N91357	zb39d02.s1	c 801	30	1.2	325	17	AQ000933	CIT-HSP-2
c 729	30	1.2	203	17	AQ059130	CIT-HSP-2	c 802	30	1.2	329	9	AA224236	zr14g09.s
c 730	30	1.2	206	9	AA975291	oq36g04.s	c 803	30	1.2	330	14	Z21713	HS2H25C04.S
c 731	30	1.2	206	10	AA878020	MR3-OT000	c 804	30	1.2	332	17	BE0516	CIT-HSP-205
c 732	30	1.2	208	9	AA374775	EST86967	c 805	30	1.2	333	9	AA826844	nr50a06.s
c 733	30	1.2	209	9	AA599556	ag08b03.s	c 806	30	1.2	334	9	AI754544	cr26f08.x
c 734	30	1.2	213	10	AA855982	RC3-CT028	c 807	30	1.2	334	10	AA194802	xn31603.x
c 735	30	1.2	215	10	BE002911	QV4-BN009.	c 808	30	1.2	335	12	BF813915	RC4-CI019
c 736	30	1.2	215	17	AQ044864	CIT-HSP-2	c 809	30	1.2	335	14	M77870	EST01454.Fe

810	30	1.2	340	9	AA666295	AA666295 ac39a10.s	883	30	1.2	394	10	BE677029	BE677029 7d51f07.x
811	30	1.2	342	12	BF859011	BF859011 MR0-FT018	C 884	30	1.2	394	12	BF061272	BF061272 7d55906.x
812	30	1.2	343	10	BE243948	BE243948 TCBAPIE14	C 885	30	1.2	395	10	AA666059	AA666059 ac41b06.s
813	30	1.2	345	17	AQ676759	AQ676759 HS 5496.B	C 886	30	1.2	395	17	AI240701	AI240701 qh53e06.x
814	30	1.2	346	9	AA345064	AA345064 EST51047_	C 887	30	1.2	395	9	AA112925	AA112925 zn54912.x
815	30	1.2	346	17	B35322	B35322 HS-1028-B1-	C 888	30	1.2	395	17	AI690497	AI690497 tx99e08.x
816	30	1.2	347	9	AA643448	AA643448 nu31hl1.s	C 889	30	1.2	396	9	AA167178	AA167178 zpi5a11.x
817	30	1.2	347	9	AI247002	AI247002 qx52b04.x	C 890	30	1.2	397	9	AA167556	AA167556 zpi5a11.x
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ALIGNMENTS

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DEFINITION DKEZP761D0110 5', mRNA sequence.
ACCESSION AL118597.1 GI:5924496
VERSION EST.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 705)
REFERENCE Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
AUTHORS EST (Blum, et al.)
TITLE Unpublished (1999)
JOURNAL Contact: Blum H
COMMENT MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by LMU (Ludwig Maximilians University,

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Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No si sequence available.
 This clone (DKFZp761D0110) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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RESULT 2

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ACCESSION      AL536293
VERSION      AL536293.1 GI:12799786
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
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               /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
               cDNA was primed with a NotI-oligo(dT) primer. Five prime
               end enriched, double-stranded cDNA was digested with Not I
               and cloned into the Not I and Eco RV sites of the
               pCMVSPORT 6 vector. Library was constructed by Life
               Technologies. Contact : Peng Liang Life Technologies, a
               division of Invitrogen 9800 Medical Center Drive Rockville
               , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
               fliang@lifetech.com URL :
               http://fulllength.invitrogen.com"
BASE COUNT      198 a      248 c      278 g      196 t      2 others
ORIGIN
Query Match      23.7%; Score 570; DB 9; Length 922;
Best Local Similarity 99.6%; Pred. No. 1.3e-270;
Matches 790; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY      2258      TTGGGCAAGTGGCC 2270
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Db      |||||||

RESULT 3
LOCUS      BM560284
DEFINITION      AGENCOURT 6597802 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5432019
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ACCESSION      BM560284
VERSION      BM560284.1 GI:18804585
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
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               adaptor: GGCACGAG(G). Library constructed by Ling Hong
               in the laboratory of Gerald M. Rubin (University of
               California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH MGC library."
BASE COUNT      198 a      288 c      264 g      179 t

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adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC library."
High quality sequence stop: 498.
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http://image.llnl.gov

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ORIGIN

Query Match 19.0%; Score 456; DB 13; Length 929;
Best Local Similarity 99.6%; Pred. No. 3.7e-214;
Matches 556; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 241 CTCCCTCTCTCCAGGAAAGTGGCCACAGCAAGTACAGCGGCTCCCTCGCTTCAT 300

QY 1349 CCAACCTCTTTTCTCTCGGACACATTTGAATGCTTGGAAATAGAAAGACCATAT 1408
Db 301 CCAACCTCTTTTCTCTCGGACACATTTGAATGCTTGGAAATAGAAAGACCATAT 360

QY 1409 ATGACCAAGAGCTTTGAAACAGCCCATCAGACCTGAGCTATTTTCTCTGCGCCAG 1468
Db 361 ATGACCAAGAGCTTTGAAACAGCCCATCAGACCTGAGCTATTTTCTCTGCGCCAG 420

QY 1469 AGGTGTAGGGGTGAATGAGCGGGGAGAGCTGGCTTTGAAACCTCAGGCGTCTCCAG 1528
Db 421 AGGTGTAGGGGTGAATGAGCGGGGAGAGCTGGCTTTGAAACCTCAGGCGTCTCCAG 480

QY 1529 CCCCAGGACACAGAGAGGGGAGAGACAGGACCCAGCAGCTGTGAGACCTGTC 1588
Db 481 CCCCAGGACACAGAGAGGGGAGAGACAGGACCCAGCAGCTGTGAGACCTGTC 540

QY 1589 CACAGCCAGAGGGGCA 1606
Db 541 CACAGCCAGAGGGGCA 558

RESULT 4
BF689781

LOCUS 60218505F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298593 5',
mRNA sequence.

DEFINITION BF689781.1 GI:11975189

VERSION BF689781.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCT/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1154 row: j column: 02

FEATURES High quality sequence stop: 602.

source Location/Qualifiers

1..1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4298593"
/clone_lib="NIH_MGC_49"
/issue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 345 a 254 c 283 g 138 t

ORIGIN

Query Match 15.9%; Score 383; DB 12; Length 1020;
Best Local Similarity 100.0%; Pred. No. 5.5e-178;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 CAGAGCCTTGGACAGCCCATCAGACCTGAGCTATTTCTCTGCGCCAGAGGTG 1473
Db 2 CAGAGCCTTGGACAGCCCATCAGACCTGAGCTATTTCTCTGCGCCAGAGGTG 61

QY 1474 TAGGGGTGGAATCAGCGCGGGGAGCTGGCTTTGAAACCTCAGGCTGTCCAGCCCCG 1533
Db 62 TAGGGGTGGAATCAGCGCGGGGAGCTGGCTTTGAAACCTCAGGCTGTCCAGCCCCG 121

QY 1534 GCAAGCCACAGGAAGAGGAGGAGAGACAGCAGCCAGCAGTGTGAGACCTGTCACAG 1593
Db 122 GCAAGCCACAGGAAGAGGAGGAGAGACAGCAGCCAGCAGTGTGAGACCTGTCACAG 181

QY 1594 CAGAGAGGGGACAGGAGGAGATCCAGGGTTGAGAGCCAGTGTGAGCTGTATGGAGCC 1653
Db 182 CAGAGAGGGGACAGGAGGAGATCCAGGGTTGAGAGCCAGTGTGAGCTGTATGGAGCC 241

QY 1654 CTGGGGCCAGCCCTGTTTACTGGTTCTTGCAATGGAGAGTGTGAGCAGCTGTGACA 1713
Db 242 CTGGGGCCAGCCCTGTTTACTGGTTCTTGCAATGGAGAGTGTGAGCAGCTGTGACA 301

QY 1714 GCCAGTGAACCTTGAACCTGCTGACCACTTCTTTAAGCCATAGACCTGAGCCCTGG 1773
Db 302 GCCAGTGAACCTTGAACCTGCTGACCACTTCTTTAAGCCATAGACCTGAGCCCTGG 361

QY 1774 GCTGGGTGCTGGGAAGGAGGGT 1796
Db 362 GCTGGGTGCTGGGAAGGAGGGT 384

RESULT 5
AL134288

LOCUS AL134288

DEFINITION DKFZP547J194_r1 547 (synonym: hEbrl) Homo sapiens cDNA clone
DKFZP547J194 5', mRNA sequence.

ACCESSION AL134288

VERSION AL134288.1 GI:6602475

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 296)
Bloeker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
S.

TITLE EST (Bloeker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
S.)

JOURNAL Unpublished (1999)

COMMENT Contact: Bloeker H


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FEATURES
source
Location/Qualifiers
1. 432
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4129205"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life technologies).
Note: this is a NIH_MGC Library."
BASE COUNT      88 a 128 c 135 g 81 t
ORIGIN
Query Match      10.0%; Score 240; DB 12; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.7e-107;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 989 CTGGGAAGGCGAGTCTGGGACCTGGGACCTGGGAGGCGAGGCTCTCCCGTGCAATCCCGCC 1048
Db 72 CTGGGAAGGCGAGTCTGGGACCTGGGACCTGGGAGGCGAGGCTCTCCCGTGCAATCCCGCC 131
Qy 1049 TGCTCAGCAATTCAGACCCCTCTGAGAGAGCCCTCTCCCTGGGACACAGACCCAGACCC 1108
Db 132 TGCTCAGCAATTCAGACCCCTCTGAGAGAGCCCTCTCCCTGGGACACAGACCCAGACCC 191
Qy 1109 CCGAGGGGAGGCGAGGATGGCTTTCTTCCCTCTCTGATGTCCCGAGTCCACGAGCC 1168
Db 192 CCGAGGGGAGGCGAGGATGGCTTTCTTCCCTCTCTGATGTCCCGAGTCCACGAGCC 251
Qy 1169 TGCAGCCACACAGACGTCAGCCCTGACTCTCTGGCTTTCCAGGAGATGGGTCCAGGG 1228
Db 252 TGCAGCCACACAGACGTCAGCCCTGACTCTCTGGCTTTCCAGGAGATGGGTCCAGGG 311
RESULT 8
BG765063 602737675F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4862970 5',
LOCUS mRNA sequence.
DEFINITION BG765063 939 bp mRNA linear EST 15-MAY-2001
ACCESSION BG765063.1 GI:14075716
VERSION BG765063.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI724 row: e column: 19
High quality sequence stop: 759.
FEATURES
source
Location/Qualifiers
1. 939
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4862970"
/clone_lib="NIH_MGC_49"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life technologies).
Note: this is a NIH_MGC Library."
BASE COUNT      88 a 128 c 135 g 81 t
ORIGIN
Query Match      9.7%; Score 233; DB 12; Length 939;
Best Local Similarity 99.8%; Pred. No. 1e-103;
Matches 283; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1639 GGGTGATGGCCAGCCCTGGGGCCAGCCCTGTTTACTGGTTCTTGGCAATGGGAGCTG 1698
Db 231 GGGTGATGGCCAGCCCTGGGGCCAGCCCTGTTTACTGGTTCTTGGCAATGGGAGCTG 290
Qy 1699 AGCAGCCTCTGGACACCCAGTACCTTTGACCTCGGTGACCACTCTCTTTAAGCCATAG 1758
Db 291 AGCAGCCTCTGGACACCCAGTACCTTTGACCTCGGTGACCACTCTCTTTAAGCCATAG 350
Qy 1759 ACCTGAGGCCCTGGGCTGGGTGCTGGGAGGAGGAGGTTGAAACCAACCCGTAACCCAGG 1818
Db 351 ACCTGAGGCCCTGGGCTGGGTGCTGGGAGGAGGAGGTTGAAACCAACCCGTAACCCAGG 410
Qy 1819 GTGTGGCTTTCCAGKACCCCTCAGGGAGCCTCCCCATCTGTCCAGCTGGGGCCAGAGGCT 1878
Db 411 GTGTGGCTTTCCAGTACCTCAGGGAGCCTCCCCATCTGTCCAGCTGGGGCCAGAGGCT 470
Qy 1879 GGGAGTCCCTTACCTGTCTTACGTTGGCGCGGCTACTCTGGAA 1922
Db 471 GGGAGTCCCTTACCTGTCTTACGTTGGCGCGGCTACTCTGGAA 514
RESULT 9
BF317160 601901286F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130469 5',
LOCUS mRNA sequence.
DEFINITION BF317160 901 bp mRNA linear EST 21-NOV-2000
ACCESSION BF317160
VERSION BF317160.1 GI:11265566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 901)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI026 row: 1 column: 22
High quality sequence start: 2
High quality sequence stop: 589.
FEATURES
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Location/Qualifiers
1. 901
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4130469"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 199 a 247 c 311 g 144 t
ORIGIN

Query Match 8.8%; Score 212; DB 12; Length 901;
Best Local Similarity 100.0%; Pred. No. 2.6e-93;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 918 TTGAGGTTGACCTGGAGGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATC 977
Db 3 TTGAGGTTGACCTGGAGGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATC 62
Qy 978 TGAGGGGCTGCTGGGAGGCGAGCTCTGGGACCTGGCACTGGGAGGCGAGGCTCTCCCG 1037
Db 63 TGAGGGGCTGCTGGGAGGCGAGCTCTGGGACCTGGCACTGGGAGGCGAGGCTCTCCCG 122
Qy 1038 TGCATCCCCCTGCTAGCAATTCAGACCCCTCTGAGAGCGCCACTCCCTGGGACACAG 1097
Db 123 TGCATCCCCCTGCTAGCAATTCAGACCCCTCTGAGAGCGCCACTCCCTGGGACACAG 182
Qy 1098 ACCGAGGACCCCGAGGGGAGGAGGATGCG 1129
Db 183 ACCGAGGACCCCGAGGGGAGGAGGATGCG 214

RESULT 10
BI034804/c
LOCUS BI034804 446 bp mRNA linear EST 14-JUN-2001
DEFINITION RC4-NN1176-090401-013-903 NN1176 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI034804
VERSION BI034804.1 GI:14441430
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 446)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-NN1176-
090401-013-903&t3=2001-04-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 67
High quality sequence stop: 389.

FEATURES
Location/Qualifiers
1..446
/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone_lib="NN1176"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent Application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 102 a 106 c 134 g 104 t
ORIGIN

Query Match 7.4%; Score 177; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 4.4e-76;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2020 TACAGCCAGTTTACGGGCAAACTTTCCCTTAGCACCTTACGGCTGAGTTCTGGGT 2079
Db 305 TACAGCCAGTTTACGGGCAAACTTTCCCTTAGCACCTTACGGCTGAGTTCTGGGT 246
Qy 2080 TTCTAGAGGTTCAGAGCGGCTCTCAGAGCGCCAGGAGCCAGAGCCCAAGCAGGACGAA 2139
Db 245 TTCTAGAGGTTCAGAGCGGCTCTCAGAGCGCCAGGAGCCAGAGCCCAAGCAGGACGAA 186
Qy 2140 AAAGAGGCATACACAGCAGTGTGAATAGCTGGCCAGCAGGCATCTCCCTCCAC 2196
Db 185 AAAGAGGCATACACAGCAGTGTGAATAGCTGGCCAGCAGGCATCTCCCTCCAC 129

RESULT 11
AA020852/c
LOCUS AA020852 463 bp mRNA linear EST 30-JAN-1997
DEFINITION ze64b08.r1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:363735 5', mRNA sequence.

ACCESSION AA020852
VERSION AA020852.1 GI:1484623

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 463)

AUTHORS

Chissoe, S., Dietrich, N., DuBuque, T., Pavello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Matra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 4323 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 342.

Location/Qualifiers

1..463

/organism="Homo sapiens"

/db_xref="GDB:1280438"

/db_xref="taxon:9606"

/clone="IMAGE:363735"

/clone_lib="Soares retina N2b4HR"

/sex="male"

/tissue_type="retina"

/dev_stage="55 year old"

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/lab host="DH10B (ampicillin resistant)"
/notes="Organ: eye; Vector: pTT3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTT3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      97 a 138 c 127 g 95 t      6 others
ORIGIN

Query Match      6.4%; Score 153; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 3.4e-64;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1677 TGGTCTTTCGAAATGGAGCTGACAGCCCTTGACAGCCAGTGACCTTTGACCTCGGTG 1736
Db 334 TGGTCTTTCGAAATGGAGCTGACAGCCCTTGACAGCCAGTGACCTTTGACCTCGGTG 275

Qy 1737 ACCACTCTCTTTAAGCCATAGACCTGAGCCCTGGCTGGCTGGAGGAGGCT 1796
Db 274 ACCACTCTCTTTAAGCCATAGACCTGAGCCCTGGCTGGCTGGAGGAGGCT 215

Qy 1797 TGAACACACCTGTAACAGAGGCTGTGGCTTTC 1829
Db 214 TGAACACACCTGTAACAGAGGCTGTGGCTTTC 182

RESULT 12
LOCUS      N35845      643 bp mRNA linear EST 16-JAN-1996
DEFINITION Y89f10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone
IMAGE:268939 5', mRNA sequence.
ACCESSION  N35845
VERSION     N35845.1 GI:1156987
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 643)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Matra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT:  Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 360
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 17
High quality sequence stop: 360.
Location/Qualifiers
FEATURES
source
1..643
/organism="Homo sapiens"
/db_xref="GDB:3878581"
/db_xref="taxon:9606"
/clone="IMAGE:268939"
/sex="Male"

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/tissue type="melanocyte"
/lab host="DH10B (ampicillin resistant)"
/notes="vector: pTT3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTT3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      143 a 171 c 171 g 145 t      13 others
ORIGIN

Query Match      5.6%; Score 134; DB 14; Length 643;
Best Local Similarity 100.0%; Pred. No. 9.8e-55;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1913 TACTCTGGATGTTTTTCCTCCCGAATCATATGATCTGGCAATTTTCCTCCTCTGCTACAGCCAGTTT 2032
Db 263 TACTCTGGATGTTTTTCCTCCCGAATCATATGATCTGGCAATTTTCCTCCTCTGCTACAGCCAGTTT 322

Qy 1973 ATCACAAGATGCAATATATGATCTGGCAATTTTCCTCCTCTGCTACAGCCAGTTT 2032
Db 323 ATCACAAGATGCAATATATGATCTGGCAATTTTCCTCCTCTGCTACAGCCAGTTT 382

Qy 2033 AGCGCAAAACCTTT 2046
Db 383 AGCGCAAAACCTTT 396

RESULT 13
LOCUS      BE384676      558 bp mRNA linear EST 21-JUL-2000
DEFINITION 601276954F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617820 5',
mRNA sequence.
ACCESSION  BE384676
VERSION     BE384676.1 GI:9330041
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 558)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC285 row: 1 column: 13
High quality sequence start: 17
High quality sequence stop: 555.
Location/Qualifiers
FEATURES
source
1..558
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3617820"
/tissue type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of

```

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 122 a 160 c 175 g 101 t

ORIGIN

Query Match 4.3%; Score 104; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 6.7e-40;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1499 GCTGGCTTTGAAACCTCAGGCTCTCCAGCCCGCAAGCCACAGGAGGGGAGAG 1558
|||||

Db 63 GCTGGCTTTGAAACCTCAGGCTCTCCAGCCCGCAAGCCACAGGAGGGGAGAG 122
|||||

Qy 1559 ACAGGACCCAGCAGTGTGGAGACCTTGCACAGCCAGGAG 1602
|||||

Db 123 ACAGGACCCAGCAGTGTGGAGACCTTGCACAGCCAGGAG 166
|||||

RESULT 14
BE540725 797 bp mRNA linear EST 09-AUG-2000
LOCUS 601065002P1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451321 5',
DEFINITION mRNA sequence.
ACCESSION BE540725
VERSION BE540725.1 GI:9769370
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8431 row: c column: 02
High quality sequence start: 4
High quality sequence stop: 677.
Location/Qualifiers
1..797
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3451321"
/cell_line="NIH_MGC_10"
/lab_host="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."

BASE COUNT 158 a 219 c 235 g 184 t 1 others

ORIGIN

Query Match 4.1%; Score 98; DB 10; Length 797;
Best Local Similarity 100.0%; Pred. No. 7.1e-37;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2218 AGACTAAGGATCCAGAGAGCAGCTCCCTTTCTCAGAGCTTGGCAGTCCCCCAGGAG 2277
|||||

Db 304 AGACTAAGGATCCAGAGAGCAGCTCCCTTTCTCAGAGCTTGGCAGTCCCCCAGGAG 363
|||||

Qy 2278 TCAGGGTTTCTCTGCAGATGTCGGAGCGGAGCGG 2315
|||||

Db 364 TCAGGGTTTCTCTGCAGATGTCGGAGCGGAGCGG 401
|||||

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 122 a 160 c 175 g 101 t

ORIGIN

Query Match 4.3%; Score 104; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 6.7e-40;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1499 GCTGGCTTTGAAACCTCAGGCTCTCCAGCCCGCAAGCCACAGGAGGGGAGAG 1558
|||||

Db 63 GCTGGCTTTGAAACCTCAGGCTCTCCAGCCCGCAAGCCACAGGAGGGGAGAG 122
|||||

Qy 1559 ACAGGACCCAGCAGTGTGGAGACCTTGCACAGCCAGGAG 1602
|||||

Db 123 ACAGGACCCAGCAGTGTGGAGACCTTGCACAGCCAGGAG 166
|||||

RESULT 14
BE540725 797 bp mRNA linear EST 09-AUG-2000
LOCUS 601065002P1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451321 5',
DEFINITION mRNA sequence.
ACCESSION BE540725
VERSION BE540725.1 GI:9769370
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8431 row: c column: 02
High quality sequence start: 4
High quality sequence stop: 677.
Location/Qualifiers
1..797
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3451321"
/cell_line="NIH_MGC_10"
/lab_host="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."

BASE COUNT 158 a 219 c 235 g 184 t 1 others

ORIGIN

Query Match 4.1%; Score 98; DB 10; Length 797;
Best Local Similarity 100.0%; Pred. No. 7.1e-37;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2218 AGACTAAGGATCCAGAGAGCAGCTCCCTTTCTCAGAGCTTGGCAGTCCCCCAGGAG 2277
|||||

Db 304 AGACTAAGGATCCAGAGAGCAGCTCCCTTTCTCAGAGCTTGGCAGTCCCCCAGGAG 363
|||||

Qy 2278 TCAGGGTTTCTCTGCAGATGTCGGAGCGGAGCGG 2315
|||||

Db 364 TCAGGGTTTCTCTGCAGATGTCGGAGCGGAGCGG 401
|||||

RESULT 15
BG769644 1120 bp mRNA linear EST 15-MAY-2001
LOCUS 602744561F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4877655 5',
DEFINITION mRNA sequence.
ACCESSION BG769644
VERSION BG769644.1 GI:14080297
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1120)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1762 row: i column: 16
High quality sequence start: 22
High quality sequence stop: 611.
Location/Qualifiers
1..1120
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4877655"
/cell_line="NIH_MGC_49"
/lab_host="DH10B (phage-resistant)"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 328 a 278 c 343 g 171 t

ORIGIN

Query Match 3.7%; Score 89; DB 12; Length 1120;
Best Local Similarity 100.0%; Pred. No. 2.3e-32;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1432 CCCCATCAGAACCTGAGCTATTTCTCTGCGCGCAGAGGTAGGGGTGAATGAGCCG 1491
|||||

Db 21 CCCCATCAGAACCTGAGCTATTTCTCTGCGCGCAGAGGTAGGGGTGAATGAGCCG 80
|||||

Qy 1492 CGGGGAGCTGCTTTGAACCTCAGGCC 1520
|||||

Db 81 CGGGGAGCTGCTTTGAACCTCAGGCC 109
|||||

Search completed: June 17, 2003, 06:24:58
Job time : 2779.07 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 344.575 Seconds
(without alignments)
15794.017 Million cell updates/sec

Title: US-09-513-888c-1_COPY_6939_7125

Perfect score: 187

Sequence: 1 atgatcatgctactgacg.....tggcctcaagcaatccacct 187

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_rts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_rts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	187	100.0	5492	9	AF123659 Homo sapi
2	187	100.0	9108	9	AF123653 Homo sapi
3	187	100.0	173284	2	AC025853 Homo sapi
C 4	42	22.5	105051	2	AC009449 Homo sapi
C 5	42	22.5	147760	9	AC011846 Homo sapi
C 6	42	22.5	156197	9	HS97K10 Z81365 Human DNA s
C 7	42	22.5	198295	9	AC105129 Homo sapi
C 8	42	22.5	212505	2	AC027220 Homo sapi
C 9	41	21.9	112732	2	AC092367 Homo sapi
C 10	41	21.9	120186	9	AF001184 Homo sapi
C 11	41	21.9	155877	2	AC073631 Homo sapi
C 12	41	21.9	165662	9	AC009930 Homo sapi
C 13	41	21.9	166098	9	AC020641 Homo sapi
C 14	41	21.9	180423	9	AC012152 Homo sapi
C 15	41	21.9	187266	2	AC073984 Homo sapi
C 16	41	21.9	202760	2	AC021987 Homo sapi
C 17	40	21.4	2580	9	AK026402 Homo sapi
C 18	40	21.4	11170	9	AL512429 Human DNA
C 19	40	21.4	18999	6	AX473126 Sequence
C 20	40	21.4	53269	9	AP002404 Homo sapi
C 21	40	21.4	66867	2	AC073170 Homo sapi
C 22	40	21.4	71091	9	AC106052 Homo sapi
C 23	40	21.4	79560	9	AL591471 Human DNA
C 24	40	21.4	86295	2	AC078810 Homo sapi
C 25	40	21.4	92651	9	AC002527 Human BAC
C 26	40	21.4	100000	9	AP000081 Homo sapi
C 27	40	21.4	109296	9	AC083949 Homo sapi
C 28	40	21.4	110000	2	AC125619 4
C 29	40	21.4	110000	2	AC027294 2
C 30	40	21.4	112597	9	HS82L10 Continuation (5 of
C 31	40	21.4	120488	9	AC073257 Homo sapi
C 32	40	21.4	123070	9	AC020656 Homo sapi
C 33	40	21.4	125146	9	AL512770 Human DNA
C 34	40	21.4	140974	9	AC085533 Homo sapi
C 35	40	21.4	141771	9	AC091821 Homo sapi
C 36	40	21.4	142666	9	AC114745 Homo sapi
C 37	40	21.4	145100	2	AC024641 Homo sapi
C 38	40	21.4	147297	2	AF215850 Homo sapi
C 39	40	21.4	149015	9	AC107992 Homo sapi
C 40	40	21.4	150526	2	AC092339 Homo sapi
C 41	40	21.4	153201	9	AC006454 Homo sapi
C 42	40	21.4	153342	2	AL591646 Homo sapi
C 43	40	21.4	153832	2	AC116447 Homo sapi
C 44	40	21.4	156100	2	AC011934 Homo sapi
C 45	40	21.4	156623	9	AC083838 Homo sapi
C 46	40	21.4	157438	2	AC036165 Homo sapi
C 47	40	21.4	157910	9	CNS01DTR AL132855 Human chr
C 48	40	21.4	157918	9	AL512422 Human DNA
C 49	40	21.4	158758	9	AC093591 Homo sapi
C 50	40	21.4	158785	2	AC027699 Homo sapi
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C 52	40	21.4	161422	2	AC021544 Homo sapi
C 53	40	21.4	161737	2	AC087809 Homo sapi
C 54	40	21.4	162427	9	AC010205 Homo sapi
C 55	40	21.4	162482	9	AC022740 Homo sapi
C 56	40	21.4	162691	2	AC013523 Homo sapi
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C 61	40	21.4	168366	9	AL353667 Human DNA
C 62	40	21.4	168425	2	AC012198 Homo sapi
C 63	40	21.4	168862	9	AC073464 Homo sapi
C 64	40	21.4	169552	9	AC015976 Homo sapi
C 65	40	21.4	170227	2	AC019161 Homo sapi

c 66	40	21.4	171173	2	AC127454	AC127454 Homo sapi	139	38	20.3	204505	9	AC089983	Homo sapi
c 67	40	21.4	177219	2	AC021286	AC021286 Homo sapi	c 140	38	20.3	209162	9	AC090955	Homo sapi
c 68	40	21.4	177527	9	AC092719	AC092719 Homo sapi	c 141	38	20.3	210791	9	CNS01D7	Human chr
c 69	40	21.4	178377	9	AC007685	AC007685 Homo sapi	c 142	38	20.3	236486	9	AC021188	Homo sapi
c 70	40	21.4	180498	9	AL513478	AL513478 Human DNA	c 143	38	20.3	243810	2	AC093405	Lemur cat
c 71	40	21.4	185000	2	AC007799	AC007799 Homo sapi	c 144	38	20.3	254437	9	AP000500	Homo sapi
c 72	40	21.4	186202	9	AC108516	AC108516 Homo sapi	c 145	37	19.8	41313	2	U82205	Homo sapien
c 73	40	21.4	186886	2	AC016297	AC016297 Homo sapi	c 146	37	19.8	50843	9	AC074114	Homo sapi
c 74	40	21.4	187431	9	AC107219	AC107219 Homo sapi	c 147	37	19.8	74509	2	AF260012	Homo sapi
c 75	40	21.4	188256	2	AP001927	AP001927 Homo sapi	c 148	37	19.8	75148	9	AC091545	Homo sapi
c 76	40	21.4	188410	2	AC124073	AC124073 Homo sapi	c 149	37	19.8	76075	9	AL590387	Homo sapi
c 77	40	21.4	192554	2	AC024170	AC024170 Homo sapi	c 150	37	19.8	82151	9	AC079987	Homo sapi
c 78	40	21.4	194832	9	AC025287	AC025287 Homo sapi	c 151	37	19.8	99408	9	AL359385	Homo sapi
c 79	40	21.4	195529	2	AC025714	AC025714 Homo sapi	c 152	37	19.8	104656	9	AL731576	Human DNA
c 80	40	21.4	202004	9	H0AF001549	AF001549 Human chr	c 153	37	19.8	118906	9	AL353583	Human DNA
c 81	40	21.4	207830	2	AC007998	AC007998 Homo sapi	c 154	37	19.8	125293	2	AC073582	Homo sapi
c 82	40	21.4	210723	9	AC012215	AC012215 Homo sapi	c 155	37	19.8	125674	2	AP002018	Homo sapi
c 83	40	21.4	215994	9	AC067941	AC067941 Homo sapi	c 156	37	19.8	129272	9	AL451125	Human DNA
c 84	40	21.4	232964	2	AC015501	AC015501 Homo sapi	c 157	37	19.8	135405	9	AC000025	Homo sapi
c 85	40	21.4	249325	2	AC015501	AC015501 Homo sapi	c 158	37	19.8	139485	2	AC025597	Homo sapi
c 86	40	21.4	290625	2	AL442068	AL442068 Homo sapi	c 159	37	19.8	143146	9	AC079855	Homo sapi
c 87	39	20.9	71404	2	AC103701	AC103701 Homo sapi	c 160	37	19.8	145428	2	AC026068	Homo sapi
c 88	39	20.9	83798	9	HS1013A22	AL132772 Human DNA	c 161	37	19.8	146889	9	AL358937	Human DNA
c 89	39	20.9	100664	9	AL512651	AL512651 Human DNA	c 162	37	19.8	147484	2	AL590088	Homo sapi
c 90	39	20.9	109876	2	AC091497	AC091497 Homo sapi	c 163	37	19.8	149308	9	AC005527	Homo sapi
c 91	39	20.9	120192	2	AC093220	AC093220 Homo sapi	c 164	37	19.8	151853	9	CNS01RHL	Human chr
c 92	39	20.9	140469	2	AC025066	AC025066 Homo sapi	c 165	37	19.8	152118	2	AC013263	Homo sapi
c 93	39	20.9	159910	9	AC009235	AC009235 Homo sapi	c 166	37	19.8	154606	9	AC097358	Homo sapi
c 94	39	20.9	167206	9	AL392044	AL392044 Human DNA	c 167	37	19.8	156378	2	AC084267	Homo sapi
c 95	39	20.9	169988	9	AC064846	AC064846 Homo sapi	c 168	37	19.8	157672	9	AC113143	Homo sapi
c 96	39	20.9	170758	9	AC004965	AC004965 Homo sapi	c 169	37	19.8	159098	2	AC016484	Homo sapi
c 97	39	20.9	170926	9	AC095034	AC095034 Homo sapi	c 170	37	19.8	162314	9	AC061965	Homo sapi
c 98	39	20.9	171343	2	AC016676	AC016676 Homo sapi	c 171	37	19.8	165260	2	AC093928	Homo sapi
c 99	39	20.9	178446	2	AC109450	AC109450 Homo sapi	c 172	37	19.8	167386	2	AL159993	Homo sapi
c 100	39	20.9	182703	2	AC022939	AC022939 Homo sapi	c 173	37	19.8	168056	9	AC004458	Homo sapi
c 101	39	20.9	185784	2	AC009719	AC009719 Homo sapi	c 174	37	19.8	169650	2	AC024629	Homo sapi
c 102	39	20.9	186531	2	AC109464	AC109464 Homo sapi	c 175	37	19.8	170404	9	AC012493	Homo sapi
c 103	38	20.3	33931	2	AC022156	AC022156 Homo sapi	c 176	37	19.8	170586	2	AL356126	Homo sapi
c 104	38	20.3	58826	2	AC116536	AC116536 Homo sapi	c 177	37	19.8	178137	9	AC011302	Homo sapi
c 105	38	20.3	71406	2	AC027434	AC027434 Homo sapi	c 178	37	19.8	179372	2	AC040922	Homo sapi
c 106	38	20.3	81951	2	AC022814	AC022814 Homo sapi	c 179	37	19.8	180595	9	AC008280	Homo sapi
c 107	38	20.3	96253	9	AC090083	AC090083 Homo sapi	c 180	37	19.8	181856	9	AC093227	Homo sapi
c 108	38	20.3	102517	2	AP002876	AP002876 Homo sapi	c 181	37	19.8	182241	9	AC022909	Homo sapi
c 109	38	20.3	110000	2	AC008576	Continuation (2 of	c 182	37	19.8	190076	9	AC008403	Homo sapi
c 110	38	20.3	120890	2	AC079517	Continuation (4 of	c 183	37	19.8	194034	9	AL592148	Human DNA
c 111	38	20.3	120890	9	AL606760	AL606760 Human DNA	c 184	37	19.8	195773	2	AL592148	Human DNA
c 112	38	20.3	122176	2	AL358233	AL358233 Homo sapi	c 185	37	19.8	198396	9	AC010355	Homo sapi
c 113	38	20.3	131398	9	HS445C9	Z95115 Human DNA	c 186	37	19.8	198751	9	AC022148	Homo sapi
c 114	38	20.3	142391	2	AC092507	AC092507 Homo sapi	c 187	37	19.8	222106	2	AC018570	Homo sapi
c 115	38	20.3	142839	9	AL356218	AL356218 Human DNA	c 188	37	19.8	222275	9	CNS05TCN	Human chr
c 116	38	20.3	152741	2	AC021606	AC021606 Homo sapi	c 189	37	19.8	226171	9	AP003730	Homo sapi
c 117	38	20.3	152824	9	AC107072	AC107072 Homo sapi	c 190	37	19.8	266941	9	AF213884S2	Homo sapi
c 118	38	20.3	157442	9	AC105001	AC105001 Homo sapi	c 191	37	19.8	318488	9	AC005529	Homo sapi
c 119	38	20.3	157921	2	AC027726	AC027726 Homo sapi	c 192	36	19.3	41907	9	AC009001	Homo sapi
c 120	38	20.3	159488	2	AC025141	AC025141 Homo sapi	c 193	36	19.3	44679	9	CH19F21246	Homo sapi
c 121	38	20.3	166007	9	CNS01DRC	AL117186 Human chr	c 194	36	19.3	50793	9	AC092592	Homo sapi
c 122	38	20.3	167358	2	AC010673	AC010673 Homo sapi	c 195	36	19.3	68035	9	AL158199	Human DNA
c 123	38	20.3	168672	2	AC027102	AC027102 Homo sapi	c 196	36	19.3	75547	9	AC004919	Homo sapi
c 124	38	20.3	168798	2	AC012683	AC012683 Homo sapi	c 197	36	19.3	89944	9	AC093127	Papio cyn
c 125	38	20.3	169223	2	AL353675	AL353675 Homo sapi	c 198	36	19.3	112416	2	AP000482	Homo sapi
c 126	38	20.3	173137	2	AC107017	AC107017 Homo sapi	c 199	36	19.3	112875	2	AP000638	Homo sapi
c 127	38	20.3	173845	9	AC018662	AC018662 Human chr	c 200	36	19.3	119555	9	AL353790	Human DNA
c 128	38	20.3	175045	2	AC022728	AC022728 Homo sapi	c 201	36	19.3	127051	9	AL355538	Human DNA
c 129	38	20.3	176046	9	AC073366	AC073366 Homo sapi	c 202	36	19.3	130932	9	AC092658	Homo sapi
c 130	38	20.3	176584	2	AC027812	AC027812 Homo sapi	c 203	36	19.3	137830	9	AC003029	Homo sapi
c 131	38	20.3	178628	2	AC015715	AC015715 Homo sapi	c 204	36	19.3	145616	9	Z85986 Human DNA s	
c 132	38	20.3	181629	2	AC087738	AC087738 Homo sapi	c 205	36	19.3	154738	9	AC023355	Homo sapi
c 133	38	20.3	183099	2	AC034144	AC034144 Homo sapi	c 206	36	19.3	156300	2	AC023355	Homo sapi
c 134	38	20.3	189635	2	HUAC002287	AC002287 Homo sapi	c 207	36	19.3	157347	2	AP001882	Homo sapi
c 135	38	20.3	191265	2	AC130450	AC130450 Homo sapi	c 208	36	19.3	158952	9	AC096745	Homo sapi
c 136	38	20.3	198402	9	AC069546	AC069546 Homo sapi	c 209	36	19.3	161487	2	AC119571	Pan trogl
c 137	38	20.3	202750	2	AC116942	AC116942 Pan trogl	c 210	36	19.3	161874	9	AC114482	Homo sapi
c 138	38	20.3	203200	9	AC008744	AC008744 Homo sapi	c 211	36	19.3	164646	2	AP002877	Homo sapi

212	36	19.3	167005	9	AL158070	Human DNA	AK023833	9	AK023833	18.7	6133	9	AK023833
213	36	19.3	167633	2	AC129096	Papio cyn	U12022	Human	AK023833	18.7	6581	9	HSCADMG2
214	36	19.3	169505	9	CNS0101TV	Human chr	U33446	Human	AK023833	18.7	7008	9	HSU33446
215	36	19.3	169671	2	AC087485	Human sapi	AL590374	Human DNA	AL590374	18.7	9775	9	AL590374
216	36	19.3	169867	2	AC087485	Human sapi	AL592286	Human DNA	AL592286	18.7	10988	9	AL592286
217	36	19.3	170102	9	AC008079	Human sapi	HS417C12	Human sapi	HS417C12	18.7	11663	9	HS417C12
218	36	19.3	171449	9	AC008079	Human sapi	AF494057	Human sapi	AF494057	18.7	12064	9	AF494057
219	36	19.3	172327	2	AC012345	Human sapi	AF494057	Human sapi	AF494057	18.7	12248	9	AF494057
220	36	19.3	175108	2	AC011982	Human sapi	AF494057	Human sapi	AF494057	18.7	15966	9	AF494057
221	36	19.3	175249	9	AC119038	Human sapi	AF494057	Human sapi	AF494057	18.7	18332	9	AF494057
222	36	19.3	175776	2	AC112511	Human sapi	AF494057	Human sapi	AF494057	18.7	22038	9	AF494057
223	36	19.3	175837	2	AC022045	Human sapi	AF494057	Human sapi	AF494057	18.7	26000	9	AF494057
224	36	19.3	176010	2	AC069125	Human sapi	AF494057	Human sapi	AF494057	18.7	26316	9	AF494057
225	36	19.3	176117	9	AC092352	Human sapi	AF494057	Human sapi	AF494057	18.7	27103	9	AF494057
226	36	19.3	176421	9	AC096888	Human sapi	AF494057	Human sapi	AF494057	18.7	28142	9	AF494057
227	36	19.3	176512	9	AC012323	Human sapi	AF494057	Human sapi	AF494057	18.7	32303	9	AF494057
228	36	19.3	179460	9	AC012512	Human sapi	AF494057	Human sapi	AF494057	18.7	33528	9	AF494057
229	36	19.3	179611	2	AC084348	Human sapi	AF494057	Human sapi	AF494057	18.7	33615	9	AF494057
230	36	19.3	179844	9	AC009265	Human sapi	AF494057	Human sapi	AF494057	18.7	34568	9	AF494057
231	36	19.3	183617	9	AC007731	Human sapi	AF494057	Human sapi	AF494057	18.7	34746	9	AF494057
232	36	19.3	183637	9	AC1139002	Human sapi	AF494057	Human sapi	AF494057	18.7	35730	9	AF494057
233	36	19.3	184138	2	AC087177	Human sapi	AF494057	Human sapi	AF494057	18.7	36594	9	AF494057
234	36	19.3	187863	9	AL589740	Human sapi	AF494057	Human sapi	AF494057	18.7	37088	9	AF494057
235	36	19.3	188034	2	AC036169	Human sapi	AF494057	Human sapi	AF494057	18.7	38055	9	AF494057
236	36	19.3	190305	2	AC090267	Human sapi	AF494057	Human sapi	AF494057	18.7	38429	9	AF494057
237	36	19.3	190415	9	AC096612	Human sapi	AF494057	Human sapi	AF494057	18.7	39186	9	AF494057
238	36	19.3	191098	2	AC073518	Human sapi	AF494057	Human sapi	AF494057	18.7	39198	6	AF494057
239	36	19.3	191329	2	AC090269	Human sapi	AF494057	Human sapi	AF494057	18.7	39854	9	AF494057
240	36	19.3	191957	2	AC015845	Human sapi	AF494057	Human sapi	AF494057	18.7	40166	9	AF494057
241	36	19.3	192592	9	AC005500	Human sapi	AF494057	Human sapi	AF494057	18.7	40205	9	AF494057
242	36	19.3	193963	9	AC007336	Human sapi	AF494057	Human sapi	AF494057	18.7	40876	9	AF494057
243	36	19.3	194197	9	AC064871	Human sapi	AF494057	Human sapi	AF494057	18.7	40981	9	AF494057
244	36	19.3	199869	9	AC092378	Human sapi	AF494057	Human sapi	AF494057	18.7	41220	9	AF494057
245	36	19.3	202414	2	AC090966	Human sapi	AF494057	Human sapi	AF494057	18.7	41319	2	AF494057
246	36	19.3	207183	9	AP001533	Human sapi	AL3359082	Human sapi	AL3359082	18.7	41372	9	AL3359082
247	36	19.3	215225	9	AP001972	Human sapi	AL3333H9	Human sapi	AL3333H9	18.7	42098	9	AL3333H9
248	36	19.3	219436	9	AC005046	Human sapi	AC074203	Human sapi	AC074203	18.7	42479	9	AC074203
249	35	18.7	272	9	AF032273	Eulemur m	AC006277	Human sapi	AC006277	18.7	42642	9	AC006277
250	35	18.7	275	9	AF032256	Eulemur m	AL136450	Human sapi	AL136450	18.7	43480	9	AL136450
251	35	18.7	275	9	AF032322	Propithec	AL159172	Human sapi	AL159172	18.7	43958	9	AL159172
252	35	18.7	300	9	HAI9344	Human sapi	AC005781	Human sapi	AC005781	18.7	44052	9	AC005781
253	35	18.7	417	6	AX072460	Sequence	AX008040	Human sapi	AX008040	18.7	44100	6	AX008040
254	35	18.7	535	11	HUMUT6283	Human SRS U	HSXSL1LM2	Human sapi	HSXSL1LM2	18.7	44373	9	HSXSL1LM2
255	35	18.7	567	6	AX387669	Sequence	AL33719	Human sapi	AL33719	18.7	44653	9	AL33719
256	35	18.7	1000	9	S83170	tissue-type	AL336135	Human sapi	AL336135	18.7	46699	9	AL336135
257	35	18.7	1203	9	HUMDY5KW	Human dyetr	AC004611	Human sapi	AC004611	18.7	47055	9	AC004611
258	35	18.7	1341	9	HSA244000	Human sapi	AC021101	Human sapi	AC021101	18.7	47069	9	AC021101
259	35	18.7	1341	9	HSG6P	H. sapiens G	AC104688	Human sapi	AC104688	18.7	47088	9	AC104688
260	35	18.7	1580	9	BC000052	Human sapi	AC003660	Human sapi	AC003660	18.7	48000	2	AC003660
261	35	18.7	1690	9	AC000028	Human sapi	AC079455	Human sapi	AC079455	18.7	50479	9	AC079455
262	35	18.7	1777	9	HSTECXTL1	Human sapi	AC004762	Human sapi	AC004762	18.7	50651	9	AC004762
263	35	18.7	1927	9	AC024132	Human sapi	AL118558	Human sapi	AL118558	18.7	51825	9	AL118558
264	35	18.7	1927	9	HSM803388	Human sapi	AL139251	Human sapi	AL139251	18.7	52935	9	AL139251
265	35	18.7	1949	9	AK055117	Human sapi	AL356535	Human sapi	AL356535	18.7	53067	9	AL356535
266	35	18.7	2138	9	HSM802532	Human sapi	AP001415	Human sapi	AP001415	18.7	53797	9	AP001415
267	35	18.7	2308	6	AX399200	Sequence	AC104538	Human sapi	AC104538	18.7	54423	9	AC104538
268	35	18.7	2320	9	AK096458	Human sapi	AC084353	Human sapi	AC084353	18.7	55488	9	AC084353
269	35	18.7	2335	6	AX399198	Sequence	AC073841	Human sapi	AC073841	18.7	55588	9	AC073841
270	35	18.7	2391	9	HSIL2REC	Human mRNA	AX329572	Sequence	AX329572	18.7	56093	6	AX329572
271	35	18.7	2391	9	HSM804140	Human sapi	AC000064	Human sapi	AC000064	18.7	56093	9	AC000064
272	35	18.7	2439	9	AK025301	Human sapi	AP002355	Human sapi	AP002355	18.7	56331	9	AP002355
273	35	18.7	2642	9	AF160477	Human sapi	AB065501	Human sapi	AB065501	18.7	56423	3	AB065501
274	35	18.7	2674	9	HSM805065	Human sapi	AC107969	Human sapi	AC107969	18.7	57662	2	AC107969
275	35	18.7	2744	9	AK027753	Human sapi	AL513314	Human sapi	AL513314	18.7	58205	9	AL513314
276	35	18.7	2841	9	AK091320	Human sapi	AC021303	Human sapi	AC021303	18.7	58546	2	AC021303
277	35	18.7	2870	9	AK056213	Human sapi	AC021303	Human sapi	AC021303	18.7	58546	2	AC021303
278	35	18.7	2995	9	HSM804013	Human sapi	AC009799	Human sapi	AC009799	18.7	59396	2	AC009799
279	35	18.7	3040	9	HSA7P2A19	Human sapi	AC074013	Human sapi	AC074013	18.7	59657	9	AC074013
280	35	18.7	3251	9	AK001638	Human sapi	AC005179	Human sapi	AC005179	18.7	59765	9	AC005179
281	35	18.7	3840	9	HSAPOC2G	Human sapi	AC103985	Human sapi	AC103985	18.7	60079	2	AC103985
282	35	18.7	4034	6	A98026	Sequence 1	AL139130	Human sapi	AL139130	18.7	61145	9	AL139130
283	35	18.7	4034	9	AF051355	Human sapi	AC090748	Human sapi	AC090748	18.7	61309	2	AC090748
284	35	18.7	4057	9	HUMAPOC2	Human sapi	AC108469	Human sapi	AC108469	18.7	62038	9	AC108469

358	35	18.7	63402	9	AP0000260	AP0000260 Homo sapi	C 431	35	18.7	86165	9	AC107048	Homo sapi
359	35	18.7	63701	9	AL353693	AL353693 Human DNA	C 432	35	18.7	86203	9	AC017116	Homo sapi
360	35	18.7	64071	2	AC084122	AC084122 Homo sapi	C 433	35	18.7	86226	2	AC013812	Homo sapi
361	35	18.7	64323	9	AL356976	AL356976 Human DNA	434	35	18.7	86829	9	AC011382	Homo sapi
362	35	18.7	64529	2	AC108449	AC108449 Homo sapi	435	35	18.7	86973	9	AC011394	Homo sapi
363	35	18.7	64597	2	AC131571	AC131571 Homo sapi	436	35	18.7	87201	9	AC007623	Homo sapi
364	35	18.7	64924	2	AC090131	AC090131 Homo sapi	437	35	18.7	88027	2	AL162401	Homo sapi
365	35	18.7	65541	2	AC021375	AC021375 Homo sapi	438	35	18.7	88251	2	AL126325	Homo sapi
366	35	18.7	65705	2	AC024394	AC024394 Homo sapi	C 439	35	18.7	88295	9	AC004612	Homo sapi
367	35	18.7	65755	2	AC011160	AC011160 Homo sapi	C 440	35	18.7	89211	9	AL669821	Human DNA
368	35	18.7	66092	2	AC125435	AC125435 Homo sapi	441	35	18.7	89290	9	CNS01DVY	Human chr
369	35	18.7	66188	9	AL391136	AL391136 Human DNA	442	35	18.7	89448	9	AC005067	Homo sapi
370	35	18.7	66565	9	AC092103	AC092103 Homo sapi	C 443	35	18.7	90169	9	HS398A12	Human DNA
371	35	18.7	66610	9	AC074386	AC074386 Homo sapi	444	35	18.7	90171	9	AC095040	Homo sapi
372	35	18.7	67335	9	HS436B3	AL449212 Homo sapi	C 445	35	18.7	90175	9	HS07858B6	Human DNA
373	35	18.7	67618	2	AC109634	AC109634 Homo sapi	C 446	35	18.7	90476	9	AC015910	Homo sapi
374	35	18.7	68764	9	AL389921	AL389921 Human DNA	C 447	35	18.7	90766	9	AL392166	Human DNA
375	35	18.7	68791	9	AC091961	AC091961 Homo sapi	448	35	18.7	90968	2	AC108722	Homo sapi
376	35	18.7	68808	2	AC022708	AC022708 Homo sapi	C 449	35	18.7	91071	2	AC022589	Homo sapi
377	35	18.7	68808	2	AC022708	AC022708 Homo sapi	C 450	35	18.7	91073	2	AC011426	Homo sapi
378	35	18.7	69492	2	AC111157	AC111157 Homo sapi	451	35	18.7	91076	9	AC073892	Homo sapi
379	35	18.7	69587	9	AF146367	AF146367 Homo sapi	C 452	35	18.7	91099	9	AL139045	Human DNA
380	35	18.7	69778	9	AC022411	AC022411 Homo sapi	C 453	35	18.7	91388	9	AC005994	Homo sapi
381	35	18.7	70589	2	AC087515	AC087515 Homo sapi	C 454	35	18.7	92644	2	AF186995	Homo sapi
382	35	18.7	70946	9	AL161614	AL161614 Human DNA	C 455	35	18.7	92932	9	AC091788	Homo sapi
383	35	18.7	70972	2	AC130332	AC130332 Homo sapi	456	35	18.7	93273	9	AC004084	Homo sapi
384	35	18.7	71382	9	AL590965	AL590965 Human DNA	C 457	35	18.7	93294	9	AL607144	Human DNA
385	35	18.7	71627	9	AC004851	AC004851 Homo sapi	458	35	18.7	93778	9	AC016999	Homo sapi
386	35	18.7	71736	9	AC022540	AC022540 Homo sapi	459	35	18.7	93911	2	HSAC000002	Homo sapi
387	35	18.7	71864	2	AC130372	AC130372 Homo sapi	C 460	35	18.7	93964	2	AL359456_5	Continuation (6 of
388	35	18.7	73568	2	AC025967	AC025967 Homo sapi	461	35	18.7	95484	2	AC015854	Homo sapi
389	35	18.7	73643	2	AC018773	AC018773 Homo sapi	462	35	18.7	96398	9	AL591367	Human DNA
390	35	18.7	74515	9	AL355482	AL355482 Human DNA	463	35	18.7	96625	9	HSAC000118	Human BAC
391	35	18.7	75525	9	AL391561	AL391561 Human DNA	C 464	35	18.7	96764	9	AL732325	Human DNA
392	35	18.7	75698	9	AP000228	AP000228 Homo sapi	C 465	35	18.7	96799	9	AC104647	Homo sapi
393	35	18.7	76241	9	HS07336M4	AL096775 Human DNA	C 466	35	18.7	97110	9	AL591521	Human DNA
394	35	18.7	76410	2	AC016093	AC016093 Homo sapi	467	35	18.7	97234	9	AL137859	Human DNA
395	35	18.7	76416	9	AC005370	AC005370 Homo sapi	C 468	35	18.7	97826	9	AL591647	Human DNA
396	35	18.7	76634	2	AC126335	AC126335 Homo sapi	C 469	35	18.7	97898	9	AL353613	Human DNA
397	35	18.7	76856	2	AC021526	AC021526 Homo sapi	470	35	18.7	97982	9	AP000687	Homo sapi
398	35	18.7	77164	9	AL133514	AL133514 Human DNA	471	35	18.7	98271	9	AL162590	Human DNA
399	35	18.7	77239	9	AL583844	AL583844 Human DNA	C 472	35	18.7	98360	9	AL049713	Human DNA
400	35	18.7	78200	9	AP001866	AP001866 Homo sapi	C 473	35	18.7	98433	9	AC097483	Homo sapi
401	35	18.7	78371	9	HSJ668P24	AL110114 Human DNA	474	35	18.7	98697	9	AC004854	Homo sapi
402	35	18.7	78386	2	AC015466	AC015466 Homo sapi	475	35	18.7	99003	2	AL390756	Homo sapi
403	35	18.7	78507	9	AC110743	AC110743 Homo sapi	476	35	18.7	99011	2	AC004937	Homo sapi
404	35	18.7	79237	9	HS0761M11	AL109624 Human DNA	477	35	18.7	99227	9	AC114737	Homo sapi
405	35	18.7	79516	9	AC004834	AC004834 Homo sapi	478	35	18.7	99342	9	HS201D17	Human DNA
406	35	18.7	80421	9	AL663100	AL663100 Human DNA	479	35	18.7	99411	9	AC005207	Homo sapi
407	35	18.7	80796	9	AC073136	AC073136 Homo sapi	C 480	35	18.7	99876	9	HS0790108	Human DNA
408	35	18.7	80796	9	AC073136	AC073136 Homo sapi	481	35	18.7	100000	9	AP000017	Homo sapi
409	35	18.7	80824	9	AL513480	AL513480 Human DNA	482	35	18.7	100000	9	AP000099	Homo sapi
410	35	18.7	81001	6	AX063464	AX063464 Sequence	C 483	35	18.7	100000	9	AP000140	Homo sapi
411	35	18.7	81001	6	AX063464	AX063464 Sequence	484	35	18.7	100000	9	AP000159	Homo sapi
412	35	18.7	81157	9	AC114963	AC114963 Homo sapi	485	35	18.7	100000	9	AP000175	Homo sapi
413	35	18.7	81364	2	AC021072_3	Continuation (4 of	C 486	35	18.7	100575	9	AL049762	Human DNA
414	35	18.7	81759	2	AC023211	AC023211 Homo sapi	C 487	35	18.7	100919	9	HS0781P6	Human DNA
415	35	18.7	81759	2	AC023211	AC023211 Homo sapi	488	35	18.7	100976	9	AL359378	Human DNA
416	35	18.7	82183	9	HSJ1037B9	AL117377 Human DNA	489	35	18.7	100998	9	HS1005F21	Human DNA
417	35	18.7	82517	9	HS341D10	Z97985 Human DNA s	490	35	18.7	101261	2	AC010628	Human DNA
418	35	18.7	82921	9	AL356747	AL356747 Human DNA	C 491	35	18.7	101269	9	AC005300	Homo sapi
419	35	18.7	83167	9	AL590423	AL590423 Human DNA	C 492	35	18.7	101584	9	CNS01DS5	BAC sequ
420	35	18.7	83175	9	AC110995	AC110995 Homo sapi	C 493	35	18.7	101744	9	AL512783	Human DNA
421	35	18.7	83684	9	AC105290	AC105290 Homo sapi	C 494	35	18.7	102259	2	AC015916	Homo sapi
422	35	18.7	83820	9	AL133264	AL133264 Human DNA	C 495	35	18.7	102282	9	AL158033	Human DNA
423	35	18.7	83888	9	AC008412	AC008412 Homo sapi	C 496	35	18.7	102326	9	AC087407	Homo sapi
424	35	18.7	84388	9	AL589984	AL589984 Human DNA	497	35	18.7	102500	2	AC096507	Homo sapi
425	35	18.7	85000	9	AC009772	AC009772 Homo sapi	498	35	18.7	102663	2	AC008399	Homo sapi
426	35	18.7	85132	9	AC092171	AC092171 Homo sapi	499	35	18.7	103347	9	AL136086	Human DNA
427	35	18.7	85195	9	AL136093	AL136093 Human DNA	C 500	35	18.7	103347	9	AC022027	Homo sapi
428	35	18.7	85378	2	AL356577	AL356577 Homo sapi	C 501	35	18.7	103574	9	HSAC002115	Human DNA
429	35	18.7	85565	9	AL136133	AL136133 Human DNA	C 502	35	18.7	103727	9	AL136360	Human DNA
430	35	18.7	85946	9	AC004240	AC004240 Homo sapi	C 503	35	18.7	103875	9	AL136223	Human DNA

504	35	18.7	103926	9	AC093164	AC093164 Homo sapi
505	35	18.7	104228	9	AL135917	AL135917 Human DNA
506	35	18.7	104357	9	AL139213	AL139213 Human DNA
507	35	18.7	104726	9	AC008087	AC008087 Homo sapi
508	35	18.7	104810	9	AC003012	AC003012 Human PAC
509	35	18.7	104844	9	HSJ105707	HSJ105707 Human DNA
510	35	18.7	105702	9	AC034203	AC034203 Homo sapi
511	35	18.7	106265	9	AL133294	AL133294 Human DNA
512	35	18.7	106363	9	AL166278	AL166278 Human DNA
513	35	18.7	106427	9	AL356417	AL356417 Human DNA
514	35	18.7	106499	9	AC023271	AC023271 Homo sapi
515	35	18.7	106773	9	AP003097	AP003097 Homo sapi
516	35	18.7	106945	9	AC024337	AC024337 Homo sapi
517	35	18.7	107325	9	AC009189	AC009189 Homo sapi
518	35	18.7	107418	9	HS551E13	HS551E13 Human DNA
519	35	18.7	107480	9	AL596094	AL596094 Human DNA
520	35	18.7	107487	9	AC011483	AC011483 Homo sapi
521	35	18.7	107567	9	AC011481	AC011481 Homo sapi
522	35	18.7	107967	9	AL353701	AL353701 Human DNA
523	35	18.7	108131	9	AL139321	AL139321 Human DNA
524	35	18.7	108765	2	AF216674	AF216674 Homo sapi
525	35	18.7	108969	9	AC004813	AC004813 Homo sapi
526	35	18.7	109056	2	AC074053	AC074053 Homo sapi
527	35	18.7	109609	9	AL138785	AL138785 Human DNA
528	35	18.7	110000	2	AC008576	AC008576 Homo sapi
529	35	18.7	110000	2	AC013391	AC013391 Homo sapi
530	35	18.7	110000	2	AC112773	AC112773 Homo sapi
531	35	18.7	110000	2	AC116301	AC116301 Homo sapi
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533	35	18.7	110000	2	AC050792	Continuation (3 of
534	35	18.7	110000	9	AC005079	Continuation (4 of
535	35	18.7	110000	9	AC005079	Continuation (4 of
536	35	18.7	110001	9	AC084880	AC084880 Homo sapi
537	35	18.7	110394	9	AC003086	AC003086 Homo sapi
538	35	18.7	111075	2	AC114337	AC114337 Homo sapi
539	35	18.7	111163	2	AL533214	AL533214 Homo sapi
540	35	18.7	111517	9	AC074366	AC074366 Homo sapi
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542	35	18.7	111998	9	AC011509	AC011509 Homo sapi
543	35	18.7	112187	9	AC096749	AC096749 Homo sapi
544	35	18.7	112291	9	AC107067	AC107067 Homo sapi
545	35	18.7	113656	9	AC112253	AC112253 Homo sapi
546	35	18.7	113853	9	AF196971	AF196971 Homo sapi
547	35	18.7	114148	9	AC112655	AC112655 Homo sapi
548	35	18.7	114298	9	HSJ543C6	HSJ543C6 Human DNA
549	35	18.7	114302	9	AL162413	AL162413 Human DNA
550	35	18.7	114411	9	HUAC002551	HUAC002551 Human Chr
551	35	18.7	114596	9	HS1063B2	HS1063B2 Human DNA
552	35	18.7	114624	9	AC099485	AC099485 Homo sapi
553	35	18.7	115027	2	AP001480	AP001480 Homo sapi
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556	35	18.7	115626	9	AC103792	AC103792 Homo sapi
557	35	18.7	115663	9	AC093029	AC093029 Homo sapi
558	35	18.7	115793	9	AC025166	AC025166 Homo sapi
559	35	18.7	116106	2	AL162611	AL162611 Homo sapi
560	35	18.7	116370	9	HS569M23	HS569M23 Human DNA
561	35	18.7	116430	9	AL359513	AL359513 Human DNA
562	35	18.7	116671	9	AC087264	AC087264 Pan trogl
563	35	18.7	116879	9	AC106854	AC106854 Homo sapi
564	35	18.7	116911	9	AC093019	AC093019 Homo sapi
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569	35	18.7	117962	9	AF312032	AF312032 Homo sapi
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572	35	18.7	118234	9	AL355476	AL355476 Human DNA
573	35	18.7	118439	9	AL135905	AL135905 Human DNA
574	35	18.7	118582	2	AC115989	AC115989 Homo sapi
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582	35	18.7	119884	9	AL139814	AL139814 Human DNA
583	35	18.7	119951	2	AC025267	AC025267 Homo sapi
584	35	18.7	120538	9	AC004815	AC004815 Homo sapi
585	35	18.7	120766	9	AC004150	AC004150 Homo sapi
586	35	18.7	121129	9	AL357315	AL357315 Human DNA
587	35	18.7	121348	9	AC106874	AC106874 Homo sapi
588	35	18.7	122073	2	AC090831	AC090831 Homo sapi
589	35	18.7	122289	9	AL389925	AL389925 Human DNA
590	35	18.7	122568	9	AF196972	AF196972 Homo sapi
591	35	18.7	122912	9	AC073182	AC073182 Homo sapi
592	35	18.7	123203	9	AC003036	AC003036 Homo sapi
593	35	18.7	123587	9	AC083807	AC083807 Homo sapi
594	35	18.7	123817	9	AL713980	AL713980 Human DNA
595	35	18.7	124000	2	AC004060	AC004060 Homo sapi
596	35	18.7	124028	9	AC022417	AC022417 Homo sapi
597	35	18.7	124829	9	AC097109	AC097109 Homo sapi
598	35	18.7	125151	9	AC093821	AC093821 Homo sapi
599	35	18.7	125479	9	HSJ244F24	HSJ244F24 Human DNA
600	35	18.7	125495	9	AL359914	AL359914 Human DNA
601	35	18.7	125508	9	AC006345	AC006345 Homo sapi
602	35	18.7	125630	9	HSU91319	HSU91319 Human chrom
603	35	18.7	125644	9	AP004293	AP004293 Homo sapi
604	35	18.7	125798	2	AL390248	AL390248 Human DNA
605	35	18.7	126736	2	AC044788	AC044788 Homo sapi
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607	35	18.7	127199	9	AC084262	AC084262 Homo sapi
608	35	18.7	127321	9	AC020903	AC020903 Homo sapi
609	35	18.7	127408	9	AC098828	AC098828 Homo sapi
610	35	18.7	127805	9	AC130271	AC130271 Homo sapi
611	35	18.7	127957	9	AC006122	AC006122 Homo sapi
612	35	18.7	128615	9	AL591051	AL591051 Human DNA
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615	35	18.7	129517	2	AC016400	AC016400 Homo sapi
616	35	18.7	129559	9	AL731563	AL731563 Human DNA
617	35	18.7	129950	9	HS739H11	HS739H11 Human DNA
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622	35	18.7	130607	9	AC004875	AC004875 Homo sapi
623	35	18.7	130647	9	AL157385	AL157385 Human DNA
624	35	18.7	130701	2	AC099889	AC099889 Homo sapi
625	35	18.7	130755	9	AC004253	AC004253 Homo sapi
626	35	18.7	130986	2	AC120597	AC120597 Homo sapi
627	35	18.7	131457	9	AL356600	AL356600 Human DNA
628	35	18.7	131841	9	HSJ881L22	HSJ881L22 Human DNA
629	35	18.7	132281	2	AC095594	AC095594 Homo sapi
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631	35	18.7	133401	2	AC079257	AC079257 Homo sapi
632	35	18.7	133541	2	AC027169	AC027169 Homo sapi
633	35	18.7	133641	2	AC097005	AC097005 Pan trogl
634	35	18.7	133893	9	AC005005	AC005005 Homo sapi
635	35	18.7	133925	9	AC011444	AC011444 Homo sapi
636	35	18.7	134010	9	AL353579	AL353579 Human DNA
637	35	18.7	134059	2	AC016284	AC016284 Homo sapi
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642	35	18.7	134339	9	AC114501	AC114501 Homo sapi
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644	35	18.7	135062	9	AC026691	AC026691 Homo sapi
645	35	18.7	135405	9	AC000025	AC000025 Homo sapi
646	35	18.7	135672	9	HSAC000113	HSAC000113 Human PAC
647	35	18.7	135693	9	HSJ1167H4	HSJ1167H4 Human DNA
648	35	18.7	135837	9	AC004837	AC004837 Homo sapi
649	35	18.7	136124	9	HS3394P21	HS3394P21 Homo sapi

650	35	18.7	136131	9	AC000360	AC000360 Homo sapi	723	35	18.7	146641	2	AC011140	AC011140 Homo sapi
651	35	18.7	136159	9	AC097475	AC097475 Homo sapi	c 724	35	18.7	146746	9	HS50J22	Z84484 Human DNA s
652	35	18.7	136188	9	AL096819	AL096819 Human DNA	c 725	35	18.7	147109	9	AL591043	AL591043 Human DNA
653	35	18.7	136932	9	AC068035	AC068035 Homo sapi	c 726	35	18.7	147167	9	HS2705	AL033529 Human DNA
654	35	18.7	137101	9	AC016692	AC016692 Homo sapi	c 727	35	18.7	147172	2	AC008688	AC008688 Homo sapi
655	35	18.7	137247	2	AC015865	AC015865 Homo sapi	c 728	35	18.7	147246	2	AC023196	AC023196 Homo sapi
656	35	18.7	137247	9	AC064853	AC064853 Homo sapi	c 729	35	18.7	147246	2	AC023196	AC023196 Homo sapi
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659	35	18.7	137469	2	AC013370	AC013370 Homo sapi	c 732	35	18.7	147418	9	AC023855	AC023855 Homo sapi
660	35	18.7	138006	9	AL390074	AL390074 Human DNA	c 733	35	18.7	147458	9	AL357832	AL357832 Homo sapi
661	35	18.7	138021	9	AC090820	AC090820 Homo sapi	c 734	35	18.7	147520	9	AC117392	AC117392 Homo sapi
662	35	18.7	138215	2	AC023523	AC023523 Homo sapi	c 735	35	18.7	147520	2	AC036186	AC036186 Homo sapi
663	35	18.7	138814	30	AC068997	AC068997 Homo sapi	c 736	35	18.7	147924	2	AC036186	AC036186 Homo sapi
664	35	18.7	138928	9	AC064847	AC064847 Homo sapi	c 737	35	18.7	148049	9	HS300188	AL455884 Human chr
665	35	18.7	139086	9	AC025456	AC025456 Homo sapi	c 738	35	18.7	148166	9	AL353625	AL353625 Human DNA
666	35	18.7	139130	9	AC091504	AC091504 Homo sapi	c 739	35	18.7	148250	9	AC090510	AC090510 Homo sapi
667	35	18.7	139144	2	AC124863	AC124863 Homo sapi	c 740	35	18.7	148295	9	AL133396	AL133396 Human DNA
668	35	18.7	139189	2	AC118553	AC118553 Homo sapi	c 741	35	18.7	148497	9	AL133396	AL133396 Human DNA
669	35	18.7	139476	9	AC010377	AC010377 Homo sapi	c 742	35	18.7	148598	9	HSBA51C14	AL121875 Human DNA
670	35	18.7	139480	9	HUAC002331	AC002331 Homo sapi	c 743	35	18.7	148750	9	AL596225	AL596225 Human DNA
671	35	18.7	139488	9	AC003043	AC003043 Homo sapi	c 744	35	18.7	148824	2	AC025640	AC025640 Homo sapi
672	35	18.7	139737	9	HS228H13	AL031985 Human DNA	c 745	35	18.7	148897	2	AL139034	AL139034 Human DNA
673	35	18.7	139996	9	AL161799	AL161799 Human DNA	c 746	35	18.7	149002	2	AL445484	AL445484 Homo sapi
674	35	18.7	140330	9	AC026777	AC026777 Homo sapi	c 747	35	18.7	149194	9	AC007566	AC007566 Homo sapi
675	35	18.7	140425	9	AC005479	AC005479 Homo sapi	c 748	35	18.7	149246	9	AC066580	AC066580 Homo sapi
676	35	18.7	140783	9	AC027373	AC027373 Homo sapi	c 749	35	18.7	149271	9	AC022144	AC022144 Homo sapi
677	35	18.7	140856	9	AC002430	AC002430 Human BAC	c 750	35	18.7	149308	9	AC005527	AC005527 Homo sapi
678	35	18.7	140966	9	AC023058	AC023058 Homo sapi	c 751	35	18.7	149313	2	AC023548	AC023548 Homo sapi
679	35	18.7	141056	9	AL354836	AL354836 Human DNA	c 752	35	18.7	149331	9	AC091554	AC091554 Homo sapi
680	35	18.7	141266	9	AC004671	AC004671 Homo sapi	c 753	35	18.7	149445	9	AC013264	AC013264 Homo sapi
681	35	18.7	141428	9	AL139415	AL139415 Human DNA	c 754	35	18.7	149605	9	AC005522	AC005522 Homo sapi
682	35	18.7	141442	9	AC108471	AC108471 Homo sapi	c 755	35	18.7	149745	9	AP000648	AP000648 Homo sapi
683	35	18.7	142037	9	AC025171	AC025171 Homo sapi	c 756	35	18.7	149762	9	AC011270	AC011270 Homo sapi
684	35	18.7	142105	9	AC012374	AC012374 Homo sapi	c 757	35	18.7	149866	9	AC025627	AC025627 Homo sapi
685	35	18.7	142185	2	AC022656	AC022656 Homo sapi	c 758	35	18.7	149977	30	AL355313	AL355313 Human DNA
686	35	18.7	142276	9	AC109454	AC109454 Homo sapi	c 759	35	18.7	150107	2	AC027582	AC027582 Homo sapi
687	35	18.7	142640	9	AC006399	AC006399 Homo sapi	c 760	35	18.7	150114	2	AC074004	AC074004 Homo sapi
688	35	18.7	142665	9	HS202121	AL033590 Human DNA	c 761	35	18.7	150192	9	AC008686	AC008686 Homo sapi
689	35	18.7	142667	9	AC125387	AC125387 Homo sapi	c 762	35	18.7	150199	9	AC087568	AC087568 Pan trogl
690	35	18.7	142762	2	AL391599	AL391599 Homo sapi	c 763	35	18.7	150541	9	AL136305	AL136305 Human DNA
691	35	18.7	142875	2	AC005805	AC005805 Homo sapi	c 764	35	18.7	150541	9	AL590559	AL590559 Human DNA
692	35	18.7	142978	9	AC097717	AC097717 Homo sapi	c 765	35	18.7	150651	9	CNS05TEM	AL592323 Human chr
693	35	18.7	142979	9	AC000029	AC000029 Homo sapi	c 766	35	18.7	150662	9	AL392106	AL392106 Human DNA
694	35	18.7	143084	9	AC034200	AC034200 Homo sapi	c 767	35	18.7	150771	9	AC024402	AC024402 Homo sapi
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696	35	18.7	143176	2	AC011332	AC011332 Homo sapi	c 769	35	18.7	150893	2	AC031989	AC031989 Homo sapi
697	35	18.7	143444	9	AC007541	AC007541 Homo sapi	c 770	35	18.7	151517	2	AC026636	AC026636 Homo sapi
698	35	18.7	143563	9	HS555C23	AL032821 Human DNA	c 771	35	18.7	151526	9	AL390294	AL390294 Human DNA
699	35	18.7	143585	9	AF176681	AF176681 Homo sapi	c 772	35	18.7	151559	9	AC087441	AC087441 Homo sapi
700	35	18.7	143618	9	AL137856	AL137856 Human DNA	c 773	35	18.7	151606	2	AC096995	AC096995 Homo sapi
701	35	18.7	143673	2	AC087720	AC087720 Homo sapi	c 774	35	18.7	151736	2	AC097489	AC097489 Homo sapi
702	35	18.7	143899	2	AC013606	AC013606 Homo sapi	c 775	35	18.7	152039	9	AP000830	AP000830 Homo sapi
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705	35	18.7	144555	2	AC037451	AC037451 Homo sapi	c 778	35	18.7	152322	2	AF186190	AF186190 Homo sapi
706	35	18.7	144724	2	AC021573	AC021573 Homo sapi	c 779	35	18.7	152405	9	AC104701	AC104701 Homo sapi
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708	35	18.7	145097	2	AC018888	AC018888 Homo sapi	c 781	35	18.7	152659	2	AC129985	AC129985 Homo sapi
709	35	18.7	145253	9	AC006329	AC006329 Homo sapi	c 782	35	18.7	152696	2	AC004057	AC004057 Homo sapi
710	35	18.7	145264	9	AC107939	AC107939 Homo sapi	c 783	35	18.7	152798	9	AC009066	AC009066 Homo sapi
711	35	18.7	145264	9	AP003086	AP003086 Homo sapi	c 784	35	18.7	152815	2	AC007157	AC007157 Homo sapi
712	35	18.7	145423	9	AL356862	AL356862 Human DNA	c 785	35	18.7	152937	9	AC090711	AC090711 Homo sapi
713	35	18.7	145481	9	AC012621	AC012621 Homo sapi	c 786	35	18.7	153064	2	AC017030	AC017030 Homo sapi
714	35	18.7	145535	9	AC087110	AC087110 Homo sapi	c 787	35	18.7	153148	2	AC026110	AC026110 Homo sapi
715	35	18.7	145544	9	AL391068	AL391068 Homo sapi	c 788	35	18.7	153190	9	AC023510	AC023510 Homo sapi
716	35	18.7	145673	2	AC068675	AC068675 Homo sapi	c 789	35	18.7	153241	9	HS119F19	AL132656 Human DNA
717	35	18.7	145870	2	CNS01RGD	AL157915 Human chr	c 790	35	18.7	153370	9	HS11B22	Z98200 Human DNA s
718	35	18.7	146002	9	AC005883	AC005883 Homo sapi	c 791	35	18.7	153382	2	AC110719	AC110719 Homo sapi
719	35	18.7	146224	9	AL589787	AL589787 Human DNA	c 792	35	18.7	153748	2	AC009694	AC009694 Homo sapi
720	35	18.7	146287	9	AC004953	AC004953 Homo sapi	c 793	35	18.7	153852	2	AC034114	AC034114 Homo sapi
721	35	18.7	146407	9	AC010489	AC010489 Homo sapi	c 794	35	18.7	153865	2	AC011256	AC011256 Homo sapi
722	35	18.7	146437	9	AC012468	AC012468 Homo sapi	c 795	35	18.7	153882	2	AL356292	AL356292 Human DNA
723	35	18.7	146578	9	AC012468	AC012468 Homo sapi							

796	35	18.7	154195	2	AC013641	AC013641 Homo sapi	c	869	35	18.7	158311	2	AC009589	Homo sapi
797	35	18.7	154280	2	AC037480	AC037480 Homo sapi	c	870	35	18.7	158414	9	AC005940	Homo sapi
798	35	18.7	154288	9	AL513164	AL513164 Human DNA	c	871	35	18.7	158470	2	AC009026	Homo sapi
799	35	18.7	154592	9	AL591215	AL591215 Human DNA	c	872	35	18.7	158626	9	AC009033	Homo sapi
800	35	18.7	154681	2	AC022000	AC022000 Homo sapi	c	873	35	18.7	158698	2	AC036181	Homo sapi
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c 980	35	18.7	165915	2	AC023104	Homo sapi
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REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

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100.0%;

Score 187;

DB 9;

Length 5492;

100.0%;

Pred. No. 3.3e-92;

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Mismatches

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Indels

0;

Gaps

0;

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RESULT 2

AF123653

LOCUS

AF123653

9108 bp

DNA

linear

PRI 07-APR-1999

DEFINITION

Homo sapiens FEZ1 (FEZ1) gene, complete cds.

ACCESSION

AF123653

VERSION

AF123653.1

GI:4572463

KEYWORDS

Homo sapiens.

SOURCE

Homo sapiens.

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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 9108)
          Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
          Mori, M., Fidanza, V., Alder, H. and Croce, C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
JOURNAL and its expression is altered in multiple human tumors
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
PUBMED 99199287
REFERENCE 10097140
          2 (bases 1 to 9108)
          Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
          Mori, M., Fidanza, V., Alder, H. and Croce, C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
          Institute, 2335 10th street, Philadelphia, PA 19107, USA
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   ELKPLGCSGALSGRNMSLPTHTSSSYQLDPLVTPVPTSRFGSAHNTQGV
   LQSNMMLKALFSKSGSLKSHKADKGPSCVRSPISTDEGSIQLEOKLLEKRG
   LQKQSFEBELASSLAYBERPRRCRDELEGPEPKGNLKOAKSOQRAOVHLQ
   VLQOKKROLROELSLMEQDLLETKLRSYERKTSFGPALEETQWECVKSGET
   LLQOKLESQTEYNKASEILGLKQKLDTRGKLEGLRLTQLEGLRPLKGLLEVC
   ENLQKKNKAEELLREKVNLEQLQELRAQALARDMGPPTPEDVPALQRELERL
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BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6999 ATGATACATGCTACTGACGCTCATCTCTGGGCTCAAGCATCTCTGCTCAGCC 7058
   |||||

Qy 61 TTCAACTAGTGGGACTACAGTGGCGCCGACCGTGGCTGCTGCTTTCATTTT 120
   |||||
Db 7059 TTCAACTAGTGGGACTACAGTGGCGCCGACCGTGGCTGCTGCTTTCATTTT 7118
   |||||

Qy 121 TGTAGGACGGGTCTCGTTTGTGTGCAAGTGGTCTCAAACTTGTGGCTCAAGCAA 180
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Db 7119 TGTAGGACGGGTCTCGTTTGTGTGCAAGTGGTCTCAAACTTGTGGCTCAAGCAA 7178
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Qy 181 TCCACCT 187
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Db 7179 TCCACCT 7185

RESULT 3
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LOCUS AC025853 173264 bp DNA linear HTG 17-JUN-2002
DEFINITION Homo sapiens chromosome 8 clone RP11-353K12 map 8, *** SEQUENCING
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IN PROGRESS ***, 3 unordered pieces.
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VERSION GI:21431202
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 173264)
          Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 8, clone RP11-353K12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173264)
          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
          Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,
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          Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
          Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
          Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
          Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
          Young, G., Zainoun, J., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 173264)
          Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
          Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
          Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
          Charaz, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
          Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
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          Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
          Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
          Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
          Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
          Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,
          Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
          Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
          Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
          O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
          Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
          Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
          Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
          Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
          Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
          Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
          Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jun 17, 2002 this sequence version replaced gi:21321864.
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
          ----- Genome Center
          Center: Whitehead Institute/ MIT Center for Genome Research
          Center code: WIBR
          Web site: http://www-seq.wi.mit.edu
          Contact: sequence_submissions@genome.wi.mit.edu
          ----- Project Information
```

```

Center project name: L7454
Center clone name: 353_K_12
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
-----
1 39461: contig of 39461 bp in length
* 39462 39561: gap of 100 bp
* 39562 108347: contig of 68786 bp in length
* 108348 108447: gap of 100 bp
* 108448 173264: contig of 64817 bp in length.
-----
Location/Qualifiers
1. 173264
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"
/clones="RP11-353K12"
/clone_lib="RPCI-11 Human Male BAC"
39435 a 38861 c 39235 g 47493 t 317 others
-----
BASE COUNT 47355 a 38861 c 39235 g 47493 t
ORIGIN
Query Match 100.0%; Score 187; DB 2; Length 173264;
Best Local Similarity 100.0%; Pred. NO. 2.2e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGATCAGTCTACTGCGCTCATACTCTGGCTCAGCAATCTCTGCTCAGCC 60
Db 29244 ATGATCAGTCTACTGCGCTCATACTCTGGCTCAGCAATCTCTGCTCAGCC 29303
Qy 61 TTCCAACCTAGTGGGACTACAGTGGCGGCACCGTGGCTGGCTAACTTTTCATTTTTT 120
Db 29304 TTCCAACCTAGTGGGACTACAGTGGCGGCACCGTGGCTGGCTAACTTTTCATTTTTT 29363
Qy 121 TGTAGGACGGGTCTCGTTTGTGGCAAGCTGGTCTCAAACTTGGCTCAGCAAA 180
Db 29364 TGTAGGACGGGTCTCGTTTGTGGCAAGCTGGTCTCAAACTTGGCTCAGCAAA 29423
Qy 181 TCCACCT 187
Db 29424 TCCACCT 29430
-----
RESULT 4
AC009449/c
LOCUS Homo sapiens chromosome 17 clone CTD-2291H15 map 17, WORKING DRAFT
DEFINITION AC009449
SEQUENCE, 5 unordered pieces.
AC009449
VERSION AC009449.5 GI:15291073
KEYWORDS HTG; HTGS_P3ASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105051)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeRellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kann, L.,
Karatas, A., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P.,
-----
TITLE JOURNAL
COMMENT
-----
Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,
Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyi, J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Testaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
Direct Submission
Submitted (22-AUG-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 26, 2001 this sequence version replaced gi:14626922.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L775
Center clone name: 2291_H_15
-----
Summary Statistics
Sequencing vector: M13; M77815; 19% of reads
Sequencing vector: Plasmid; n/a; 81% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 102893 bases at least Q40
Consensus quality: 103343 bases at least Q30
Consensus quality: 103573 bases at least Q20
Insert size: 104651; sum-of-contigs
Quality coverage: 16.2 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1 617: contig of 617 bp in length
* 618 717: gap of 100 bp
* 718 1791: contig of 1074 bp in length
* 1792 1891: gap of 100 bp
* 1892 11154: contig of 9263 bp in length
* 11155 11254: gap of 100 bp
* 11255 47275: contig of 36021 bp in length
* 47276 47375: gap of 100 bp
* 47376 105051: contig of 57676 bp in length.
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Location/Qualifiers
1. 105051
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="CTD-2291H15"
/clone_lib="CITD Human BAC"
1. 617
/notes="assembly_fragment"
718. 1791
/notes="assembly_fragment"
1892. 11154
/notes="assembly_fragment"
11255. 47275
/notes="assembly_fragment"
47376. 105051
/notes="assembly_fragment"
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BASE COUNT 29638 a 22552 c 21751 g 30707 t
ORIGIN
Query Match 22.5%; Score 42; DB 2; Length 105051;

```

Paro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severi,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (11-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 11, 2002 this sequence version replaced gi:14994158.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu

Project Information
Center project name: L2618
Center clone name: 346_A_8

Only the last 147.8 kb of this clone are being submitted.
The remainder overlaps accession number AC105129 [WICGR project L22971].

Location/Qualifiers
1. .147760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosomes="15"
/map="15"
/clone="RP11-346A8"
/clone_lib="RP11-11 Human Male BAC"
572. .572
/rpt_family="MIR"
697. .1138
/rpt_family="LIMB6"
1143. .1340
/rpt_family="AluJo"
1357. .1665
/rpt_family="AluSg"
1666. .1699
/rpt_family="L2"
1771. .2026
/rpt_family="AluJo"
2049. .2069
/rpt_family="(TC)n"
2072. .2096
/rpt_family="(CA)n"
2154. .2185
/rpt_family="(TC)n"
complement(2458. .2533)
/rpt_family="MIR3"
2943. .3081
/rpt_family="MIR3"
complement(3473. .3526)
/rpt_family="L2"
3584. .3758
/rpt_family="MIR"
complement(3767. .4021)
/rpt_family="AluSx"

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repeat_region complement(4075..4115)
repeat_region /rpt_family="AluSx"
repeat_region complement(4737..4774)
repeat_region /rpt_family="MIR"
repeat_region 5062..5168
repeat_region /rpt_family="MIR"
repeat_region complement(5262..5563)
repeat_region /rpt_family="AluY"
repeat_region complement(6726..7022)
repeat_region /rpt_family="AluSx"
repeat_region 7049..7166
repeat_region /rpt_family="L2"
repeat_region 7215..7332
repeat_region /rpt_family="MIR"
repeat_region complement(7387..7530)
repeat_region /rpt_family="L3"
repeat_region 8050..8168
repeat_region /rpt_family="MIR3"
repeat_region complement(8169..8480)
repeat_region /rpt_family="AluJo"
repeat_region 8481..8537
repeat_region /rpt_family="MIR3"
repeat_region complement(9062..9373)
repeat_region /rpt_family="AluSx"
repeat_region 9383..9601
repeat_region /rpt_family="L2"
repeat_region 9755..10149
repeat_region /rpt_family="L2"
repeat_region 11647..11688
repeat_region /rpt_family="(CA)n"
repeat_region 11960..11991
repeat_region /rpt_family="CC-rich"
repeat_region 12008..12028
repeat_region /rpt_family="(CCG)n"
repeat_region 12084..12161
repeat_region /rpt_family="G-rich"
repeat_region complement(12722..12877)
repeat_region /rpt_family="MIR3"
repeat_region 13023..13086
repeat_region /rpt_family="L3"
repeat_region 13212..13282
repeat_region /rpt_family="L2"
repeat_region 13283..13537
repeat_region /rpt_family="L2"
repeat_region 13538..13667
repeat_region /rpt_family="FLAM_C"
repeat_region 13668..14227
repeat_region complement(14228..14513)
repeat_region /rpt_family="AluSx"
repeat_region 14514..14525
repeat_region /rpt_family="L2"
repeat_region complement(14526..14835)
repeat_region /rpt_family="AluSx"
repeat_region 14836..14999
repeat_region /rpt_family="L2"
repeat_region complement(15356..15637)
repeat_region /rpt_family="L2"
repeat_region 15859..15991
repeat_region /rpt_family="MIR3"
repeat_region 16064..16363
repeat_region /rpt_family="AluSx"
repeat_region 16597..16909
repeat_region /rpt_family="Aluub"

Query Match 22.5%; Score 42; DB 9; Length 147760;
Best Local Similarity 100.0%; Pred.No.2.2e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 47 CTCCTGCTCAGCCCTTCCAACTAGCTGGGACTACAGGTGCGC 88
DB 61532 CTCCTGCTCAGCCCTTCCAACTAGCTGGGACTACAGGTGCGC 61573
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RESULT 6
HS97K10 156197 bp DNA linear PRI 23-NOV-1999
LOCUS Human DNA sequence from cosmid 97K10, between markers DXS6791 and
DEFINITION DXS8038 on chromosome X contains STSS and CpG island.
ACCESSION Z81365.1 GI:16555588
VERSION 281365
KEYWORDS CpG island; X.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 156197)
Wray, P.
Direct Submission
TITLE Submitted (30-OCT-1996) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 1RQ, UK. E-mail enquires: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT IMPORTANT: This sequence is the entire insert of clone 97K10. The
true left end of clone 97K10 is at 1 in this sequence. The true
right end of clone 97K10 is at 156197.
97K10 is from the Human PAC library.
FEATURES
source
1..156197
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="X"
/clone="RP1-97K10"
/clone_lib="RPC1-1"
548..673
/note="MIR repeat: matches 21..147 of consensus"
2971..5179
/notes="Putative CpG island"
5673..5771
/notes="MIR repeat: matches 141..34 of consensus"
6281..6384
/notes="MIR repeat: matches 92..190 of consensus"
8048..8192
/notes="MIR repeat: matches 14..143 of consensus"
9008..9304
/notes="AluSx repeat: matches 298..1 of consensus"
9481..9792
/note="AluJb repeat: matches 11..302 of consensus"
9962..10099
/note="MIR repeat: matches 118..259 of consensus"
10787..10881
/notes="MIR repeat: matches 52..145 of consensus"
11201..11509
/note="AluSx repeat: matches 1..299 of consensus"
13071..13181
/note="MIR repeat: matches 193..80 of consensus"
14453..14712
/note="AluJb repeat: matches 14..288 of consensus"
15654..15898
/note="MIR repeat: matches 20..262 of consensus"
16041..16342
/note="AluJo repeat: matches 301..2 of consensus"
16343..16477
/partial
/note="AluJb repeat: matches 136..2 of consensus"
16775..17028
/note="L1ME3A repeat: matches 905..641 of consensus"
17018..17320
/note="MLTIE repeat: matches 568..256 of consensus"
17312..17550
/note="MLTID repeat: matches 309..82 of consensus"
17652..17887
/note="L1ME3 repeat: matches 660..412 of consensus"
18334..18480
/note="MIR2 repeat: matches 1..143 of consensus"
18930..19074


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repeat_region /note="MER3 repeat: matches 1. .148 of consensus"
repeat_region 19076. .19381
repeat_region /note="AluSg repeat: matches 301. .2 of consensus"
repeat_region 19409. .19487
repeat_region /note="MER3 repeat: matches 131. .209 of consensus"
repeat_region 20782. .20864
repeat_region /note="MIR repeat: matches 65. .152 of consensus"
repeat_region 21630. .21931
repeat_region /note="AluSx repeat: matches 302. .1 of consensus"
repeat_region 22185. .22605
repeat_region /note="MSTA repeat: matches 1. .426 of consensus"
repeat_region 23148. .23286
repeat_region /note="MIR repeat: matches 217. .65 of consensus"
repeat_region 23291. .23709
repeat_region /note="MSTA repeat: matches 426. .1 of consensus"
repeat_region 24130. .24419
repeat_region /note="AluSg repeat: matches 293. .1 of consensus"
repeat_region 25082. .25350
repeat_region /note="AluSx repeat: matches 293. .5 of consensus"
repeat_region 25366. .25649
repeat_region /note="AluJo repeat: matches 290. .1 of consensus"
repeat_region 26058. .26093
repeat_region /note="18 copies of 2 mer 100 % conserved"
repeat_region 26631. .27157
repeat_region /note="L1PA12 repeat: matches 369. .902 of consensus"
repeat_region 27183. .27475
repeat_region /note="AluJo repeat: matches 1. .301 of consensus"
repeat_region 27483. .27746
repeat_region /partial
repeat_region /note="AluY repeat: matches 301. .38 of consensus"
repeat_region 30360. .30410
repeat_region /note="MIR2 repeat: matches 94. .144 of consensus"
repeat_region 32055. .32239
repeat_region /note="MIR repeat: matches 61. .262 of consensus"
repeat_region 32571. .32781
repeat_region /note="MSTA repeat: matches 216. .425 of consensus"
repeat_region 33063. .33322
repeat_region /note="MER42B repeat: matches 1301. .1031 of consensus"
repeat_region 33684. .33746
repeat_region /note="MIR repeat: matches 81. .142 of consensus"
repeat_region 33764. .33879
repeat_region /note="MER5A repeat: matches 18. .140 of consensus"
repeat_region 34848. .35013
repeat_region /note="FRAM repeat: matches 1. .165 of consensus"
repeat_region 35846. .36152
repeat_region /note="AluSx repeat: matches 1. .291 of consensus"
repeat_region 36247. .36428
repeat_region /note="MIR repeat: matches 17. .214 of consensus"
repeat_region 37815. .38119
repeat_region /note="AluJo repeat: matches 1. .302 of consensus"
repeat_region 39991. .40270
repeat_region /note="AluJb repeat: matches 290. .1 of consensus"
repeat_region 40862. .41163
repeat_region /note="AluSx repeat: matches 302. .1 of consensus"
repeat_region 42060. .42344
repeat_region /partial
repeat_region /note="AluSx repeat: matches 1. .282 of consensus"
repeat_region 43932. .44218
repeat_region /note="L1PA1 repeat: matches 762. .1051 of consensus"
repeat_region 47698. .47929
repeat_region /partial
repeat_region /note="AluJb repeat: matches 1. .229 of consensus"
repeat_region 47940. .48038
repeat_region /partial
repeat_region /note="AluJo repeat: matches 200. .294 of consensus"
repeat_region 49174. .49246
repeat_region /note="L1PA2 repeat: matches 954. .885 of consensus"
repeat_region 49266. .49326
repeat_region /partial
repeat_region /note="AluSx/g repeat: matches 302. .240 of consensus"
repeat_region 49339. .49545
repeat_region /partial
repeat_region /note="AluJb repeat: matches 98. .300 of consensus"
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repeat_region 50987. .51276
repeat_region /note="AluSg repeat: matches 1. .300 of consensus"
repeat_region 51955. .52996
repeat_region /note="MLT2_internal repeat: matches 4017. .5042 of
consensus"
repeat_region 53263. .53562
repeat_region /note="AluSx repeat: matches 1. .298 of consensus"
repeat_region 53772. .54167
repeat_region /note="MSTA repeat: matches 1. .426 of consensus"
repeat_region 54416. .54785
repeat_region /note="MLT1D repeat: matches 505. .119 of consensus"
repeat_region 54829. .54949
repeat_region /partial
repeat_region /note="AluSp repeat: matches 300. .177 of consensus"
repeat_region 54994. .55100
repeat_region /note="MLT1D repeat: matches 107. .1 of consensus"
repeat_region 55707. .56029
repeat_region /note="MER2 repeat: matches 345. .1 of consensus"
repeat_region 56258. .61666
repeat_region /note="L1 repeat: matches 13. .5390 of consensus"
repeat_region 61517. .62409
repeat_region /note="L1PA2 repeat: matches 1. .893 of consensus"
repeat_region 64264. .64323
repeat_region /note="30 copies of 2 mer 83 % conserved"
repeat_region 64850. .65196
repeat_region /note="MLT2FA repeat: matches 1. .358 of consensus"
repeat_region 65197. .65251
repeat_region /note="MLT2CA repeat: matches 503. .449 of consensus"
repeat_region 65197. .65237
repeat_region /note="MLT2CB repeat: matches 501. .461 of consensus"
repeat_region 65300. .65629
repeat_region /note="MLT2CB repeat: matches 462. .145 of consensus"
repeat_region 65635. .65932
repeat_region /note="AluSx repeat: matches 298. .1 of consensus"
repeat_region 65935. .66064
repeat_region /note="MLT2D repeat: matches 140. .1 of consensus"
repeat_region 66065. .66180
repeat_region /note="MLT2FB repeat: matches 318. .414 of consensus"
repeat_region 66931. .67287
repeat_region /note="MER39 repeat: matches 80. .460 of consensus"
repeat_region 68857. .68940
repeat_region /note="MLT1D repeat: matches 6. .91 of consensus"
repeat_region 68956. .69258
repeat_region /note="AluJo repeat: matches 1. .293 of consensus"
repeat_region 69278. .69653
repeat_region /note="MLT1D repeat: matches 117. .505 of consensus"
repeat_region 71353. .71521
repeat_region /note="MER5A repeat: matches 188. .1 of consensus"
repeat_region 71538. .71669
repeat_region /partial
repeat_region /note="AluJo repeat: matches 49. .171 of consensus"
repeat_region 71697. .71820
repeat_region /partial
repeat_region /note="AluJo repeat: matches 174. .300 of consensus"
repeat_region 78248. .78379
repeat_region /note="MIR2 repeat: matches 146. .6 of consensus"
repeat_region 78449. .78752
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Query Match 22.5%; Score 42; DB 9; Length 156197;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AGCTCACTGCAGCTCATACTCTCTGGCTCAAGCAATCTCTCC 50
|||||
Db 34942 AGCTCACTGCAGCTCATACTCTCTGGCTCAAGCAATCTCTCC 34901

RESULT 7

AC105129/c AC105129 198295 bp DNA linear PRI 26-APR-2002
LOCUS AC105129
DEFINITION Homo sapiens chromosome 15, clone RP11-349G13, complete sequence.
ACCESSION AC105129
VERSION AC105129.4 GI:20330981


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repeat_region complement(8227..8312)
repeat_region /rpt_family="AluMB3"
repeat_region 8313..8347
repeat_region /rpt_family="AT_Rich"
repeat_region complement(8350..8617)
repeat_region /rpt_family="AluSx"
repeat_region complement(8621..9274)
repeat_region /rpt_family="AluMB3"
repeat_region 9403..9445
repeat_region /rpt_family="AT_Rich"
repeat_region 9706..10007
repeat_region /rpt_family="AluJb"
repeat_region complement(10940..11000)
repeat_region /rpt_family="AluMB5"
repeat_region 11001..11284
repeat_region /rpt_family="AluJb"
repeat_region complement(11285..11366)
repeat_region /rpt_family="AluJb"
repeat_region complement(11641..11934)
repeat_region /rpt_family="AluSg"
repeat_region complement(12071..12294)
repeat_region /rpt_family="AluJb"
repeat_region complement(12410..12697)
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Best Local Similarity 100.0%; Pred. No. 2-2e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 CTCCTGCTCAGCTTCCAACTAGCTGGACTACAGTGGCC 88
Db 13355 CTCCTGCTCAGCTTCCAACTAGCTGGACTACAGTGGCC 13314

RESULT 8
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LOCUS HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
DEFINITION Homo sapiens chromosome 15 clone RP11-731G9 map 15, *** SEQUENCING
IN PROGRESS ***, 9 unordered pieces.
ACCESSION AC027220
VERSION AC027220.5 GI:17977449
KEYWORDS HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 212505)

```

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
Homo sapiens chromosome 15, clone RP11-731G9
Unpublished
2 (bases 1 to 212505)
Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
Boguslavsky, L., Bouckgeer, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Collins, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehotzky, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
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Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Ollivier, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tasfave, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 22, 2001 this sequence version replaced g1:13959268.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8347
Center clone name: 731_G_9

TITLE
JOURNAL
COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 32125: contig of 32125 bp in length
* 32126 32225: gap of 100 bp
* 32226 45347: contig of 13122 bp in length
* 45348 45447: gap of 100 bp
* 45448 51661: contig of 6214 bp in length
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* 51762 59880: contig of 8119 bp in length
* 59881 59980: gap of 100 bp
* 59981 70999: contig of 11019 bp in length
* 71000 71099: gap of 100 bp
* 71100 97542: contig of 26443 bp in length
* 97543 97642: gap of 100 bp
* 97643 176551: contig of 78909 bp in length
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Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 CTCCTGGCTCAGCTTCCAACTAGCTGGAGTACAGTGCGC 88
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/chromosomes="16"
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Best Local Similarity 100.0%; Pred. No. 8.3e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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LOCUS AP001184 120186 bp DNA linear PRI 27-APR-2002
DEFINITION Homo sapiens genomic DNA, chromosome.11q clone:RP11-715F10,
complete sequences.
ACCESSION AP001184
VERSION AP001184.4 GI:203334320
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
clone:RP11-715F10.

REFERENCE
1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (2000)
REFERENCE
2 (bases 1 to 120186)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (16-FEB-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba-shi, Ibaraki, Japan 305-8565, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Apr 26, 2002 this sequence version replaced gi:11320825.
COMMENT
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/db_xref="taxon:9606"
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/clone="RP11-715F10"
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ORIGIN

Query Match 21.9%; Score 41; DB 9; Length 120186;
Best Local Similarity 100.0%; Pred. No. 8.2e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAGCTCCTCTCTGCTCAGCTTCCAAAC 67
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Db      84093 ACTCCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAAC 84053
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AC073631.1 GI:8748850
VERSION HTG: HTGS PHASE1.
KEYWORDS Homo sapiens.
SOURCE  Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 155877)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 155877)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

----- Genome Center -----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1086: contig of 1086 bp in length
* 1087 1186: gap of unknown length
* 1187 2446: contig of 1260 bp in length
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* 18554 18654: gap of unknown length
* 18654 29773: contig of 11120 bp in length
* 29773 29874: gap of unknown length
* 29874 42606: contig of 12732 bp in length
* 42606 42706: gap of unknown length
* 42706 56735: contig of 14029 bp in length
* 56735 56834: gap of unknown length
* 56834 70734: contig of 13900 bp in length
* 70734 70835: gap of unknown length
* 70835 83357: contig of 14523 bp in length
* 83357 85458: gap of unknown length
* 85458 101145: contig of 15688 bp in length
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* 121898 121999: gap of unknown length
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Query Match 21.9%; Score 41; DB 2; Length 155877;
Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC009930
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VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 165662)
AUTHORS Birren,B., Nussbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-11408
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165662)
AUTHORS Birren,B., Linton,L., Nussbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
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Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 165662)
AUTHORS Birren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camrata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (13-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Oct 8, 2001 this sequence version replaced gi:15421962.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1961
Center clone name: 114_O_8

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 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Homo sapiens chromosome 10 clone RP11-222A11, complete sequence.
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 VERSION AC020641.8 GI:20901839
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Smith,D.R.
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 166098)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 3 (bases 1 to 166098)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (29-NOV-2001) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 4 (bases 1 to 166098)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 COMMENT On May 17, 2002 this sequence version replaced gi:17149359.
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 Query Match 21.9%; Score 41; DB 9; Length 166098;
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGATCATAGCTACTGCAGCTCATCTCTCTGGGCTCAAG 41
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 DEFINITION Homo sapiens 3 BAC RP11-552C10 (Roswell Park Cancer Institute Human
 BAC library) complete sequence.
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 VERSION AC012152.12 GI:6649262
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Muzny,D.M., Adams,C., Bailey,M., Barabara,J., Blankenburg,K.,
 Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
 Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
 David,R., Delgado,O., Deshazo,D., Ding,Y., Donah-Rashid,N.,
 Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
 Forcum-Tansey,J., Frantz,P., Ganesha,R., Garcia,D.K., Gorrell,J.H.,
 Horrell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J.,
 Hodgson,A., Hogues,M., Holloway,C., Hosak,H., Jackson,L.E.,
 Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondejewski,N., Kong,Y.,
 Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O.,
 Lozado,R.J., Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P.,

Mei,G., Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S.,
 Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Osawa,G., Parish,B.,
 Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D.,
 Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H.,
 Simon,M., Sparks,A., Stamps,A., Sugang,R., Tabor,P., Taylor,T.,
 Vasquez,L., Vinson,R., Vo,Q., Wahban,M., Watlington,S.,
 Weinstock,G., Weinstock,I.R., Williamson,A., Worley,K., Wren,J.,
 Wrensford,G., Yu,W., Zhou,X., Naylor,S.L., Nelson,D. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 180423)
 Worley,K.C.
 Direct Submission
 Submitted (21-OCT-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 180423)
 Worley,K.C.
 Direct Submission
 Submitted (31-DEC-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 31, 1999 this sequence version replaced gi:6646737.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches
 of a local database that includes entries from dbSTS, GDB, and
 local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
 unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
 (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
 EST and cDNA sequences. Genes demonstrate at least two exons
 flanked by consensus splice sites that maintained sequence
 continuity across the splice junctions. Sequences that are not
 identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
 standard of double strand coverage with a minimum of 2 clones and 2
 reads with no ambiguities or 2 chemistries with a minimum of 2
 clones and 3 reads with no ambiguities. If the sequence quality for
 a region does not meet this standard, it will be indicated in the
 annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
 standards - estimated error rate less than 1 per 10,000 bases.
 Reports of lowest quality individual bases and measures of base
 quality are listed below. Description of the metrics can be found
 at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
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repeat_region	complement(638..976) /rpt_family="L1M4"
repeat_region	complement(1188..1445) /rpt_family="L1M4"

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complement(15316..15766)
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17198..17279
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Best Local Similarity 100.0%; Pred.No. 7.8e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCTCATACTCTGGGCTCAAGCAATCTCTGCTGCTCAGCCT 61
Db 108235 CCTCATACTCTGGGCTCAAGCAATCTCTGCTGCTCAGCCT 108275

RESULT 15
AC073984 187266 bp DNA linear HTG 02-SEP-2000
LOCUS Homo sapiens chromosome 3 clone RP11-394K18, WORKING DRAFT
DEFINITION SEQUENCE, 9 unordered pieces.
ACCESSION AC073984
VERSION AC073984.4 GI:9965004
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 187266)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 187266)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Sep 2, 2000 this sequence version replaced gi:9739341.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0394K18
----- Summary Statistics -----
```


Sequencing vector: M13; 100%
 Sequencing vector: plasmid; 0%
 Chemistry: Dye-primer ET; 100% of reads
 Chemistry: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 181863 bases at least Q40
 Consensus quality: 183568 bases at least Q30
 Consensus quality: 184222 bases at least Q20
 Insert size: 196000; agarose-fp
 Insert size: 186466; sum-of-contigs
 Quality coverage: 6.15 in Q20 bases; agarose-fp
 Quality coverage: 6.52 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1735: contig of 1735 bp in length
 * 1736 1835: gap of unknown length
 * 1836 9195: contig of 7360 bp in length
 * 9196 9295: gap of unknown length
 * 9296 16758: contig of 7463 bp in length
 * 16759 16858: gap of unknown length
 * 16859 27746: contig of 10888 bp in length
 * 27747 27846: gap of unknown length
 * 27847 41286: contig of 13440 bp in length
 * 41287 41386: gap of unknown length
 * 41387 64712: contig of 23326 bp in length
 * 64713 64812: gap of unknown length
 * 64813 100745: contig of 35933 bp in length
 * 100746 100845: gap of unknown length
 * 100846 141830: contig of 40985 bp in length
 * 141831 141931: gap of unknown length
 * 141931 187266: contig of 45336 bp in length.

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="3"
 /clone="RP11-394K18"
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 141931..187266
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 ORIGIN

Query Match 21.9%; Score 41; DB 2; Length 187266;
 Best Local Similarity 100.0%; Pred.No. 7.8e-12;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CCTCATACTCCTGGGCTCAAGCAATCCTCTGCTCAGCCT 61
 |||||
 Db 107131 CCTCATACTCCTGGGCTCAAGCAATCCTCTGCTCAGCCT 107171

Search completed: June 17, 2003, 03:58:43
 Job time : 391.575 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 33.0127 Seconds
(without alignments)

Title: US-09-513-888c-1_COPY_6939_7125

Perfect score: 187
Sequence: 1 atgacatgactcactgcag.....tggcctcaagcaatccacct 187
12756.396 Million cell updates/sec

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_101002.*

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- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	187	100.0	5492	21	AAA64508
2	187	100.0	9048	21	AAA64507
3	40	21.4	12767	22	ABAI7068
4	40	21.4	18997	24	AAD36072
5	40	21.4	84495	24	AAS20588
6	40	21.4	160552	22	AAD02697
7	38	20.3	24843	24	AAS17764
8	37	19.8	328	22	ABAI5496
9	36	19.3	831	22	AA196106
CDNA sequence of t					
Nucleotide sequenc					
Human nervous syst					
Human POLD2 genom					
Human methionine a					
Human glycosyl sul					
Human Genomic DNA					
Human nervous syst					
Human neuroblastom					

Human musculoskele
Human reproductive
Human ovarian canc
Human polynucleoti
Human polynucleoti
Novel human polynu
Human polynucleoti
Human polynucleoti
Human breast cance
Human immune/haema
Human cDNA clone
Human cancer relat
Human immune/haema
Human reproductive
Human breast cance
Human breast cance
Human LNXp80 homol
Human breast cance
DNA encoding novel
Human immune/haema
Human immune/haema
Human immune/haema
Human immune/haema
Human PRO1722 homo
Human cancer suppr
cDNA sequence #425
Human cDNA sequenc
Human immunoglobul
Human cDNA SEQ ID
cDNA encoding huma
Human secreted pro
Human low adenosin
Human adenosine re
CD25 T cell activa
Human TANGO 364 al
Human secreted pro
Human cDNA sequenc
Human cDNA sequenc
Human TANGO 364 CD
Human prostate exp
Human prostate exp
Human glucose 6-ph
Human immune/haema
Human cDNA sequenc
Genomic sequence #
Genomic sequence #
DNA encoding human
Human excretory re
Human kidney relat
Human IL-1ra BAC c
Human immune/haema
Genomic sequence #
Human low adenosin
Human adenosine re
Human pancreatic c
Human genomic DNA
Human cardiac vascul
Human DNA for a no
Human DNA for a no
Genomic DNA encodi
Human polynucleoti
Human polynucleoti
Genomic sequence #
Human nervous syst
Human immune/haema
Human polyamine-mo
Human retroviral s
Human immune/haema
Human immune/haema
Colon adenocarcino
Human nibrin DNA
Human apolipoprote

83	35	18.7	143899	24	AA138336	Genomic sequence e	C 156	32	17.1	814	21	AA75898	Human OREF ORF1453
84	35	18.7	144460	21	AA293815	Olfactory receptor	C 157	32	17.1	5916	22	AAK90637	Human digestive sy
85	34	18.2	51	22	AA404296	Human SNP flanking	C 158	32	17.1	5553	22	ABA14823	Human nervous syst
86	34	18.2	411	22	AA186466	Human polynucleoti	C 159	32	17.1	7993	22	AAK73139	Human immune/haema
87	34	18.2	441	22	AA835908	Human cardiovascular	C 160	32	17.1	13646	22	AAK79787	Human neuroblastom
88	34	18.2	441	22	AA835910	Human cardiovascular	C 161	32	17.1	24884	22	AAK67892	Human immune/haema
89	34	18.2	473	22	AA844700	Human full-length	C 162	32	17.1	34878	22	AAK66167	Human immune/haema
90	34	18.2	514	24	AB133540	Human ovarian canc	C 163	32	17.1	34878	22	AAK80088	Human immune/haema
91	34	18.2	558	24	ABQ56499	Human colon cancer	C 164	32	17.1	44100	21	AAK97975	Human retroviral s
92	34	18.2	797	21	AAK77141	Human OREF ORF2696	C 165	32	17.1	172570	24	ABQ88207	Human osteoblast d
93	34	18.2	876	22	AA840689	DNA encoding huma	C 166	31	16.6	364	21	AAK13155	Human secreted pro
94	34	18.2	876	22	AA840692	Human reproductive	C 167	31	16.6	476	23	ABV01550	Human prostate exp
95	34	18.2	1531	22	AA204666	Human nervous syst	C 168	31	16.6	477	23	ABA14998	Human nervous syst
96	34	18.2	2589	20	AA228760	Human cyclophilin	C 169	31	16.6	514	23	ABV31884	Human prostate exp
97	34	18.2	2813	22	AAK85585	Human immune/haema	C 170	31	16.6	514	23	ABV40843	Human prostate exp
98	34	18.2	2814	22	AAK85584	Human immune/haema	C 171	31	16.6	540	23	ABV60384	Human prostate exp
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103	34	18.2	5686	24	ABK14231	Human related RAS	C 176	31	16.6	1258	22	AAK75907	Human immune/haema
104	34	18.2	5686	24	ABK14253	Human related RAS	C 177	31	16.6	1259	22	AAK75908	Human immune/haema
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106	34	18.2	9324	22	AAK75610	Human immune/haema	C 179	31	16.6	1607	21	AAK59256	Human secreted pro
107	34	18.2	15734	22	AAK36422	Human cardiovascular	C 180	31	16.6	1779	24	ABK34995	Human cDNA encodin
108	34	18.2	17146	22	AA137485	Human musculoskele	C 181	31	16.6	2164	22	AAH17265	Human cDNA sequenc
109	34	18.2	26928	22	ABA82620	Human HBM gene reg	C 182	31	16.6	2703	22	AAK65263	CDNA encoding huma
110	34	18.2	26928	24	AAK22779	Human high bone ma	C 183	31	16.6	6302	22	AAK65687	Human immune/haema
111	34	18.2	30568	22	AA137486	Human musculoskele	C 184	31	16.6	13138	22	AAK65690	Human immune/haema
112	34	18.2	32196	22	ABA18857	Human nervous syst	C 185	31	16.6	15848	20	AAK232190	Human heparin cofa
113	34	18.2	32199	22	AAK90296	Human digestive sy	C 186	31	16.6	15849	24	ABN95864	Gene #2362 used to
114	34	18.2	32199	22	AA157673	Human colorectal c	C 187	31	16.6	18664	22	AAK65421	Human immune/haema
115	34	18.2	35959	22	AAK78275	Human immune/haema	C 188	31	16.6	18664	22	AAK84438	Human immune/haema
116	34	18.2	41765	22	AAK76675	Human immune/haema	C 189	31	16.6	22791	22	AAK69857	Human immune/haema
117	34	18.2	41772	22	AAK76676	Human immune/haema	C 190	31	16.6	25975	22	AAK69855	Human reproductive
118	34	18.2	112460	24	ABK83567	Human cDNA differe	C 191	31	16.6	25975	23	ABL97849	Human testicular a
119	34	17.6	252	22	ABA17318	Human nervous syst	C 192	31	16.6	32174	22	ABA15665	Human nervous syst
120	33	17.6	276	24	ABK80285	Bacillus clausii g	C 193	31	16.6	32174	22	ABA19477	Human nervous syst
121	33	17.6	347	24	ABL83445	Human ovarian canc	C 194	31	16.6	32174	22	ABA20359	Human nervous syst
122	33	17.6	380	22	AA186608	Human polynucleoti	C 195	31	16.6	32174	22	ABA21505	Human nervous syst
123	33	17.6	393	22	AA180381	Human polynucleoti	C 196	31	16.6	32174	22	AAK36280	Human musculoskele
124	33	17.6	410	22	AA186660	Human polynucleoti	C 197	31	16.6	32174	22	AAK32655	Human musculoskele
125	33	17.6	566	24	ABL62267	Colon adenocarcino	C 198	31	16.6	32174	22	AAK34394	Human DNA for a no
126	33	17.6	566	24	ABL63618	Breast cancer rela	C 199	31	16.6	32174	22	AAK30638	DNA encoding novel
127	33	17.6	566	24	ABL64029	Breast cancer rela	C 200	31	16.6	32174	22	AAK03792	Human reproductive
128	33	17.6	589	23	AAH50429	Human prostate exp	C 201	31	16.6	32174	22	AAK07447	Human reproductive
129	33	17.6	2133	22	AAH15667	Human cDNA sequenc	C 202	31	16.6	32174	22	AAK07491	Human reproductive
130	33	17.6	2207	21	AAK59244	Human secreted pro	C 203	31	16.6	32174	22	AAK28700	Genomic sequence #
131	33	17.6	2634	24	ABK35089	Human cDNA encodin	C 204	31	16.6	32174	22	AAI62606	Human breast or ov
132	33	17.6	2664	24	ABK51251	Human cDNA encodin	C 205	31	16.6	32174	22	AAI62904	Human genomic DNA
133	33	17.6	5030	23	AAK76216	DNA encoding novel	C 206	31	16.6	32174	22	AAK72131	Human ovarian anti
134	33	17.6	11646	22	AAK70925	Human immune/haema	C 207	31	16.6	32174	24	ABK91723	Novel ovarian rela
135	33	17.6	14148	22	AAK70926	Human immune/haema	C 208	31	16.6	32220	22	AAK37568	Human musculoskele
136	33	17.6	16183	22	AAK74819	Human immune/haema	C 209	31	16.6	38771	22	AAK66361	Human immune/haema
137	33	17.6	16281	22	AAK70314	Human immune/haema	C 210	31	16.6	38771	22	AAK68883	Human immune/haema
138	33	17.6	16281	22	ABK42480	Genomic sequence #	C 211	31	16.6	38771	22	AAK69604	Human immune/haema
139	33	17.6	16281	22	AAK70315	Human immune/haema	C 212	31	16.6	38771	22	AAK71499	Human immune/haema
140	33	17.6	16285	22	AAK70316	Human immune/haema	C 213	31	16.6	38771	22	AAK72925	Human immune/haema
141	33	17.6	16285	23	ABK42481	Genomic sequence #	C 214	31	16.6	38771	22	AAK75870	Human immune/haema
142	33	17.6	16285	23	ABK42482	Genomic sequence #	C 215	31	16.6	38771	22	AAK80325	Human immune/haema
143	33	17.6	17150	22	AAK29282	Human DNA methyltr	C 216	31	16.6	38771	22	AAK83538	Human immune/haema
144	33	17.6	17595	22	AAK71154	Human immune/haema	C 217	31	16.6	109906	24	ABK94411	DNA encoding endot
145	33	17.6	17792	22	AAK322727	Human genomic DNA	C 218	31	16.6	121162	21	AAK66548	Human kinein-like
146	33	17.6	17792	22	AAK36099	Human cardiovascular	C 219	31	16.6	222930	24	ABK84349	Human cDNA differe
147	33	17.6	21693	22	AAK79930	Human immune/haema	C 220	31	16.6	227968	24	AAK83497	Human cDNA differe
148	33	17.6	24079	22	AAK71153	Human immune/haema	C 221	31	16.6	325791	22	AAK43104	Human Oestrogen re
149	33	17.6	30115	21	AAK59651	Modified adenovira	C 222	30	16.0	122	22	AAK86623	Human immune/haema
150	33	17.6	65608	24	ABL62910	Breast cancer rela	C 223	30	16.0	122	22	AAK86623	Human immune/haema
151	33	17.6	65608	24	ABL64414	Stomach cancer rel	C 224	30	16.0	278	23	ABV53552	Human prostate exp
152	33	17.6	65608	24	ABL67668	Oesophagus cancer	C 225	30	16.0	289	23	AAK29315	Human secreted pro
153	33	17.6	84495	24	AAK20588	Human methionine a	C 226	30	16.0	338	22	AAK75949	Human immune/haema
154	33	17.6	172570	24	ABQ88207	Human osteoblast d	C 227	30	16.0	338	22	AAK75950	Human immune/haema
155	32	17.1	403	21	AAH30457	Human colon cancer	C 228	30	16.0	345	22	AAI86872	Human polynucleoti

229	30	16.0	387	23	ABV43001	Human prostate exp	302	29	15.5	338	14	AAQ59619	Human brain expres
230	30	16.0	388	23	ABV03849	Human prostate exp	c 303	29	15.5	348	22	AAF65880	Novel human polynu
231	30	16.0	406	23	AAI85057	Human polynucleoti	c 304	29	15.5	364	22	AAI88966	Human polynucleoti
232	30	16.0	409	23	ABV04720	Human prostate exp	c 305	29	15.5	366	22	AAS27779	DNA encoding novel
233	30	16.0	421	20	AAV87192	EST clone BN139.	c 306	29	15.5	373	22	AAI85901	Human polynucleoti
234	30	16.0	434	22	AAI93309	Human polynucleoti	c 307	29	15.5	398	22	AAI86942	Human polynucleoti
235	30	16.0	436	23	ABV34139	Human prostate exp	c 308	29	15.5	408	24	ABQ58163	Human colon cancer
236	30	16.0	438	23	ABV13889	Human prostate exp	c 309	29	15.5	410	22	ABA17229	Human nervous syst
237	30	16.0	459	23	ABV35001	Human prostate exp	c 310	29	15.5	412	22	AAF64900	Novel human polynu
238	30	16.0	459	23	ABV43849	Human prostate exp	c 311	29	15.5	412	22	AAI83800	Human polynucleoti
239	30	16.0	471	23	ABV13018	Human prostate exp	c 312	29	15.5	416	22	ABA17230	Human nervous syst
240	30	16.0	490	22	AAI86033	Human polynucleoti	c 313	29	15.5	433	24	ABU87836	Human ovarian canc
241	30	16.0	492	22	AAH71568	Human cervical can	c 314	29	15.5	495	22	AAS60582	Human cancer agent
242	30	16.0	540	22	AAH70143	Human cervical can	c 315	29	15.5	496	22	AAI12047	Human breast cancer
243	30	16.0	589	24	ABN64952	Human cancer relat	c 316	29	15.5	496	24	ABN65848	Human cancer relat
244	30	16.0	620	22	AAI07458	Human reproductive	c 317	29	15.5	504	22	AAS60340	Human cancer agent
245	30	16.0	637	22	AAI33384	Human colon cancer	c 318	29	15.5	524	22	AAI93453	Human polynucleoti
246	30	16.0	674	21	AAZ79992	Human colon cancer	c 319	29	15.5	543	22	ABA60844	Human foetal liver
247	30	16.0	1069	23	AAS80995	DNA encoding novel	c 320	29	15.5	543	22	ABA28851	Human genome-deriv
248	30	16.0	1610	22	AAH15274	Human CDNA sequenc	c 321	29	15.5	543	22	AAK09131	Human brain expres
249	30	16.0	1746	22	AAK70288	Human immune/haema	c 322	29	15.5	543	22	AAK35020	Human bone marrow
250	30	16.0	1746	22	AAK70289	Human immune/haema	c 323	29	15.5	543	22	AAI16900	Probe #6833 for ge
251	30	16.0	1757	22	ABAI5128	Human nervous syst	c 324	29	15.5	543	22	AAI40737	Probe #9423 used t
252	30	16.0	1990	22	AAK87330	Human immune/haema	c 325	29	15.5	543	24	ABS09501	Human genome-deriv
253	30	16.0	1990	22	AAK87331	Human immune/haema	c 326	29	15.5	554	22	AAK64110	Human immune/haema
254	30	16.0	2006	22	AAK87389	Human immune/haema	c 327	29	15.5	569	22	AAK62069	Human immune/haema
255	30	16.0	2044	22	AAK65721	Human immune/haema	c 328	29	15.5	571	24	ABN63980	Human cancer relat
256	30	16.0	2044	22	AAK65722	Human immune/haema	c 329	29	15.5	590	22	AAI82752	Human polynucleoti
257	30	16.0	2044	22	AAK69117	Human immune/haema	c 330	29	15.5	600	22	AAI20932	Human breast cancer
258	30	16.0	2044	22	AAK69118	Human immune/haema	c 331	29	15.5	605	22	AAS35625	Human cardiovascular
259	30	16.0	2045	22	AAK65720	Human immune/haema	c 332	29	15.5	623	23	ABV48087	Human prostate exp
260	30	16.0	2045	22	AAK65725	Human immune/haema	c 333	29	15.5	684	24	ABN60127	Human cancer relat
261	30	16.0	2045	22	AAK69116	Human immune/haema	c 334	29	15.5	725	22	AAH03539	Human CDNA clone (
262	30	16.0	2045	22	AAK69119	Human immune/haema	c 335	29	15.5	795	22	AAK82472	Human immune/haema
263	30	16.0	2607	22	AAK97848	Human neuroblastom	c 336	29	15.5	795	22	AAK82473	Human immune/haema
264	30	16.0	4066	19	AAK59181	Human bak gene pro	c 337	29	15.5	950	23	ABK42761	Genomic sequence #
265	30	16.0	4156	22	AAK83412	Human immune/haema	c 338	29	15.5	950	23	ABK42762	Genomic sequence #
266	30	16.0	7640	22	AAK91239	Human digestive sy	c 339	29	15.5	950	23	ABK42763	Genomic sequence #
267	30	16.0	7703	22	AAK90904	Human digestive sy	c 340	29	15.5	1031	23	ABV30293	Human prostate exp
268	30	16.0	7703	22	AAK90945	Human digestive sy	c 341	29	15.5	1040	22	AAK69263	Human immune/haema
269	30	16.0	7703	22	AAK91939	Human liver associ	c 342	29	15.5	1253	22	AAI36111	Human musculoskele
270	30	16.0	7703	22	AAK91980	Human liver associ	c 343	29	15.5	1254	22	AAI36110	Human musculoskele
271	30	16.0	7703	24	ABN90294	Human liver antige	c 344	29	15.5	1276	20	AAZ06248	Human secreted pro
272	30	16.0	7703	24	ABN90335	Human liver antige	c 345	29	15.5	2160	22	AAI36895	Human musculoskele
273	30	16.0	8764	22	AAK91240	Human digestive sy	c 346	29	15.5	2218	14	AAO47929	Paired basic amino
274	30	16.0	10195	22	AAS26626	Human genomic DNA	c 347	29	15.5	2268	22	AAS42150	Genomic sequence #
275	30	16.0	15366	22	AAS28623	Genomic sequence #	c 348	29	15.5	2270	22	AAS42152	Genomic sequence #
276	30	16.0	15843	22	AAS36896	Human cardiovascular	c 349	29	15.5	2465	24	AAU47848	Human basic helix-
277	30	16.0	15843	22	AAK67635	Human immune/haema	c 350	29	15.5	2944	9	AAH0253	Insert of lambda 3
278	30	16.0	16774	22	AAS36895	Human cardiovascular	c 351	29	15.5	2971	22	AAI02843	Human reproductive
279	30	16.0	16774	22	AAS36898	Human cardiovascular	c 352	29	15.5	2971	22	AAI02959	Human cancer agent
280	30	16.0	16774	22	AAK67634	Human immune/haema	c 353	29	15.5	5092	22	AAS61001	Human activation-i
281	30	16.0	16774	22	AAK67637	Human immune/haema	c 354	29	15.5	5514	21	AAS55313	Human CDNA sequenc
282	30	16.0	21721	22	ABA06775	Human genomic DNA	c 355	29	15.5	5573	22	AAH18243	Human tumour-assoc
283	30	16.0	21721	22	AAS41719	Genomic sequence #	c 356	29	15.5	5957	24	ABA99506	Human tumour-assoc
284	30	16.0	21721	22	AAK69459	Human immune/haema	c 357	29	15.5	5955	22	ABA20275	Human nervous syst
285	30	16.0	33795	24	ABN95686	Gene #2184 used to	c 358	29	15.5	5998	22	ABA20274	Human nervous syst
286	30	16.0	47090	22	AAK68725	Human immune/haema	c 359	29	15.5	6163	24	ABA99507	Human tumour-assoc
287	30	16.0	47090	22	AAK78219	Human immune/haema	c 360	29	15.5	6428	22	AAK78562	Human immune/haema
288	30	16.0	48727	22	AAK67375	Human immune/haema	c 361	29	15.5	6517	22	AAK72855	Human immune/haema
289	30	16.0	54863	22	AAK86025	Human immune/haema	c 362	29	15.5	7152	22	AAK84144	Human immune/haema
290	30	16.0	54877	22	AAK86026	Human immune/haema	c 363	29	15.5	7683	23	ABK42286	Genomic sequence #
291	30	16.0	90220	24	ABK83576	Human CDNA differe	c 364	29	15.5	10097	22	AAF97856	Human neuroblastom
292	30	16.0	106746	21	AAI10225	Human PCTA-1 genom	c 365	29	15.5	10302	22	ABA16133	Human nervous syst
293	30	16.0	110096	24	ABN95044	Gene #1542 used to	c 366	29	15.5	10437	22	AAS41709	Genomic sequence #
294	30	16.0	145831	24	ABL62309	Colon adenocarcino	c 367	29	15.5	11204	21	AAS55339	Human activation-1
295	30	16.0	145831	24	ABL66806	Lung cancer relate	c 368	29	15.5	12339	22	AAK81687	Human immune/haema
296	30	16.0	145831	24	ABL68588	Kidney cancer rela	c 369	29	15.5	12339	22	AAK81691	Human immune/haema
297	30	16.0	145831	24	ABL69213	Prostate cancer re	c 370	29	15.5	12392	22	ABA15896	Human nervous syst
298	30	16.0	167343	24	ABL64403	Stomach cancer rel	c 371	29	15.5	12620	22	ABA16891	Human nervous syst
299	30	16.0	167343	24	ABL67239	Thyroid cancer rel	c 372	29	15.5	13608	22	AAK87529	Human immune/haema
300	29	15.5	51	22	AAH89505	Human coding sequ	c 373	29	15.5	13934	22	AAK81690	Human immune/haema
301	29	15.5	246	21	AAI16539	Human secreted pro	c 374	29	15.5	17104	22	AAS30249	DNA encoding rena

C 375	29	15.5	17104	22	AAS26973	Human genomic DNA
C 376	29	15.5	17104	22	AAS30484	DNA encoding human
C 377	29	15.5	17107	22	AAS30248	DNA encoding rena
C 378	29	15.5	17107	22	AAS26972	Human genomic DNA
C 379	29	15.5	17107	22	AAS33483	DNA encoding human
C 380	29	15.5	21129	22	AAS36234	Human cardiovascular
C 381	29	15.5	21936	22	ABAI5865	Human nervous syst
C 382	29	15.5	21936	22	AAI06119	Human reproductive
C 383	29	15.5	21936	22	AAI06758	Human reproductive
C 384	29	15.5	21936	22	ABAI62664	Human breast or ov
C 385	29	15.5	21936	23	ABAI98684	Human testicular a
C 386	29	15.5	22700	22	AAK70746	Human immune/haema
C 387	29	15.5	22700	22	AAK66230	Human immune/haema
C 388	29	15.5	23580	22	AAK93578	Human immune/haema
C 389	29	15.5	24000	21	AAAS8851	Human dual-specifi
C 390	29	15.5	24977	22	AAI03263	Human reproductive
C 391	29	15.5	24977	22	AAI05788	Human reproductive
C 392	29	15.5	24977	23	ABAI98352	Human testicular a
C 393	29	15.5	24983	22	AAI03262	Human reproductive
C 394	29	15.5	24983	22	AAI05787	Human reproductive
C 395	29	15.5	24983	23	ABAI98351	Human testicular a
C 396	29	15.5	27148	22	AAS28612	Genomic sequence #
C 397	29	15.5	29329	22	ABAI18026	Human nervous syst
C 398	29	15.5	29329	22	ABA20511	Human nervous syst
C 399	29	15.5	29329	22	AAK70791	Human immune/haema
C 400	29	15.5	29329	22	AAK78512	Human immune/haema
C 401	29	15.5	32134	22	AAI199172	Human excretory re
C 402	29	15.5	32134	22	AAI63522	Human kidney relat
C 403	29	15.5	32184	22	ABA20589	Human nervous syst
C 404	29	15.5	32184	22	ABA20590	Human nervous syst
C 405	29	15.5	32192	22	AAI199173	Human excretory re
C 406	29	15.5	32192	22	AAI63523	Human kidney relat
C 407	29	15.5	32199	22	AAK90286	Human digestive sy
C 408	29	15.5	32199	22	AAI57673	Human colorectal c
C 409	29	15.5	35100	22	AAK65700	Human immune/haema
C 410	29	15.5	35100	22	AAK659767	Human immune/haema
C 411	29	15.5	35115	22	AAK65699	Human immune/haema
C 412	29	15.5	35115	22	AAK69766	Human immune/haema
C 413	29	15.5	35871	22	AAK84974	Human immune/haema
C 414	29	15.5	38272	22	AAK84952	Human immune/haema
C 415	29	15.5	38348	22	AAK84953	Human immune/haema
C 416	29	15.5	43599	24	ABK84242	Human cDNA differe
C 417	29	15.5	48037	22	AAK84729	Human immune/haema
C 418	29	15.5	48037	22	AAK85983	Human immune/haema
C 419	29	15.5	48045	22	AAK84730	Human immune/haema
C 420	29	15.5	48045	22	AAK85984	Human immune/haema
C 421	29	15.5	110096	24	ABN95044	Gene #1542 used to
C 422	29	15.5	110608	24	ABK83572	Human cDNA differe
C 423	29	15.5	117574	24	AAI45288	Human KCNB1 gene.
C 424	29	15.5	121162	21	AAK656548	Human kinesin-like
C 425	28	15.0	196	21	AAK12258	Human secreted pro
C 426	28	15.0	347	22	ABAI19979	Human nervous syst
C 427	28	15.0	348	22	ABAI19978	Human nervous syst
C 428	28	15.0	351	22	AAI83981	Human polynucleoti
C 429	28	15.0	353	22	AAI86190	Human polynucleoti
C 430	28	15.0	390	23	ABV50386	Human prostate exp
C 431	28	15.0	401	22	AAK36414	Human neuregulin g
C 432	28	15.0	401	22	AAK97907	Human neuregulin g
C 433	28	15.0	404	22	AAI86627	Human polynucleoti
C 434	28	15.0	416	22	AAI93349	Human polynucleoti
C 435	28	15.0	407	22	AAK76092	Human immune/haema
C 436	28	15.0	417	22	AAK76091	Human immune/haema
C 437	28	15.0	417	24	ABAI83801	Human ovarian canc
C 438	28	15.0	449	22	AAI86596	Human polynucleoti
C 439	28	15.0	478	21	ABAI9773	Human secreted pro
C 440	28	15.0	514	24	ABN63452	Human cancer relat
C 441	28	15.0	544	23	ABV53170	Human prostate exp
C 442	28	15.0	555	23	ABV54906	Human prostate exp
C 443	28	15.0	592	23	ABV58987	Human prostate exp
C 444	28	15.0	593	23	AAK67044	Human immune/haema
C 445	28	15.0	617	23	ABV51224	Human prostate exp
C 446	28	15.0	827	22	ABA20530	Human nervous syst
C 447	28	15.0	1631	22	AAS01475	Human secreted pro
C 448	28	15.0	1644	24	ABK35053	Human cDNA encodin
C 449	28	15.0	1738	21	AAZ65086	Membrane-bound pro
C 450	28	15.0	1738	22	AAZ46044	Human DNA encoding
C 451	28	15.0	1738	22	AAZ46044	Human PRO156 (UNQ
C 452	28	15.0	1776	22	AAK94697	Human full-length
C 453	28	15.0	4748	22	ABA07182	Human pancreatic c
C 454	28	15.0	4748	22	AAK89814	Human digestive sy
C 455	28	15.0	5139	22	AAK36394	Human cardiovascular
C 456	28	15.0	5366	22	ABA20542	Human nervous syst
C 457	28	15.0	5366	22	AAK87126	Human immune/haema
C 458	28	15.0	6519	22	AAK97859	Human neuroblastom
C 459	28	15.0	6928	22	ABA21109	Human nervous syst
C 460	28	15.0	10093	22	ABA07184	Human pancreatic c
C 461	28	15.0	10093	22	AAK55890	Human cardiovascular
C 462	28	15.0	10093	22	AAK89816	Human digestive sy
C 463	28	15.0	10538	22	AAK71513	Human immune/haema
C 464	28	15.0	11186	24	AAK36213	Human cytochrome p
C 465	28	15.0	11216	22	AAK39593	Genomic sequence #
C 466	28	15.0	11216	22	AAK88992	Human digestive sy
C 467	28	15.0	11811	20	AAV83943	Bacterial artifici
C 468	28	15.0	12891	22	AAK85953	Human immune/haema
C 469	28	15.0	13608	22	AAK87529	Human immune/haema
C 470	28	15.0	13864	22	AAK97861	Human neuroblastom
C 471	28	15.0	17947	22	AAK77679	Human immune/haema
C 472	28	15.0	19012	14	AAQ36952	HSA gene. Homo sa
C 473	28	15.0	22756	22	AAK40321	DNA encoding human
C 474	28	15.0	22756	22	AAI03921	Human reproductive
C 475	28	15.0	32195	22	AAK36517	Human cardiovascular
C 476	28	15.0	32219	22	AAK36516	Human cardiovascular
C 477	28	15.0	32249	22	AAK36814	Human cardiovascular
C 478	28	15.0	35973	24	ABK13076	Human amyloid beta
C 479	28	15.0	36651	24	AAD28072	Human kinase genom
C 480	28	15.0	53552	22	AAK13655	Genomic DNA sequen
C 481	28	15.0	59065	24	ABU42416	Human serine/chreo
C 482	28	15.0	59747	24	ABQ88209	Human osteoblast d
C 483	28	15.0	123219	23	AAK88703	Human DNA sequence
C 484	28	15.0	128978	24	AAK83459	Human cDNA differe
C 485	28	15.0	143306	24	ABK49586	Human transporter
C 486	28	15.0	143899	24	AAK38336	Genomic sequence e
C 487	28	15.0	1503900	22	AAK95240	Human neuregulin-1
C 488	28	15.0	1503900	22	AAK95240	Human neuregulin-1
C 489	28	15.0	1503900	22	AAK96733	Human neuregulin-1
C 490	28	15.0	1503900	22	AAK96733	Human neuregulin-1
C 491	27	14.4	239	14	AAO60227	Human brain Expres
C 492	27	14.4	285	21	AAK26614	Human secreted pro
C 493	27	14.4	286	21	AAK77171	Human immune/haema
C 494	27	14.4	291	21	AAK01150	Human colon cancer
C 495	27	14.4	294	22	AAI22271	Human breast canc
C 496	27	14.4	300	20	AAI214874	Human gene express
C 497	27	14.4	300	20	AAI214219	Human gene express
C 498	27	14.4	301	21	AAK27970	Human secreted pro
C 499	27	14.4	320	22	AAI13401	Human breast canc
C 500	27	14.4	357	22	AAK26671	Human genomic DNA
C 501	27	14.4	372	24	ABU77513	Human ovarian canc
C 502	27	14.4	382	24	AAI87908	Human polynucleoti
C 503	27	14.4	402	24	AAK96275	Gene #2773 used to
C 504	27	14.4	442	22	AAK67377	Human immune/haema
C 505	27	14.4	487	22	AAH10346	Human cDNA clone (
C 506	27	14.4	493	23	ABV18906	Human prostate exp
C 507	27	14.4	542	22	AAH12053	Human cDNA clone (
C 508	27	14.4	544	23	ABV48686	Human prostate exp
C 509	27	14.4	558	22	AAK92557	Human cDNA 3'-end
C 510	27	14.4	616	22	AAK78123	Human immune/haema
C 511	27	14.4	627	24	ABN62667	Human cancer relat
C 512	27	14.4	700	22	AAH92467	Human inflammatory
C 513	27	14.4	731	22	AAI95571	Human neuroblastom
C 514	27	14.4	741	20	AAI216697	Human gene express
C 515	27	14.4	758	20	AAI217480	Human gene express
C 516	27	14.4	759	20	AAI216373	Human gene express
C 517	27	14.4	760	21	AAK69550	Human secreted pro
C 518	27	14.4	808	20	AAK89617	Human cDNA encodin
C 519	27	14.4	808	22	AAS59248	Human cDNA encodin
C 520	27	14.4	808	24	ABA90917	Human polynucleoti

c 521	27	14.4	820	22	AAK75851	Human immune/haema
c 522	27	14.4	951	22	AAI86541	Human polynucleoti
c 523	27	14.4	1055	22	AAI64168	Human immune/haema
c 524	27	14.4	1068	22	AAK86818	Human immune/haema
c 525	27	14.4	1081	22	AAK68843	Human immune/haema
c 526	27	14.4	1276	22	ABA16339	Human nervous syst
c 527	27	14.4	1466	22	ABA08564	Human Grb7 effecto
c 528	27	14.4	1675	24	ABQ78825	Human Mch2 protein
c 529	27	14.4	1763	22	AAK94891	Human full-length
c 530	27	14.4	1852	22	AAH18681	Human cDNA sequenc
c 531	27	14.4	1886	22	AAH17946	Human cDNA sequenc
c 532	27	14.4	1923	22	AAK89342	Human S-HT3-B DNA
c 533	27	14.4	2027	22	AAH17405	Human cDNA sequenc
c 534	27	14.4	2040	23	AAK85019	DNA encoding novel
c 535	27	14.4	2151	24	ABK34851	Human cDNA for nov
c 536	27	14.4	2154	22	AAH17497	Human cDNA sequenc
c 537	27	14.4	2277	22	AAK68770	Human immune/haema
c 538	27	14.4	2399	24	ABK34922	Human cDNA encodin
c 539	27	14.4	2449	22	AAK32585	Human genomic DNA
c 540	27	14.4	2903	24	AAI44608	Human muscle creat
c 541	27	14.4	3408	22	AAK05598	Human secreted pro
c 542	27	14.4	4054	22	AAK74209	Human immune/haema
c 543	27	14.4	4461	22	AAK72635	Human immune/haema
c 544	27	14.4	4553	22	AAK85916	Human immune/haema
c 545	27	14.4	4976	24	ABN83973	Human gene sequenc
c 546	27	14.4	6111	22	AAK36193	Human cardiovascular
c 547	27	14.4	6111	22	AAK78300	Human immune/haema
c 548	27	14.4	7282	22	AAK72425	Human immune/haema
c 549	27	14.4	7379	19	AAV49653	Human SCL DNA, Ho
c 550	27	14.4	7491	22	AAK78292	Human immune/haema
c 551	27	14.4	8276	22	AAK70800	Human immune/haema
c 552	27	14.4	8705	22	ABA82624	Human HBM gene reg
c 553	27	14.4	9496	22	AAI61328	Human nervous syst
c 554	27	14.4	9591	22	AAI03355	Human reproductive
c 555	27	14.4	9591	22	AAK28906	Human immunoglobul
c 556	27	14.4	9968	22	AAK32240	Human DNA repair a
c 557	27	14.4	10448	22	AAI999191	Human excretory re
c 558	27	14.4	10448	22	AAI63541	Human kidney relat
c 559	27	14.4	12415	22	AAI03356	Human reproductive
c 560	27	14.4	12415	22	AAK28907	Human immunoglobul
c 561	27	14.4	13585	17	AAI11549	Tumour rejection a
c 562	27	14.4	15261	22	AAU07498	Human reproductive
c 563	27	14.4	15399	22	ABA18197	Human nervous syst
c 564	27	14.4	15399	22	ABA18198	Human nervous syst
c 565	27	14.4	17979	22	AAK64964	Human immune/haema
c 566	27	14.4	17979	22	AAK71664	Human immune/haema
c 567	27	14.4	20565	22	AAI03357	Human reproductive
c 568	27	14.4	20565	22	AAK28908	Human immunoglobul
c 569	27	14.4	20565	22	AAK89083	Human digestive sy
c 570	27	14.4	23164	22	AAK79678	Human immune/haema
c 571	27	14.4	27359	22	ABA19957	Human nervous syst
c 572	27	14.4	27371	22	ABA19958	Human nervous syst
c 573	27	14.4	28818	22	AAI35901	Human musculoskele
c 574	27	14.4	29329	22	ABA18026	Human nervous syst
c 575	27	14.4	29329	22	ABA20511	Human nervous syst
c 576	27	14.4	29329	22	AAK70791	Human immune/haema
c 577	27	14.4	29329	22	AAK78512	Human immune/haema
c 578	27	14.4	30037	22	ABA20038	Human nervous syst
c 579	27	14.4	31949	22	AAI05410	Human reproductive
c 580	27	14.4	31949	23	ABU98289	Human testicular a
c 581	27	14.4	32152	22	AAK39621	Genomic sequence #
c 582	27	14.4	32152	22	AAK89020	Human digestive sy
c 583	27	14.4	32152	22	AAK91534	Human digestive sy
c 584	27	14.4	32152	22	AAI57791	Human colorectal c
c 585	27	14.4	32186	22	AAI61117	Human nervous syst
c 586	27	14.4	32186	22	AAI05411	Human reproductive
c 587	27	14.4	32186	23	ABU98270	Human testicular a
c 588	27	14.4	32187	22	AAK32249	Human DNA repair a
c 589	27	14.4	32188	22	AAK28365	Genomic sequence #
c 590	27	14.4	32204	22	AAK39620	Genomic sequence #
c 591	27	14.4	32204	22	AAK89019	Human digestive sy
c 592	27	14.4	32204	22	AAK91533	Human digestive sy
c 593	27	14.4	32204	22	AAI57790	Human colorectal c
c 594	27	14.4	36305	24	ABK22783	Human high bone ma
c 595	27	14.4	36933	22	AAK66362	Human immune/haema
c 596	27	14.4	52562	22	AAK86669	Human immune/haema
c 597	27	14.4	53075	22	AAK86671	Human immune/haema
c 598	27	14.4	54108	24	AAK22782	Human high bone ma
c 599	27	14.4	72049	22	ABA82623	Genomic sequence o
c 600	27	14.4	97662	22	AAK83908	Human cDNA differe
c 601	27	14.4	97835	24	ABK84796	Nucleotide sequenc
c 602	27	14.4	110000	22	AAK48000	Colon adenocarcino
c 603	27	14.4	149480	24	ABL61947	Colon adenocarcino
c 604	27	14.4	149480	24	ABL61948	Kidney cancer rela
c 605	27	14.4	149480	24	ABL68365	Human cDNA differe
c 606	27	14.4	149671	24	ABK84797	Human osteoblast d
c 607	27	14.4	159400	24	ABQ88126	Ovary cancer relat
c 608	27	14.4	174424	24	ABL68122	Ovary cancer relat
c 609	27	14.4	174424	24	ABL68122	Hereditary haemoch
c 610	27	14.4	235033	19	AAV57926	Human single nucle
c 611	26	13.9	129	20	AAH85825	Human ovarian canc
c 612	26	13.9	182	24	ABL87181	Human secreted pro
c 613	26	13.9	225	21	AAK25960	Human secreted pro
c 614	26	13.9	239	21	AAK11964	Human secreted pro
c 615	26	13.9	248	21	AAK20340	EST clone HH404
c 616	26	13.9	258	20	AAV88716	Activated T-cell d
c 617	26	13.9	279	24	AAI69101	Human immune/haema
c 618	26	13.9	319	22	AAK62615	Human immune/haema
c 619	26	13.9	319	22	AAK82895	Human immune/haema
c 620	26	13.9	319	22	AAK82896	Human immune/haema
c 621	26	13.9	323	21	AAK41492	Human secreted exp
c 622	26	13.9	326	22	AAI81940	Human polynucleoti
c 623	26	13.9	335	22	AAI80295	Human polynucleoti
c 624	26	13.9	346	24	ABL64216	Stomach cancer rel
c 625	26	13.9	351	23	ABV49084	Human prostate exp
c 626	26	13.9	354	22	AAK64027	Human immune/haema
c 627	26	13.9	356	21	AAK280255	Human colon cancer
c 628	26	13.9	370	21	AAK02646	Human secreted pro
c 629	26	13.9	372	22	ABA18488	Human nervous syst
c 630	26	13.9	386	21	AAH30469	Human colon cancer
c 631	26	13.9	398	22	AAK58627	Human immune/haema
c 632	26	13.9	401	22	AAK96108	Human neuregulin g
c 633	26	13.9	401	22	AAK96109	Human neuregulin g
c 634	26	13.9	401	22	AAK97601	Human neuregulin g
c 635	26	13.9	401	22	AAK97602	Human neuregulin g
c 636	26	13.9	412	24	ABL778970	Human ovarian canc
c 637	26	13.9	423	24	ABL77253	Human ovarian canc
c 638	26	13.9	431	23	ABV16978	Human prostate exp
c 639	26	13.9	436	24	ABL81158	Human ovarian canc
c 640	26	13.9	438	22	AAK70880	Human immune/haema
c 641	26	13.9	442	22	AAI83526	Human polynucleoti
c 642	26	13.9	461	24	ABQ54456	Human ovarian anti
c 643	26	13.9	475	23	ABV13017	Human prostate exp
c 644	26	13.9	476	23	ABV03848	Human prostate exp
c 645	26	13.9	478	22	AAI86439	Human polynucleoti
c 646	26	13.9	478	23	ABV46773	Human prostate exp
c 647	26	13.9	507	22	AAK70049	Human immune/haema
c 648	26	13.9	507	22	AAK70050	Human immune/haema
c 649	26	13.9	508	23	ABV21474	Human prostate exp
c 650	26	13.9	508	23	ABV27292	Human prostate exp
c 651	26	13.9	508	23	ABV60406	Human prostate exp
c 652	26	13.9	513	23	ABV34138	Human prostate exp
c 653	26	13.9	513	23	ABV43000	Human prostate exp
c 654	26	13.9	522	24	ABL77779	Human ovarian canc
c 655	26	13.9	533	20	AAH10131	Human cDNA clone (
c 656	26	13.9	537	20	AAH10131	Human gene express
c 657	26	13.9	538	22	AAH10203	Human cDNA clone (
c 658	26	13.9	538	23	ABV41555	Human prostate exp
c 659	26	13.9	542	23	ABV19310	Human prostate exp
c 660	26	13.9	548	22	AAH10712	Human cDNA clone (
c 661	26	13.9	558	24	ABN64455	Human cancer relat
c 662	26	13.9	561	22	AAH12647	Human cDNA clone (
c 663	26	13.9	571	22	AAK69674	Human immune/haema
c 664	26	13.9	574	22	AAK69673	Human immune/haema
c 665	26	13.9	574	22	AAK69675	Human cDNA clone (
c 666	26	13.9	609	22	AAH09405	Human cDNA clone (

C 667	26	13.9	614	24	ABN61386	Human cancer relat	C 740	26	13.9	15914	22	AAK73222	Human immune/haema
C 668	26	13.9	628	22	AAS22853	Human cDNA encodin	C 741	26	13.9	16146	22	AAK84529	Human immune/haema
C 669	26	13.9	628	23	ABV54668	Human prostate exp	C 742	26	13.9	16891	20	AAK37084	MEFV gene sequence
C 670	26	13.9	629	22	AAK57818	Human immune/haema	C 743	26	13.9	16939	22	AAU04817	Human reproductive
C 671	26	13.9	634	24	ABN60146	Human cancer relat	C 744	26	13.9	16939	23	ABL97711	Human testicular a
C 672	26	13.9	634	24	ABN61981	Human cancer relat	C 745	26	13.9	17327	14	AAQ44278	Serglycin - proteo
C 673	26	13.9	644	24	ABN61351	Human cancer relat	C 746	26	13.9	17327	14	AAQ44278	Human cytoskeletal
C 674	26	13.9	663	24	ABQ57171	Human cancer relat	C 747	26	13.9	17730	22	AAK529826	Human immune/haema
C 675	26	13.9	795	24	ABN59620	Human colon cancer	C 748	26	13.9	19243	22	AAK71662	Human reproductive
C 676	26	13.9	934	21	AAK59512	Novel human coding	C 749	26	13.9	22689	22	AAU04819	Human cytoskeletal
C 677	26	13.9	978	20	AAK51732	Human secreted pro	C 750	26	13.9	22689	23	ABL97713	Human testicular a
C 678	26	13.9	988	22	AAI93555	DNA encoding a hum	C 751	26	13.9	22735	23	ABL97713	Human ion3 coding
C 679	26	13.9	988	22	AAI93557	Human polynucleoti	C 752	26	13.9	26928	20	AAK32184	Human prothrombin
C 680	26	13.9	1458	21	AAK59929	Human secreted pro	C 753	26	13.9	26928	24	ABN95780	Gene #2278 used to
C 681	26	13.9	1554	20	AAZ10643	DNA encoding a hu	C 754	26	13.9	27841	22	AAK29820	Human cytoskeletal
C 682	26	13.9	1596	22	AAH17127	Human cDNA sequenc	C 755	26	13.9	27841	22	AAK29827	Human cytoskeletal
C 683	26	13.9	1688	24	ABL68589	Kidney cancer rela	C 756	26	13.9	31952	22	AAK89370	Human digestive sy
C 684	26	13.9	1753	22	AAH18420	Human cDNA sequenc	C 757	26	13.9	32192	22	AAK89452	Human digestive sy
C 685	26	13.9	1753	22	AAH18445	Human cDNA sequenc	C 758	26	13.9	32217	22	AAK41738	Genomic sequence #
C 686	26	13.9	1767	22	AAH15897	Human cDNA sequenc	C 759	26	13.9	33718	22	AAK65257	Human immune/haema
C 687	26	13.9	1821	22	AAH17442	Human cDNA sequenc	C 760	26	13.9	33718	22	AAK86411	Human immune/haema
C 688	26	13.9	1899	22	AAH14906	Human cDNA sequenc	C 761	26	13.9	35959	22	AAK78275	Human immune/haema
C 689	26	13.9	2081	24	ABK11363	Human cDNA encodin	C 762	26	13.9	37783	22	AAK70780	Human immune/haema
C 690	26	13.9	2391	22	AAI92576	Human polynucleoti	C 763	26	13.9	37783	22	AAK76625	Human immune/haema
C 691	26	13.9	2575	22	AAK82973	Human immune/haema	C 764	26	13.9	37783	22	AAK80913	Human immune/haema
C 692	26	13.9	2588	24	AAK52260	cDNA sequence #47	C 765	26	13.9	40308	22	AAK68184	Human cDNA differe
C 693	26	13.9	2750	22	AAH16544	Human cDNA sequenc	C 766	26	13.9	57248	24	ABK83563	Gene #3952 used to
C 694	26	13.9	2752	21	AAK69119	Human secreted pro	C 767	26	13.9	76798	24	ABN97454	Human cDNA differe
C 695	26	13.9	2789	22	AAK67124	Human immune/haema	C 768	26	13.9	81800	24	ABK84756	Human cDNA differe
C 696	26	13.9	2810	19	AAV17099	Human brain derive	C 769	26	13.9	89328	24	ABL61995	Human ATP-binding
C 697	26	13.9	2990	22	AAK560842	Human cancer agent	C 770	26	13.9	107820	22	AAK16230	Human transporter
C 698	26	13.9	3121	20	AAK03037	Human IL-1ra BAC C	C 771	26	13.9	126512	24	ABN83429	Human cDNA differe
C 699	26	13.9	3127	23	AAK576376	DNA encoding novel	C 772	26	13.9	175737	24	ABK83571	Human osteoblast d
C 700	26	13.9	3144	22	AAH13942	Human cDNA sequenc	C 773	26	13.9	17896	24	ABQ88146	Human cDNA differe
C 701	26	13.9	3361	22	AAK81871	Human immune/haema	C 774	26	13.9	220895	24	ABK84798	Human cDNA differe
C 702	26	13.9	3566	23	AAK56905	DNA encoding novel	C 775	26	13.9	240825	22	AAK24497	Human PG-3 gene.
C 703	26	13.9	3648	24	ABA95675	Human interleukin-	C 776	26	13.9	325791	22	AAK43104	Human oestrogen re
C 704	26	13.9	3729	22	AAK03253	Human reproductive	C 777	26	13.9	465237	24	ABO87681	Human oestrogen re
C 705	26	13.9	3809	24	AAK45769	Human acid phospho	C 778	26	13.9	465237	24	ABA90193	Human secreted pro
C 706	26	13.9	4837	22	AAK36474	Human musculoskele	C 779	25	13.4	108	21	AAK21941	Human immune/haema
C 707	26	13.9	4932	22	AAK82980	Human immune/haema	C 780	25	13.4	117	22	AAK78904	Human immune/haema
C 708	26	13.9	4933	22	AAK82972	Human immune/haema	C 781	25	13.4	145	21	AAK14944	Human secreted pro
C 709	26	13.9	5204	24	ABK83946	Human cDNA differe	C 782	25	13.4	152	21	AAK65545	Human immune/haema
C 710	26	13.9	5331	22	AAK76629	Human immune/haema	C 783	25	13.4	158	21	AAK04856	Human secreted pro
C 711	26	13.9	5332	22	AAK32735	Human genomic DNA	C 784	25	13.4	176	21	AAK04856	Human secreted pro
C 712	26	13.9	5670	24	ABL65836	Lung cancer relate	C 785	25	13.4	178	22	AAK65541	Human immune/haema
C 713	26	13.9	5690	22	AAI99536	Human polynucleoti	C 786	25	13.4	191	22	AAA41380	Human secreted exp
C 714	26	13.9	6149	22	AAK90925	Human digestive sy	C 787	25	13.4	210	22	AAI80988	Human polynucleoti
C 715	26	13.9	6149	22	AAK90926	Human digestive sy	C 788	25	13.4	229	22	AAI80988	Human polynucleoti
C 716	26	13.9	6149	22	AAK90926	Human liver associ	C 789	25	13.4	239	22	AAK65273	Human immune/haema
C 717	26	13.9	6149	22	AAK90926	Human liver associ	C 790	25	13.4	239	22	AAK69836	Human polynucleoti
C 718	26	13.9	6149	22	AAK90926	Human liver associ	C 791	25	13.4	243	24	AAI80854	Human polynucleoti
C 719	26	13.9	6149	22	AAK90926	Human liver associ	C 792	25	13.4	252	21	ABL85663	Human ovarian canc
C 720	26	13.9	6259	22	AAK93975	Human immune/haema	C 793	25	13.4	257	21	AAK03720	Human ovarian canc
C 721	26	13.9	6389	22	ABA17557	Human nervous syst	C 794	25	13.4	289	21	AAK21549	Human secreted pro
C 722	26	13.9	6744	20	AAZ38125	Human FATP genomic	C 795	25	13.4	294	21	AAK25334	Human secreted pro
C 723	26	13.9	7099	22	AAK04882	Human reproductive	C 796	25	13.4	307	22	ABA20816	Human nervous syst
C 724	26	13.9	7099	22	AAK04882	Human reproductive	C 797	25	13.4	307	22	AAK20816	Human polynucleoti
C 725	26	13.9	7099	22	AAK04882	Human reproductive	C 798	25	13.4	307	22	AAK20816	Human polynucleoti
C 726	26	13.9	12192	22	AAK28195	Genomic sequence #	C 799	25	13.4	313	21	AAK29194	Human secreted pro
C 727	26	13.9	12729	22	AAK97873	Human neuroblastom	C 800	25	13.4	320	22	AAI86771	Human polynucleoti
C 728	26	13.9	12842	22	ABA20815	Human nervous syst	C 801	25	13.4	338	24	ABL85243	Human ovarian canc
C 729	26	13.9	13001	22	AAK92979	Human immune/haema	C 802	25	13.4	340	22	AAK05529	Human reproductive
C 730	26	13.9	13294	22	AAK85255	Human immune/haema	C 803	25	13.4	340	22	AAK70517	Human immune/haema
C 731	26	13.9	14796	19	AAV27941	Survivin gene. Ho	C 804	25	13.4	343	21	AAK12745	Human secreted pro
C 732	26	13.9	14796	22	AAK21523	DNA encoding human	C 805	25	13.4	344	22	AAK01608	Human reproductive
C 733	26	13.9	14796	22	AAH47531	Human Her-3 genomi	C 806	25	13.4	344	22	AAK55080	Human immune/haema
C 734	26	13.9	14796	24	ABN96924	Gene #3422 used to	C 807	25	13.4	346	21	AAK10697	Human secreted pro
C 735	26	13.9	14796	24	ABL65663	Lung cancer relate	C 808	25	13.4	350	22	ABA11527	Human nervous syst
C 736	26	13.9	14796	24	ABL656326	Lung cancer relate	C 809	25	13.4	353	22	AAI80926	Human polynucleoti
C 737	26	13.9	14796	24	ABL68655	Kidney cancer rela	C 810	25	13.4	355	22	ABA18242	Human nervous syst
C 738	26	13.9	15054	22	AAK04025	DNA encoding human	C 811	25	13.4	355	22	AAK23986	Human breast cance
C 739	26	13.9	15054	22	AAK04033	Human reproductive	C 812	25	13.4	365	21	AAK28473	Human breast cance
C 739	26	13.9	15295	22	AAK37039	Human musculoskele				371	22	AAK15140	Human breast cance

C 813	25	13.4	373	22	AA186899	Human polynucleoti	C 886	25	13.4	1457	22	AAK77700	Human immune/haema
C 814	25	13.4	377	22	AA183591	Human polynucleoti	C 887	25	13.4	1473	22	AAF45097	Human secreted pro
C 815	25	13.4	377	22	AAK86977	Human immune/haema	C 888	25	13.4	1588	20	AAK98019	Human secreted pro
C 816	25	13.4	377	22	AAK86978	Human immune/haema	C 889	25	13.4	1625	22	AAK83155	Human immune/haema
C 817	25	13.4	377	22	AAK86979	Human immune/haema	C 890	25	13.4	1625	22	AAK83171	Human immune/haema
C 818	25	13.4	383	22	AAK81123	Human immune/haema	C 891	25	13.4	1650	24	ABL55368	Human leucine zipp
C 819	25	13.4	406	22	AA181312	Human polynucleoti	C 892	25	13.4	1706	22	AAK94092	Human full-length
C 820	25	13.4	409	24	ABL83510	Human ovarian canc	C 893	25	13.4	1730	24	ABL50929	Human bubble prote
C 821	25	13.4	415	22	AA186972	Human polynucleoti	C 894	25	13.4	1780	22	AAH15367	Human cDNA sequenc
C 822	25	13.4	421	22	ABAI11360	Human nervous syst	C 895	25	13.4	1833	22	AAH22596	Human cDNA encodin
C 823	25	13.4	421	23	ABV18008	Human prostate exp	C 896	25	13.4	1833	22	AAH22832	Human cDNA encodin
C 824	25	13.4	430	22	AAK65031	Human immune/haema	C 897	25	13.4	1873	22	AAH17314	Human cDNA sequenc
C 825	25	13.4	434	22	AAK65751	Human immune/haema	C 898	25	13.4	1954	22	AAH17532	Human cDNA sequenc
C 826	25	13.4	434	22	AAK73893	Human immune/haema	C 899	25	13.4	1964	22	AAH05791	Human reproductive
C 827	25	13.4	443	21	AAK26202	Human secreted pro	C 900	25	13.4	1964	23	ABL98355	Human testicular a
C 828	25	13.4	453	22	AA187017	Human polynucleoti	C 901	25	13.4	1970	24	ABO77574	Human cyclophillin-
C 829	25	13.4	465	24	ABL85335	Human ovarian canc	C 902	25	13.4	1984	22	ABA44109	Human breast cell
C 830	25	13.4	467	22	AAK24798	Human ovarian PCR-	C 903	25	13.4	1984	22	ABA54562	Human foetal liver
C 831	25	13.4	475	22	ABA43814	Human breast cell	C 904	25	13.4	1984	22	ABA24345	Probe #2811 for ge
C 832	25	13.4	475	22	ABA54269	Human foetal liver	C 905	25	13.4	1984	22	AAK02855	Human brain expres
C 833	25	13.4	475	22	ABA24024	Probe #2490 for ge	C 906	25	13.4	1984	22	AAK28297	Human bone marrow
C 834	25	13.4	475	22	AAK02547	Human brain expres	C 907	25	13.4	1984	22	AAI12861	Probe #2794 for ge
C 835	25	13.4	475	22	AAK27986	Human bone marrow	C 908	25	13.4	1984	22	AAI13218	Probe #2904 used t
C 836	25	13.4	475	22	AAI12568	Probe #2501 for ge	C 909	25	13.4	1984	22	AAI02777	Probe #2768 used t
C 837	25	13.4	475	22	AAI33915	Probe #2601 used t	C 910	25	13.4	1984	24	ABS02806	Human genome-deriv
C 838	25	13.4	475	22	AAI02475	Probe #2466 used t	C 911	25	13.4	2071	24	AAH98877	cDNA encoding an e
C 839	25	13.4	475	24	ABS02452	Human genome-deriv	C 912	25	13.4	2225	22	AAH16675	Human cDNA sequenc
C 840	25	13.4	477	22	ABA06379	Human cDNA SEQ ID	C 913	25	13.4	2236	22	ABA07878	Human ovarian and
C 841	25	13.4	477	22	AAK50843	cDNA encoding nove	C 914	25	13.4	2236	22	AAK03695	Human reproductive
C 842	25	13.4	477	22	AAK57097	Human immune/haema	C 915	25	13.4	2236	22	AAK66847	Human immune/haema
C 843	25	13.4	484	21	AAK86955	Human immune/haema	C 916	25	13.4	2236	22	AAK69056	Human immune/haema
C 844	25	13.4	489	21	AAK28371	Human secreted pro	C 917	25	13.4	2236	22	AAK72813	Human immune/haema
C 845	25	13.4	513	22	AA186094	Human polynucleoti	C 918	25	13.4	2373	22	AAH13864	Human cDNA sequenc
C 846	25	13.4	513	22	AAH12118	Human cDNA clone (C 919	25	13.4	2404	22	AAH17310	Human cDNA sequenc
C 847	25	13.4	523	23	ABV47797	Human prostate exp	C 920	25	13.4	2583	22	AAK81358	Human immune/haema
C 848	25	13.4	527	22	AAK83169	Human immune/haema	C 921	25	13.4	2627	22	AAH17965	Human cDNA sequenc
C 849	25	13.4	544	23	ABV18300	Human prostate exp	C 922	25	13.4	2656	22	AAK87660	Human immune/haema
C 850	25	13.4	553	22	AAH09954	Human cDNA clone (C 923	25	13.4	2854	22	AAK83164	Human immune/haema
C 851	25	13.4	556	22	AAH83432	Human ovarian tumo	C 924	25	13.4	2901	24	ABA01040	Human uterine glob
C 852	25	13.4	556	22	AAH10417	Human cDNA clone (C 925	25	13.4	3116	22	AAK39688	Genomic sequence #
C 853	25	13.4	557	22	AAH10283	Human cDNA clone (C 926	25	13.4	3116	22	AAK90031	Human digestive sy
C 854	25	13.4	562	21	AAK99969	Human secreted pro	C 927	25	13.4	3304	22	ABA18014	Human nervous syst
C 855	25	13.4	565	24	ABN64837	Human cancer relat	C 928	25	13.4	3396	22	AAK27756	DNA encoding novel
C 856	25	13.4	566	23	ABV56854	Human prostate exp	C 929	25	13.4	3585	22	AAK27755	DNA encoding novel
C 857	25	13.4	574	22	ABA07578	Human ovarian and	C 930	25	13.4	3622	22	AAK86394	Human immune/haema
C 858	25	13.4	574	22	AAI00647	Human reproductive	C 931	25	13.4	3666	24	ABN96799	Gene #3297 used to
C 859	25	13.4	574	22	AAH09363	Human cDNA clone (C 932	25	13.4	3760	22	AAK72031	Human immune/haema
C 860	25	13.4	629	23	ABV58132	Human prostate exp	C 933	25	13.4	4283	22	AAK83180	Human immune/haema
C 861	25	13.4	655	24	ABN62513	Human cancer relat	C 934	25	13.4	4340	24	ABN95734	Gene #2232 used to
C 862	25	13.4	679	21	AAK02065	Human colon cancer	C 935	25	13.4	4412	22	ABA16083	Human immune/haema
C 863	25	13.4	682	22	AAK64694	Human immune/haema	C 936	25	13.4	4678	22	AAK87310	Human immune/haema
C 864	25	13.4	687	22	ABA16476	Human nervous syst	C 937	25	13.4	5025	22	AAK84573	Human immune/haema
C 865	25	13.4	692	21	AAK02064	Human colon cancer	C 938	25	13.4	5029	22	AAK84574	Human immune/haema
C 866	25	13.4	694	22	AAK64203	Human immune/haema	C 939	25	13.4	5054	22	AAK83477	Human immune/haema
C 867	25	13.4	700	22	AAH92688	Human inflammatory	C 940	25	13.4	5216	22	AAK28261	Genomic sequence #
C 868	25	13.4	728	21	AAK99894	Human secreted pro	C 941	25	13.4	5216	22	AAK31528	Human DNA for a no
C 869	25	13.4	738	20	AAK27431	Human cDNA clone (C 942	25	13.4	5216	24	ABO66852	Human polynucleoti
C 870	25	13.4	765	22	AAH08429	Human secreted pro	C 943	25	13.4	5441	22	AAI98937	Human excretory re
C 871	25	13.4	773	24	ABQ89708	Human prostate exp	C 944	25	13.4	5441	22	AAI63287	Human kidney relat
C 872	25	13.4	775	24	ABQ89633	Human prostate exp	C 945	25	13.4	5814	22	AAK83448	Human immune/haema
C 873	25	13.4	781	20	AAI21516	Human gene expres	C 946	25	13.4	5932	22	AAI03052	Human reproductive
C 874	25	13.4	806	22	AAH04371	Human cDNA clone (C 947	25	13.4	5932	23	ABL97388	Human testicular a
C 875	25	13.4	938	24	ABQ88881	Human prostate exp	C 948	25	13.4	5966	22	ABA07890	Human ovarian and
C 876	25	13.4	1032	22	AAK83157	Human immune/haema	C 949	25	13.4	5966	22	AAI03707	Human reproductive
C 877	25	13.4	1032	22	AAK83479	Human immune/haema	C 950	25	13.4	6071	22	AAK27758	DNA encoding novel
C 878	25	13.4	1034	22	AAK83478	Human immune/haema	C 951	25	13.4	6440	22	AAK68762	Human immune/haema
C 879	25	13.4	1241	21	AAK79745	Human secreted pro	C 952	25	13.4	6440	22	AAK68763	Human immune/haema
C 880	25	13.4	1242	22	AAH15609	Human cDNA sequenc	C 953	25	13.4	6440	22	AAK68764	Human immune/haema
C 881	25	13.4	1317	22	AAK84446	Human immune/haema	C 954	25	13.4	6512	22	AAK27757	DNA encoding novel
C 882	25	13.4	1381	15	AAK077883	Neural thread prot	C 955	25	13.4	6686	22	AAK81545	Human immune/haema
C 883	25	13.4	1381	17	AAI27765	AD 10-7 human neur	C 956	25	13.4	6751	22	AAK83163	Human immune/haema
C 884	25	13.4	1400	22	AAK24242	Human oxidoreducta	C 957	25	13.4	6767	22	AAK83147	Human immune/haema
C 885	25	13.4	1433	24	ABK34834	Human cDNA for nov	C 958	25	13.4	6945	22	AAK88968	Human digestive sy

c 959 25 13.4 6945 22 AAK88969 Human digestive sy
 c 960 25 13.4 6945 22 AAK31837 Human liver associ
 c 961 25 13.4 6945 22 AAK31838 Human liver associ
 c 962 25 13.4 6945 24 ABN90192 Human liver antige
 c 963 25 13.4 6945 24 ABN90193 Human liver antige
 c 964 25 13.4 7042 21 AAK84785 Apoptosis inducer
 c 965 25 13.4 7042 21 AAK24656 Human full-length
 c 966 25 13.4 7042 21 AAK91128 Wild type Apaf-1 c
 c 967 25 13.4 7042 24 AAK93574 Human apoptotic pr
 c 968 25 13.4 7075 20 AAV84798 Apoptosis inducer
 c 969 25 13.4 7166 22 AAK32736 Human genomic DNA
 c 970 25 13.4 7301 24 ABA98878 Genomic DNA encodi
 c 971 25 13.4 7633 22 AAK83159 Human immune/haema
 c 972 25 13.4 7725 22 AAK87157 Human immune/haema
 c 973 25 13.4 7858 22 AAK67290 Human immune/haema
 c 974 25 13.4 8003 22 AAK83149 Human immune/haema
 c 975 25 13.4 8021 22 AAK85877 Human immune/haema
 c 976 25 13.4 8121 22 AAK36189 Human cardiovascular
 c 977 25 13.4 8190 22 ABA18373 Human nervous syst
 c 978 25 13.4 8253 22 AAS40470 DNA encoding human
 c 979 25 13.4 8253 22 AAL04087 Human reproductive
 c 980 25 13.4 8253 22 AAS30465 DNA encoding novel
 c 981 25 13.4 8794 22 AAL06245 Human reproductive
 c 982 25 13.4 8846 22 ABA15292 Human nervous syst
 c 983 25 13.4 9133 22 AAK83165 Human immune/haema
 c 984 25 13.4 9192 22 AAL35853 Human musculoskele
 c 985 25 13.4 9192 23 AAK42359 Genomic sequence #
 c 986 25 13.4 9217 22 AAK83151 Human immune/haema
 c 987 25 13.4 9337 22 AAK76038 Human immune/haema
 c 988 25 13.4 9337 22 AAK78564 Human immune/haema
 c 989 25 13.4 9837 18 AAT96851 Intron 21 of human
 c 990 25 13.4 10102 22 AAK83072 Human immune/haema
 c 991 25 13.4 10497 22 AAK67302 Human immune/haema
 c 992 25 13.4 10497 22 AAK83166 Human immune/haema
 c 993 25 13.4 10899 22 ABA15344 Human nervous syst
 c 994 25 13.4 11079 22 AAK90954 Human digestive sy
 c 995 25 13.4 11079 22 AAK31989 Human liver associ
 c 996 25 13.4 11079 24 ABN90344 Human liver antige
 c 997 25 13.4 11244 22 AAK74606 Human immune/haema
 c 998 25 13.4 11266 24 AAL43028 Human P2X7 gene in
 c 999 25 13.4 11298 23 ABA42456 Genomic sequence #
 c1000 25 13.4 11655 22 AAK87506 Human immune/haema

ALIGNMENTS

RESULT 1
 ID AAA64508 standard; cdna; 5492 BP.
 XX
 AC AAA64508;
 XX

DT 02-JAN-2001 (first entry)
 XX

DE cdna sequence of the wild type human FEZ1 gene.
 XX

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
 KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
 KW tumorigenesis; tumour survival; metastasis; ss.
 XX

OS Homo sapiens.
 XX

XX WO200050565-A2.
 XX

XX 31-AUG-2000.
 PD

XX 25-FEB-2000; 2000WO-US04950.
 PF

XX 25-FEB-1999; 99US-0121537.
 PR

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Croce CM, Ishii H;
 XX
 DR WPI; 2000-558396/51.
 XX
 PT New polynucleotide homologous with a portion of one strand of the human
 PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
 PT cancer -
 XX
 PS Example 2; Fig 5B; 255pp; English.
 XX

XX The present sequence represents the cDNA sequence of the human FEZ1 gene.
 CC FEZ1 is a tumour suppressor gene, located at chromosome location 8p22.
 CC Decreased or no expression of FEZ1 is detected in a variety of cancer
 CC cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
 CC also interacts with tubulin, with microtubules, and with protein
 CC Efi-gamma. Post-translational phosphorylation and dephosphorylation
 CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
 CC expression are useful for inducing cells to proliferate. Compounds
 CC which modulate FEZ1 association with tubulin are useful for alleviating
 CC tubulin hyper- or hypo- polymerisation disorders, such as those
 CC associated with aberrant initiation of mitosis, modulation of the
 CC initiation and rate of cell proliferation and cell growth, modulation of
 CC cell shape, cell rigidity, cell motility, rate and stage of cellular
 CC DNA replication, intracellular distribution of organelles, metastatic
 CC potential of cell and cellular transformation from a non-cancerous to
 CC cancerous phenotype. Compounds which modulate FEZ1 binding and
 CC phosphorylation are also useful for alleviating a disorder, such as
 CC tumorigenesis, tumour survival, growth and metastasis.
 XX

SQ Sequence 5492 BP; 1137 A; 1704 C; 1565 G; 1086 T; 0 other;

Query Match 100.0%; Score 187; DB 21; Length 5492;
 Best Local Similarity 100.0%; Pred. No. 1.3e-82;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATATAGTCTCAGCTGCGCTCTACTCTCTGGCTCAAGCAATCTCTGCTCAGCC 60
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Db 3348 ATCATATAGTCTCAGCTGCGCTCTACTCTCTGGCTCAAGCAATCTCTGCTCAGCC 3407
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QY 61 TTCCAACATAGCTGGGACTCAGTGGCGGCCACCGTGGCTGCTAACTTTTCAATTTT 120
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Db 3408 TTCCAACATAGCTGGGACTCAGTGGCGGCCACCGTGGCTGCTAACTTTTCAATTTT 3467
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QY 121 TGTAGGACGGGTCTCGTTTGTGTCGAAGCTGGTCTCAAACTTGTGGCTCAAGCAA 180
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Db 3468 TGTAGGACGGGTCTCGTTTGTGTCGAAGCTGGTCTCAAACTTGTGGCTCAAGCAA 3527
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QY 181 TCCACCT 187
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Db 3528 TCCACCT 3534

RESULT 2

AAA64507

ID AAA64507 standard; DNA; 9048 BP.

XX AAA64507;

AC AAA64507;

XX 02-JAN-2001 (first entry)

XX Nucleotide sequence comprising the human FEZ1 gene.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
 KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
 KW tumorigenesis; tumour survival; metastasis; ss.
 XX

OS Homo sapiens.
 XX

XX WO200050565-A2.
 PN

XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US04950.
XX 25-FEB-1999; 99US-0121537.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Croce CM, Ishii H;
XX WPI; 2000-558396/51.
XX New polynucleotide homologous with a portion of one strand of the human
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
PT cancer -
XX Claim 2; Fig 5A; 255pp; English.
XX The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour
CC suppressor gene, located at chromosome location 8p22. Decreased or no
CC expression of FEZ1 is detected in a variety of cancer cells. Expression
CC of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts
CC with tubulin, with microtubules, and with protein ERF-gamma.
CC Post-translational phosphorylation and dephosphorylation modulates the
CC effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are
CC useful for inducing cells to proliferate. Compounds which modulate FEZ1
CC association with tubulin are useful for alleviating tubulin hyper- or
CC hypo- polymerisation disorders, such as those associated with aberrant
CC initiation of mitosis, modulation of the initiation and rate of cell
CC proliferation and cell growth, modulation of cell shape, cell rigidity,
CC cell motility, rate and stage of cellular DNA replication, intracellular
CC distribution of organelles, metastatic potential of cell and cellular
CC transformation from a non-cancerous to cancerous phenotype. Compounds
CC which modulate FEZ1 binding and phosphorylation are also useful for
CC alleviating a disorder, such as tumorigenesis, tumour survival, growth
CC and metastasis.
XX SQ Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;
Query Match 100.0%; Score 187; DB 21; Length 9048;
Best Local Similarity 100.0%; Pred. No. 1.3e-82;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGATCATAGCTACTGCGCTCATACTCTGGGCTCAAGCAATCTCTGCTCGCTCAGCC 60
Db 6939 ATGATCATAGCTACTGCGCTCATACTCTGGGCTCAAGCAATCTCTGCTCGCTCAGCC 6998
Qy 61 TTCAACTAGCTGGGCTGCTGCTTTGTTGCAAGCTGGTCTCAAACTTGTGGCTCAGCAA 120
Db 6999 TTCAACTAGCTGGGCTGCTGCTTTGTTGCAAGCTGGTCTCAAACTTGTGGCTCAGCAA 7058
Qy 121 TGTAGGACGGGCTGCTGCTTTGTTGCAAGCTGGTCTCAAACTTGTGGCTCAGCAA 180
Db 7059 TGTAGGACGGGCTGCTGCTTTGTTGCAAGCTGGTCTCAAACTTGTGGCTCAGCAA 7118
Qy 181 TCCACCT 187
Db 7119 TCCACCT 7125
RESULT 3
ABAI7068/c
ID ABAI7068 standard; DNA; 12767 BP.
XX ABAI7068;
AC ABAI7068;
XX 23-JAN-2002 (first entry)
XX Human nervous system related polynucleotide SEQ ID NO 9399.
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW

KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebrotective; antiinflammatory;
KW antiallergic; antidiabetic; antituber; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX Homo sapiens.
OS WO200159063-A2.
XX 16-AUG-2001.
PD 17-JAN-2001; 2001WO-US01334.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184564.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
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PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.

PR	14-SEP-2000;	2000US-02330655;
PR	21-SEP-2000;	2000US-02334223;
PR	21-SEP-2000;	2000US-02342714;
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PR	29-SEP-2000;	2000US-02363699;
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PR	02-OCT-2000;	2000US-02368002;
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PR	02-OCT-2000;	2000US-02370388;
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PR	08-NOV-2000;	2000US-02464833;
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PR	08-NOV-2000;	2000US-02464839;
PR	08-NOV-2000;	2000US-02464840;
PR	08-NOV-2000;	2000US-02464841;
PR	08-NOV-2000;	2000US-02464842;
PR	08-NOV-2000;	2000US-02464843;
PR	08-NOV-2000;	2000US-02464844;
PR	08-NOV-2000;	2000US-02464845;
PR	08-NOV-2000;	2000US-02464846;
PR	08-NOV-2000;	2000US

08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-541565/60.
Nucleic acids encoding 3224 human nervous system antigen polypeptides
useful for preventing, diagnosing and/or treating nervous system
cancers and metastases -
Disclosure; SEQ ID NO 9399; 1701pp + Sequence Listing; English.
The invention relates to novel genes (ABAl1004-ABR21534) and proteins
(ABBA14678-ABBI18001) useful for preventing, treating or ameliorating
medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification
The nucleic acids, proteins, antibodies and (ant)agonists are useful
in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
and ovarian cancer and other cancers of the adrenal gland, bone, bone
marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
(b) immune disorders e.g. Addison's disease, allergies, autoimmune
hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
disease, multiple sclerosis, rheumatoid arthritis and ulcerative
colitis; (c) cardiovascular disorders such as myocardial ischaemia;
(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections.
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Sequence 12767 BP; 4099 A; 2208 C; 2513 G; 3947 T; 0 other;

Query Match 21.4%; Score 40; DB 22; Length 12767;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 40: Conservative 0; Mismatches 0; Indels 0

QY 27 ACTCTGGGCTCAAGCAATCCTCTGCTCAGCCTTCCAA 66
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RESULT 4
AAD36072/c
ID AAD36072 standard: DNA: 18997 BP.

XX
AC

DT 09-AUG-2002 (first entry)

DE Human POLD2 genomic DNA.

Human, chromosome 7; snare YKT6; adipocyte enhancer binding protein; AEBP1; liver glucokinase; DNA directed 50 kDa regulatory subunit; POLD2; cell growth; tumour; apoptosis; virus-induced lymphocyte depletion; AIDS; acquired immune deficiency syndrome; hyperglycaemia; Alzheimer's disease; neurodegenerative disorder; gene therapy; Parkinson's disease; stroke; ALS; amyotrophic lateral sclerosis; retinitis pigmentosa; adipogenesis; spinal muscular atrophy; cerebellar degeneration; blood cell disorder; aplastic anaemia; myocardial infarction; diabetes mellitus; obesity; chronic neutropenia; myelodysplastic syndrome; osteopenic disorder; DNA repair; xeroderma pigmentosum; progeria; ataxia telangiectasia; ATP; D-hexose 6-phosphotransferase; gene; ds.

OS Homo sapiens.

XX	Key	Location/Qualifiers
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FT	CDS	11546..18814

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FT FT /tag= u
XX XX WO200224741-A2.
XX XX 28-MAR-2002.
XX XX 21-SEP-2001; 2001WO-US29454.
XX XX 21-SEP-2000; 2000US-234422P.
XX XX (RYAN/) RYAN J W.
XX XX Ryan JW;
```

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XX WPI; 2002-394128/42.
DR P-PSDB; AAE22740.
XX
PT Novel genomic polynucleotide from human chromosome-7 encoding snare
PT YKT6, liver glucokinase, adipocyte enhancer binding protein (AEBP1) and DNA
PT delta small subunit useful in gene therapy for treating e.g. diabetes,
PT cancer -
XX
PS Claim 1; Page 54-63; 94pp; English.
XX
CC The present invention relates to novel genomic polynucleotide from human
CC chromosome 7 encoding human snare YKT6, liver glucokinase (ATP: D-hexose
CC 6-phosphotransferase), adipocyte enhancer binding protein (AEBP1) and DNA
CC directed 50 kDa regulatory subunit (POLD2). Sequences of the invention
CC are used to prevent, treat or ameliorate a medical condition. Antisense
CC oligonucleotides specific for snare YKT6 are useful for inhibiting cell
CC growth and in particular to treat or prevent tumour growth. Glucokinase
CC and AEBP are useful for treating hyperglycaemia. Genomic sequences of
CC the invention are useful for gene therapy e.g., SNARE YKT6 is useful to
CC modulate or prevent cell apoptosis and treat disorder such as virus-
CC induced lymphocyte depletion (AIDS-acquired immune deficiency syndrome),
CC cell death in neurodegenerative disorders (e.g., Alzheimer's disease,
CC Parkinson's disease, ALS (amyotrophic lateral sclerosis), retinitis
CC pigmentosa, spinal muscular atrophy and various forms of cerebellar
CC degeneration), cell death in blood cell disorders resulting from the
CC deprivation of growth factors (anaemia associated with chronic disease,
CC aplastic anaemia, chronic neutropenia and myelodysplastic syndromes)
CC and disorders arising from acute loss of blood flow such as stroke and
CC myocardial infarctions. Glucokinase gene is useful for treating diabetes
CC mellitus. AEBP is useful in modulating or inhibiting adipogenesis and
CC in treating obesity, diabetes mellitus or osteopenic disorders. POLD2 is
CC useful in treating defects in DNA repair such as xeroderma pigmentosum,
CC progeria and ataxia telangiectasia. The present sequence is human POLD2
CC genomic DNA.
XX
SQ Sequence 18997 BP; 4650 A; 4852 C; 5028 G; 4467 T; 0 other;

Query Match 21.4%; Score 40; DB 24; Length 18997;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 66
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Db 6339 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 6300

RESULT 5
AAS20588
ID AAS20588 standard; DNA; 84495 BP.
XX
AC AAS20588;
XX
XX 23-APR-2002 (first entry)
XX
DE Human methionine aminopeptidase protease genomic DNA.
XX
KW Human; methionine aminopeptidase; protease; adrenal cortico adenoma; ds;
KW Cushing's syndrome; prostate embryonal carcinoma; colon tumour; brain;
KW hepatocellular carcinoma; foetal lung; testis; b cell; kidney; prostate;
KW gene.
XX
OS Homo sapiens.
XX
PN US6329188-B1.
XX
PD 11-DEC-2001.
XX
PF 05-MAR-2001; 2001US-0797906.
XX
PR 02-MAR-2001; 2001US-0797000.
XX
PA (PEKE ) PE CORP NY.
```


CC DNA encoding GST-4alpha and GST-4beta. GST-4 gene is found on
CC chromosome 16q23.1.
CC GST is a type 2 membrane protein useful for inhibiting a binding event
CC between a selectin and a selectin ligand, which comprises contacting the
CC selectin with a non-sulphated selectin ligand. GST and a small molecular
CC agent that inhibits the sulphation activity of GST. GST is also useful
CC in inhibiting a selectin mediated binding event. GST is useful in gene
CC therapy to treat disorders such as acute or chronic inflammation,
CC systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis
CC nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes,
CC glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's
CC disease, Grave's disease, adenitis, hypoparathyroidism, pernicious
CC anaemia, demyelinating diseases, cirrhosis, ulcerative colitis,
CC dermatitis, myocarditis, regional enteritis, adult respiratory distress
CC syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis,
CC bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection
CC during transplantation.

XX Sequence 160552 BP; 40281 A; 37573 C; 38015 G; 44564 T; 119 other;

Query Match 21.4%; Score 40; DB 22; Length 160552;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 66
|||||
Db 24529 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 24490

RESULT 7

AAS17764
ID AAS17764 standard; DNA; 24843 BP.

XX AAS17764;

XX 12-MAR-2002 (first entry)

XX Human Genomic DNA for CRYBB1.

XX Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmological;
KW cataract; allele specific oligonucleotide; ASO; ds; haplotype;
KW genotyping; transgenic animal.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 4014..20843
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FT replace (1830,A)
FT /*tag= b
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FT /note= "Polymorphic site 1"
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FT /note= "Polymorphic site 6"

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XX WO200185998-A1.

XX 15-NOV-2001.

XX 07-MAY-2001; 2001WO-US14715.

XX 05-MAY-2000; 2000US-202253P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Kazemi A, Kliem SE, Koshy B, Rounds E;

XX WPI; 2002-062253/08.

XX P-PSDB; AAU11447.

XX Novel polymorphic variants of crystallin, beta B1 useful in studying
FT expression and function of the protein, useful for screening candidate
FT drugs to treat diseases e.g. cataract

XX Claim 19; Fig 1; 94pp; English.

XX The invention relates to an isolated polynucleotide comprising a
CC sequence which is a polymorphic variant of a reference sequence for
CC crystallin, beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their
CC fragment, where the polymorphic variant comprises a CRYBB1 isogene
CC defined by a haplotype from haplotypes 1-16 as given in the
CC specification. Also included are a transgenic non-human animal
CC transformed or transfected with the polymorphic variant, a computer
CC system for storing and analysing polymorphism data for CRYBB1 gene, a
CC genome anthology for the CRYBB1 gene which comprises the defined CRYBB1
CC isogenes, methods of determining an individual's haplotype or
CC genotype as well as methods of determining the association of a
CC particular haplotype with a disease or trait and a composition comprising
CC at least one genotyping oligonucleotide (especially allele-specific
CC oligonucleotides (ASO)) for detecting a polymorphism in the CRYBB1.
CC The isogenes or haplotypes are useful for improving the efficiency and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with CRYBB1 activity, e.g. cataract.
CC and can also be used by the pharmaceutical research scientist to
CC validate CRYBB1 as a candidate target for, and in design of clinical
CC trials of candidate drugs for, treating a specific condition or
CC disease predicted to be associated with CRYBB1 activity. The ASOs are
CC useful as probes and primers, and for assaying a polymorphism in the
CC target region. The present sequence is the genomic DNA encoding
CC CRYBB1.

XX Sequence 24843 BP; 6532 A; 6034 C; 5997 G; 6280 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      29 TCCTGGGCTCAAGCAATCCTCTGCTCAGCCTTCCAA 66
Db      17814 TCCTGGGCTCAAGCAATCCTCTGCTCAGCCTTCCAA 17851

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ID  ABAI5496 standard; DNA; 328 BP.
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AC  ABAI5496;
XX
DT  23-JAN-2002 (first entry)
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DE  Human nervous system related polynucleotide SEQ ID NO 7827.
XX
KW  Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
KW  immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW  antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
KW  antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW  antiallergic; antidiabetic; antilulcer; anticonvulsant; antifungal;
KW  antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW  neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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OS  Homo sapiens.
XX
FN  WO200159063-A2.
XX
PD  16-AUG-2001.
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PF  17-JAN-2001; 2001WO-US01334.
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PR  31-JAN-2000; 2000US-0179065.
PR  04-FEB-2000; 2000US-0180628.
PR  24-FEB-2000; 2000US-0184664.
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PR 17-NOV-2000; 2000US-0249244.
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PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 03-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases -
XX
XX Disclosure; SEQ ID NO 7827; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABAI1004-ABA21534) and proteins
XX (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful
XX in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
XX and ovarian cancer and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.
XX
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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XX Sequence 328 BP; 86 A; 78 C; 75 G; 89 T; 0 other;
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XX Query Match 19.8%; Score 37; DB 22; Length 328;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-08;
XX Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX RESULT 9
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XX ID AA196106 standard; cDNA; 831 BP.
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XX 13-NOV-2001 (first entry)
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XX Human neuroblastoma expressed polynucleotide SEQ ID NO 2181.
XX
XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
XX
XX Homo sapiens.
XX
XX WO200166719-A1.
XX
XX 13-SEP-2001.
XX
XX 02-MAR-2001; 2001WO-JP01629.
XX
XX 07-MAR-2000; 2000JP-0159195.
XX
XX (CHIB-) CHIBA PREFECTURE.
XX
XX (HISM) HISAMITSU PHARM CO LTD.
XX
XX Nakagawara A;
XX
XX WPI; 2001-565584/63.
XX
XX Nucleic acids originating in gene expressed in human neuroblastoma,
XX useful as probe or primer in diagnosing prognosis of human
XX neuroblastoma, malignancy and susceptibility indicator or tumour marker
XX for anti-cancer agents -
XX
XX Claim 1; Page 1608-1609; 2979pp; Japanese.
XX
XX The invention relates to novel genes (AAI93926-AAI97963) expressed in
XX human neuroblastoma. The nucleic acids are applicable as a probe or
XX primer in diagnosing the prognosis of human neuroblastoma, malignancy and
XX susceptibility indicators or tumour markers for anti-cancer agents. The
XX gene information for diagnosing prognosis is related to factors similar
XX to that for N-myc and TrkA genes.
XX
XX Sequence 831 BP; 220 A; 156 C; 166 G; 256 T; 33 other;
XX
XX Query Match 19.3%; Score 36; DB 22; Length 831;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-08;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 31 CTGGGCTCAAGCAATCTCTGCTCAGCCTTCCTCAA 66
XX
XX 222 CTGGGCTCAAGCAATCTCTGCTCAGCCTTCCTCAA 257
XX
XX
XX RESULT 10
XX AAL36563
XX ID AAL36563 standard; DNA; 27483 BP.
XX
XX AAL36563;
XX
XX 08-JAN-2002 (first entry)
XX
XX Human musculoskeletal system related polynucleotide SEQ ID NO 2928.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein;
XX musculoskeletal system; ds.
XX
XX Homo sapiens.
XX
XX WO200155367-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01338.
XX
XX PF
```

XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 13-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232337.
PR 14-SEP-2000; 2000US-0232338.
PR 14-SEP-2000; 2000US-0232339.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
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PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
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PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/ or prognosing
disorders related to the musculoskeletal system including

PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246529.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249287.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX Disclosure; SEQ ID NO 9663; 1297pp + Sequence Listing; English.
XX The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
XX Sequence 32250 BP; 9497 A; 6491 C; 6656 G; 9606 T; 0 other;
XX Query Match 19.3%; Score 36; DB 22; Length 32250;
XX Best Local Similarity 100.0%; Pred. No. 4e-08;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 TACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
|||||

Db 1584 TACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 1549
RESULT 12
ABL84298/c
ID ABL84298 standard; cDNA; 359 BP.
XX AC ABL84298;
XX AC ABL84298;
DT 17-MAY-2002 (first entry)
XX Human ovarian cancer related cDNA clone SEQ ID NO:7276.
DE Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX Homo sapiens.
OS WO200192581-A2.
PN 06-DEC-2001.
PD 29-MAY-2001; 2001WO-US17756.
XX 26-MAY-2000; 2000US-207484P.
PR (CORI-) CORIXA CORP.
PA Algate PA, Harlocker SL, Jones R;
XX WPI; 2002-122075/16.
DR Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
XX polypeptide
XX Claim 1; SEQ ID 7276; 489pp; English.
XX The present invention describes a composition (I) comprising: carriers
XX and immunostimulants; and a polypeptide (II) of a ovarian tumour
XX polypeptide encoded by a polynucleotide (III) having a cDNA sequence
XX (S1) from the 10912 nucleotide sequences as given in ABL77023 to
XX ABL87934. (III) encoding (II) having a sequence (S2), a T cell
XX population of (II), or antigen presenting cells that express (II).
XX (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
XX (I) can be used for detecting ovarian cancer in a patient's biological
XX sample preferably serum or ovarian tissue. The method comprises
XX contacting a biological sample from a patient with (IV), detecting the
XX amount of polynucleotide hybridising to (IV) and comparing the amount to
XX a predetermined cutoff value and thereby detecting ovarian cancer in the
XX patient, where the amount of polynucleotide hybridising to (IV) is
XX detected preferably by polymerase chain reaction (PCR). (I) comprising
XX (III) and/or (II) is useful for stimulating and/or expanding T cells
XX specific for an ovarian tumour protein comprising contacting T cells
XX with (III) or (II). (III) is useful in design and preparation of
XX ribozyme molecules for inhibiting expression of the tumour polypeptides
XX and proteins in tumour cells; and to isolate a full length gene from a
XX suitable library e.g., a tumour cDNA library using well known
XX techniques.
XX SQ Sequence 359 BP; 116 A; 57 C; 69 G; 117 T; 0 other;
XX Query Match 18.7%; Score 35; DB 24; Length 359;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-07;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
|||||
Db 335 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 301
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RESULT 13
AAI86984/c

```

ID AAI85984 standard; cDNA; 406 BP.
XX AC
XX AAI86984;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 7044.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX
XX P-PSDB; AAO07053.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX
XX Claim 1; SEQ ID NO 7044; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 406 BP; 138 A; 64 C; 90 G; 114 T; 0 other;

Query Match 18.7%; Score 35; DB 22; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ACTCTGGGCTCAGCAATCCTCTGCTCAGCCT 61
Db 338 ACTCTGGGCTCAGCAATCCTCTGCTCAGCCT 304

RESULT 14
AAI88863
XX
XX AAI88863 standard; cDNA; 414 BP.
XX
XX AAI88863;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 8923.
XX
XX Homo sapiens.
XX
XX WO200102568-A2.
XX
XX 11-JAN-2001.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
KW
KW Homo sapiens.
KW
KW WO200164835-A2.
KW
KW 07-SEP-2001.
KW
KW 26-FEB-2001; 2001WO-US04927.
KW
KW 28-FEB-2000; 2000US-0515126.
KW
KW 18-MAY-2000; 2000US-0577409.
KW
KW (HYSE-) HYSEQ INC.
KW
KW Tang YT, Liu C, Drmanac RT;
KW
KW WPI; 2001-514838/56.
KW
KW P-PSDB; AAO08932.
KW
KW Isolated nucleic acids and polypeptides, useful for preventing
KW diagnosing and treating e.g. leukaemia, inflammation and immune
KW disorders -
KW
KW Claim 1; SEQ ID NO 8923; 1399pp + Sequence Listing; English.
KW
KW The invention relates to human polynucleotides (AAI79941-AAI93841) and
KW the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
KW cytokine, cell proliferation or cell differentiation or which may induce
KW production of other cytokines in other cell populations. The
KW polynucleotides and polypeptides are useful in gene therapy, vaccines or
KW peptide therapy. The polypeptides have various cytokine-like activities,
KW e.g. stem cell growth factor activity, haematopoiesis regulating
KW activity, tissue growth factor activity, immunomodulatory activity and
KW activin/inhibin activity and may be useful in the diagnosis and/or
KW treatment of cancer, leukaemia, nervous system disorders, arthritis and
KW inflammation.
KW
KW Note: The sequence data for this patent did not form part of the printed
KW specification, but was obtained in electronic format directly from WIPO
KW at ftp.wipo.int/pub/published_pct_sequences.
KW
KW Sequence 414 BP; 91 A; 96 C; 81 G; 146 T; 0 other;

Query Match 18.7%; Score 35; DB 22; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ACTCTGGGCTCAGCAATCCTCTGCTCAGCCT 61
Db 30 ACTCTGGGCTCAGCAATCCTCTGCTCAGCCT 64

RESULT 15
AAI67176/c
ID AAI67176 standard; cDNA; 417 BP.
XX
XX AAI67176;
XX
XX 09-APR-2001 (first entry)
XX
XX Novel human polynucleotide, SEQ ID NO: 2932.
XX
XX Human; cytostatic; gene therapy; colon cancer; prostate cancer;
XX breast cancer; lung cancer; cancer detection; ss.
XX
XX Homo sapiens.
XX
XX WO200102568-A2.
XX
XX 11-JAN-2001.
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XX 30-JUN-2000; 2000WO-US18374.
XX
XX
XX 02-JUL-1999; 99US-0142310.
XX 02-JUL-1999; 99US-0142311.
XX
XX (CHIR) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
XX Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
XX Crknenjakov R, Drmanac S, Dickson M, Labat I, Leshkowitz D;
XX Kita D, Garcia V, Jones LW, Strache-Crain B;
XX
XX WPI; 2001-091805/10.
XX
XX Library of polynucleotides for diagnosing a cancerous state of a
XX mammalian cell and detecting cancer, particularly of the colon or
XX prostate, comprises 3351 human polynucleotide sequences -
XX
XX Claim 9; Page 981; 1046pp; English.
XX
XX The present sequence is one of 3351 sequences in a library of human
XX polynucleotides. The library is used to detect differentially expressed
XX genes correlated with a cancerous state of a mammalian cell and can
XX detect colon, prostate, breast and lung cancer. The library can be used
XX to produce probes for detection of mRNA and to produce additional copies
XX of the polynucleotides. The probes can be used for chromosome mapping of
XX the polynucleotide and for detection of transcription levels. Ribozymes
XX or antisense oligonucleotides can be generated. The polynucleotides and
XX their gene products are used as genetic or biochemical markers (e.g. in
XX blood or tissues) that will detect the earliest changes along the
XX carcinogenesis pathway and/or monitor the efficacy of therapies and
XX preventive interventions. The polynucleotides, polypeptides and
XX antibodies against them can be used in pharmaceutical compositions to
XX treat the cancers and proliferative disorders such as neoplasia,
XX dysplasia and hyperplasia.
XX
XX Sequence 417 BP; 152 A; 91 C; 102 G; 72 T; 0 other;

Query Match 18.7%; Score 35; DB 22; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db |||||
94 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 60

Search completed: June 16, 2003, 20:03:54
Job time : 54.0127 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 7.32011 Seconds
(without alignments)
7834.381 Million cell updates/sec

Title: US-09-513-888C-1_COPY_6939_7125

Perfect score: 187

Sequence: 1 atgcatcatgctcactgcag.....tggcctcaagcaatccacct 187

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA.*

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- 2: /cgm2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgm2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgm2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgm2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgm2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	21.4	84495	4	US-09-797-906-3
C 2	35	18.7	81001	4	US-09-750-580-1
3	35	18.7	176373	3	US-09-128-155-17
4	34	18.2	2589	2	US-08-482-728A-3
C 5	34	18.2	3350	1	US-08-247-946A-2
C 6	34	18.2	3350	5	PCT-US95-06420-2
C 7	33	17.6	70000	4	US-09-851-896-3
C 8	33	17.6	84495	4	US-09-797-906-3
9	30	16.0	674	4	US-09-328-111-76
C 10	30	16.0	4066	4	US-09-367-750-1
C 11	29	15.5	636	2	US-08-284-941-3
C 12	29	15.5	636	2	US-08-447-642-3
C 13	29	15.5	636	4	US-09-236-503-3
C 14	29	15.5	636	5	PCT-US93-02147A-3
C 15	29	15.5	98844	4	US-09-791-211-10
16	28	15.0	11811	4	US-09-078-294-7
C 17	28	15.0	16063	4	US-09-801-052-3
C 18	28	15.0	19011	1	US-08-310-356-36
C 19	28	15.0	19557	5	PCT-US92-06300-1
C 20	28	15.0	36651	4	US-09-738-894A-3
21	28	15.0	38564	4	US-09-734-673-3
22	28	15.0	59065	4	US-09-813-817-3
23	28	15.0	59065	4	US-09-978-197-3
C 24	27	14.4	1613	4	US-09-061-154-1
C 25	27	14.4	1613	4	US-09-061-154-3
C 26	27	14.4	4129	2	US-08-370-319C-12
C 27	27	14.4	4129	4	US-08-224-834-12

c 101	23	12.3	15936	4	US-09-147-119-1	Sequence 1, Appl	174	21	11.2	3136	4	US-09-215-649A-5	Sequence 5, Appl
c 102	23	12.3	17327	1	US-07-906-871-15	Sequence 15, Appl	175	21	11.2	3136	4	US-09-577-780-5	Sequence 5, Appl
c 103	23	12.3	35100	1	US-08-306-691B-19	Sequence 19, Appl	c 176	21	11.2	3741	4	US-09-541-782-9	Sequence 9, Appl
c 104	23	12.3	35100	5	PCT-US93-06251-19	Sequence 3, Appl	c 177	21	11.2	3741	4	US-09-723-820-9	Sequence 10, Appl
c 105	23	12.3	36741	3	US-09-301-665-3	Sequence 79, Appl	c 178	21	11.2	10825	3	US-09-659-791A-10	Sequence 1, Appl
c 106	23	12.3	87350	3	US-08-781-891-79	Sequence 79, Appl	c 179	21	11.2	10825	3	US-08-652-265-1	Sequence 3, Appl
c 107	23	12.3	87350	3	US-08-781-891-79	Sequence 79, Appl	c 180	21	11.2	10825	3	US-08-652-265-3	Sequence 3, Appl
c 108	23	12.3	87543	4	US-09-791-211-3	Sequence 3, Appl	c 181	21	11.2	10825	3	US-08-652-265-5	Sequence 5, Appl
c 109	23	12.3	87543	4	US-09-791-211-3	Sequence 3, Appl	c 182	21	11.2	10825	3	US-08-652-265-7	Sequence 7, Appl
c 110	23	12.3	162450	4	US-09-345-882-1	Sequence 1, Appl	c 183	21	11.2	10825	3	US-08-834-497A-1	Sequence 1, Appl
c 111	22	11.8	247	2	US-08-602-716A-11	Sequence 11, Appl	c 184	21	11.2	10825	3	US-08-834-497A-3	Sequence 3, Appl
c 112	22	11.8	533	1	US-08-049-283A-1	Sequence 1, Appl	c 185	21	11.2	10825	3	US-08-834-497A-5	Sequence 5, Appl
c 113	22	11.8	617	2	US-08-481-658B-47	Sequence 47, Appl	c 186	21	11.2	10825	3	US-08-834-497A-7	Sequence 7, Appl
c 114	22	11.8	617	2	US-08-477-504A-47	Sequence 47, Appl	c 187	21	11.2	10825	4	US-09-503-444A-1	Sequence 1, Appl
c 115	22	11.8	617	2	US-08-486-756A-47	Sequence 47, Appl	c 188	21	11.2	10825	4	US-09-503-444A-3	Sequence 3, Appl
c 116	22	11.8	617	2	US-08-485-862B-47	Sequence 47, Appl	c 189	21	11.2	10825	4	US-09-503-444A-5	Sequence 5, Appl
c 117	22	11.8	617	3	US-08-787-739-47	Sequence 47, Appl	c 190	21	11.2	10825	4	US-09-503-444A-7	Sequence 7, Appl
c 118	22	11.8	617	3	US-08-487-077A-47	Sequence 47, Appl	c 191	21	11.2	11613	1	US-08-484-044-10	Sequence 10, Appl
c 119	22	11.8	617	3	US-08-485-863A-47	Sequence 47, Appl	c 192	21	11.2	12146	4	US-09-277-457-27	Sequence 27, Appl
c 120	22	11.8	617	4	US-08-485-049D-47	Sequence 47, Appl	c 193	21	11.2	13953	4	US-09-738-884-3	Sequence 3, Appl
c 121	22	11.8	617	4	US-08-178-115-47	Sequence 47, Appl	c 194	21	11.2	16595	4	US-09-146-053-7	Sequence 7, Appl
c 122	22	11.8	617	4	US-09-177-776-47	Sequence 47, Appl	c 195	21	11.2	17949	4	US-09-087-465-3	Sequence 3, Appl
c 123	22	11.8	645	4	US-09-328-111-9	Sequence 9, Appl	c 196	21	11.2	31571	1	US-08-323-443B-1	Sequence 1, Appl
c 124	22	11.8	672	1	US-08-599-252-102	Sequence 102, App	c 197	21	11.2	31571	1	US-08-323-443B-1	Sequence 1, Appl
c 125	22	11.8	672	5	PCT-US96-06352-102	Sequence 102, App	c 198	21	11.2	32042	4	US-09-245-281-44	Sequence 44, Appl
c 126	22	11.8	672	5	PCT-US96-06583-102	Sequence 102, App	c 199	21	11.2	53526	3	US-08-658-136-2	Sequence 2, Appl
c 127	22	11.8	1096	4	US-09-000-127-2	Sequence 2, Appl	c 200	21	11.2	53526	3	US-08-658-136-2	Sequence 2, Appl
c 128	22	11.8	1290	4	US-09-289-349-9	Sequence 9, Appl	c 201	21	11.2	53577	3	US-08-658-136-1	Sequence 1, Appl
c 129	22	11.8	1838	3	US-09-227-357-32	Sequence 32, Appl	c 202	21	11.2	53577	3	US-08-658-136-1	Sequence 1, Appl
c 130	22	11.8	1888	3	US-09-035-648-20	Sequence 20, Appl	c 203	21	11.2	81001	4	US-09-750-580-1	Sequence 1, Appl
c 131	22	11.8	1888	4	US-09-001-951-20	Sequence 20, Appl	c 204	21	11.2	99500	4	US-09-798-096-10	Sequence 10, Appl
c 132	22	11.8	1888	4	US-08-818-829-20	Sequence 20, Appl	c 205	21	11.2	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 133	22	11.8	1897	4	US-09-302-769-40	Sequence 40, Appl	c 206	21	11.2	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 134	22	11.8	2514	4	US-09-144-914-3	Sequence 3, Appl	c 207	21	11.2	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 135	22	11.8	10898	2	US-08-481-658B-5	Sequence 5, Appl	c 208	20	10.7	87	5	PCT-US94-05150-23	Sequence 23, Appl
c 136	22	11.8	10898	2	US-08-477-504A-5	Sequence 5, Appl	c 209	20	10.7	347	2	US-08-967-101-44	Sequence 44, Appl
c 137	22	11.8	10898	2	US-08-486-756A-5	Sequence 5, Appl	c 210	20	10.7	347	2	US-08-967-101-44	Sequence 44, Appl
c 138	22	11.8	10898	2	US-08-485-862B-5	Sequence 5, Appl	c 211	20	10.7	347	3	US-09-124-698-44	Sequence 44, Appl
c 139	22	11.8	10898	3	US-08-787-739-5	Sequence 5, Appl	c 212	20	10.7	347	4	US-09-127-480-44	Sequence 44, Appl
c 140	22	11.8	10898	3	US-08-487-077A-5	Sequence 5, Appl	c 213	20	10.7	347	4	US-08-496-841C-44	Sequence 44, Appl
c 141	22	11.8	10898	3	US-08-485-863A-5	Sequence 5, Appl	c 214	20	10.7	347	4	US-09-124-523-44	Sequence 44, Appl
c 142	22	11.8	10898	4	US-08-485-049D-5	Sequence 5, Appl	c 215	20	10.7	456	4	US-09-227-357-110	Sequence 110, App
c 143	22	11.8	10898	4	US-09-178-115-5	Sequence 5, Appl	c 216	20	10.7	609	4	US-09-385-982-291	Sequence 291, App
c 144	22	11.8	10898	4	US-09-177-776-5	Sequence 5, Appl	c 217	20	10.7	693	4	US-09-712-016-12	Sequence 12, Appl
c 145	22	11.8	17425	4	US-09-511-625B-5	Sequence 5, Appl	c 218	20	10.7	950	4	US-08-991-789A-6	Sequence 6, Appl
c 146	22	11.8	35100	1	US-08-306-691B-19	Sequence 19, Appl	c 219	20	10.7	950	4	US-09-062-451-6	Sequence 6, Appl
c 147	22	11.8	35100	5	PCT-US93-06251-19	Sequence 19, Appl	c 220	20	10.7	950	4	US-09-598-326-6	Sequence 6, Appl
c 148	22	11.8	45716	4	US-08-965-048-5	Sequence 5, Appl	c 221	20	10.7	1001	4	US-09-641-638-78	Sequence 78, Appl
c 149	22	11.8	45989	4	US-08-965-048-6	Sequence 6, Appl	c 222	20	10.7	1001	4	US-09-641-638-199	Sequence 199, App
c 150	22	11.8	59065	4	US-08-813-817-3	Sequence 3, Appl	c 223	20	10.7	1001	4	US-09-641-638-200	Sequence 200, App
c 151	22	11.8	59065	4	US-09-978-197-3	Sequence 3, Appl	c 224	20	10.7	1300	2	US-08-474-020A-13	Sequence 13, Appl
c 152	22	11.8	152331	3	US-09-128-155-16	Sequence 16, Appl	c 225	20	10.7	1313	1	US-08-446-925-6	Sequence 6, Appl
c 153	21	11.2	26	2	US-08-859-998-10	Sequence 10, Appl	c 226	20	10.7	1313	2	US-09-146-331-6	Sequence 6, Appl
c 154	21	11.2	26	2	US-09-225-928-10	Sequence 10, Appl	c 227	20	10.7	1313	2	US-08-896-885-6	Sequence 6, Appl
c 155	21	11.2	517	1	US-08-480-784-33	Sequence 33, Appl	c 228	20	10.7	1313	4	US-09-375-256-6	Sequence 6, Appl
c 156	21	11.2	517	1	US-08-483-553-33	Sequence 33, Appl	c 229	20	10.7	1313	4	US-09-376-156-6	Sequence 6, Appl
c 157	21	11.2	517	1	US-08-487-002-33	Sequence 33, Appl	c 230	20	10.7	1545	1	US-08-446-925-4	Sequence 4, Appl
c 158	21	11.2	517	1	US-08-483-554B-33	Sequence 33, Appl	c 231	20	10.7	1545	2	US-09-146-331-4	Sequence 4, Appl
c 159	21	11.2	517	1	US-08-488-011B-33	Sequence 33, Appl	c 232	20	10.7	1545	2	US-08-896-885-4	Sequence 4, Appl
c 160	21	11.2	517	4	US-08-850-727-33	Sequence 33, Appl	c 233	20	10.7	1545	4	US-09-375-256-4	Sequence 4, Appl
c 161	21	11.2	517	5	PCT-US95-10202-33	Sequence 33, Appl	c 234	20	10.7	1545	4	US-09-376-156-4	Sequence 4, Appl
c 162	21	11.2	517	5	PCT-US95-10203-33	Sequence 33, Appl	c 235	20	10.7	1829	2	US-08-687-080-57	Sequence 57, Appl
c 163	21	11.2	517	5	PCT-US95-10220-33	Sequence 33, Appl	c 236	20	10.7	2053	3	US-09-227-357-45	Sequence 45, Appl
c 164	21	11.2	1575	4	US-08-639-294-1	Sequence 1, Appl	c 237	20	10.7	2120	3	US-09-221-235-4	Sequence 4, Appl
c 165	21	11.2	1915	4	US-09-147-915-1	Sequence 2, Appl	c 238	20	10.7	2120	3	US-09-221-928-4	Sequence 4, Appl
c 166	21	11.2	3035	1	US-08-726-725-2	Sequence 2, Appl	c 239	20	10.7	2120	3	US-09-221-527-4	Sequence 4, Appl
c 167	21	11.2	3115	3	US-08-996-139-1	Sequence 1, Appl	c 240	20	10.7	2120	3	US-09-221-236-4	Sequence 4, Appl
c 168	21	11.2	3115	4	US-08-995-659-1	Sequence 1, Appl	c 241	20	10.7	2120	3	US-09-221-416-4	Sequence 4, Appl
c 169	21	11.2	3115	4	US-09-215-649A-1	Sequence 1, Appl	c 242	20	10.7	2120	4	US-09-221-245-4	Sequence 4, Appl
c 170	21	11.2	3136	3	US-08-577-780-1	Sequence 1, Appl	c 243	20	10.7	2120	4	US-09-163-115-4	Sequence 4, Appl
c 171	21	11.2	3136	3	US-08-996-139-5	Sequence 5, Appl	c 244	20	10.7	2120	4	US-09-221-528-4	Sequence 4, Appl
c 172	21	11.2	3136	4	US-09-435-296-3	Sequence 3, Appl	c 245	20	10.7	2120	4	US-09-593-553-4	Sequence 4, Appl
c 173	21	11.2	3136	4	US-08-995-659-5	Sequence 5, Appl	c 246	20	10.7	2120	4	US-09-221-237-4	Sequence 4, Appl

C 247	20	10.7	2394	4	US-09-414-010-3	Sequence 3, Appli	320	19	10.2	3885	1	US-08-688-145-1	Sequence 1, Appli
C 248	20	10.7	2562	1	US-08-146-421-4	Sequence 4, Appli	321	19	10.2	4016	1	US-08-410-540-3	Sequence 3, Appli
C 249	20	10.7	2972	20	US-08-453-695A-114	Sequence 114, App	322	19	10.2	4129	2	US-08-370-319C-12	Sequence 12, Appli
C 250	20	10.7	2972	1	US-08-268-161A-114	Sequence 114, App	323	19	10.2	4129	4	US-09-224-834-12	Sequence 22, Appli
C 251	20	10.7	2972	2	US-08-453-702A-114	Sequence 114, App	324	19	10.2	4177	3	US-09-023-082A-23	Sequence 23, Appli
C 252	20	10.7	2972	4	US-09-039-639-114	Sequence 114, App	325	19	10.2	4220	1	US-08-832-883-66	Sequence 66, Appli
C 253	20	10.7	2972	5	PCT-US95-08071-114	Sequence 3, Appli	326	19	10.2	4220	2	US-08-832-877-66	Sequence 66, Appli
C 254	20	10.7	3565	1	US-08-578-649-3	Sequence 3, Appli	327	19	10.2	4517	5	PCT-US93-06251-83	Sequence 83, Appli
C 255	20	10.7	4286	4	US-09-413-304-7	Sequence 7, Appli	328	19	10.2	4550	4	US-09-103-663-35	Sequence 35, Appli
C 256	20	10.7	4286	4	US-09-817-856-7	Sequence 7, Appli	329	19	10.2	5095	1	US-08-092-817-3	Sequence 3, Appli
C 257	20	10.7	4773	3	US-08-884-324-9	Sequence 9, Appli	330	19	10.2	5095	4	US-08-485-128-3	Sequence 3, Appli
C 258	20	10.7	6063	1	US-08-185-744-4	Sequence 4, Appli	331	19	10.2	5408	1	US-08-471-058-20	Sequence 20, Appli
C 259	20	10.7	6063	2	US-08-788-279-4	Sequence 4, Appli	332	19	10.2	5408	3	US-08-471-057-20	Sequence 20, Appli
C 260	20	10.7	7301	4	US-09-816-088-3	Sequence 3, Appli	333	19	10.2	5537	1	US-08-135-511-32	Sequence 32, Appli
C 261	20	10.7	7620	1	US-07-767-135-1	Sequence 1, Appli	334	19	10.2	5537	1	US-08-483-852-9	Sequence 9, Appli
C 262	20	10.7	7620	1	US-07-841-652-1	Sequence 1, Appli	335	19	10.2	5537	1	US-08-361-458-4	Sequence 4, Appli
C 263	20	10.7	8353	3	US-08-611-587-1	Sequence 1, Appli	336	19	10.2	5537	1	US-08-477-953-9	Sequence 9, Appli
C 264	20	10.7	8517	3	US-08-827-208-1	Sequence 1, Appli	337	19	10.2	5537	1	US-08-187-453-32	Sequence 32, Appli
C 265	20	10.7	8517	4	US-09-500-358-1	Sequence 1, Appli	338	19	10.2	5537	1	US-08-562-985A-5	Sequence 5, Appli
C 266	20	10.7	8517	4	US-09-498-809-1	Sequence 1, Appli	339	19	10.2	5537	2	US-08-477-952-9	Sequence 9, Appli
C 267	20	10.7	9365	4	US-09-608-285A-8	Sequence 8, Appli	340	19	10.2	5912	2	US-08-629-001A-1	Sequence 1, Appli
C 268	20	10.7	9365	4	US-09-350-836B-8	Sequence 8, Appli	341	19	10.2	5912	4	US-08-642-274D-1	Sequence 1, Appli
C 269	20	10.7	9365	4	US-09-370-265-8	Sequence 8, Appli	342	19	10.2	5912	4	US-08-352-127-1	Sequence 1, Appli
C 270	20	10.7	9721	4	US-09-345-217-2	Sequence 2, Appli	343	19	10.2	5912	4	US-08-952-014C-1	Sequence 1, Appli
C 271	20	10.7	11464	3	US-08-884-324-13	Sequence 13, Appli	344	19	10.2	6354	3	US-09-058-389A-5	Sequence 5, Appli
C 272	20	10.7	12394	4	US-09-488-856A-10	Sequence 10, Appli	345	19	10.2	6354	4	US-09-611-781-5	Sequence 5, Appli
C 273	20	10.7	12597	4	US-09-705-299-12	Sequence 12, Appli	346	19	10.2	6987	4	US-09-026-033-3	Sequence 3, Appli
C 274	20	10.7	14747	4	US-09-608-285A-42	Sequence 42, Appli	347	19	10.2	6987	4	US-09-026-033-23	Sequence 23, Appli
C 275	20	10.7	15977	4	US-09-608-285A-59	Sequence 59, Appli	348	19	10.2	7122	4	US-09-318-448-2	Sequence 2, Appli
C 276	20	10.7	28994	3	US-08-884-324-14	Sequence 14, Appli	349	19	10.2	7122	4	US-09-347-878-4	Sequence 4, Appli
C 277	20	10.7	40000	4	US-09-780-049-18	Sequence 18, Appli	350	19	10.2	7224	4	US-09-347-878-6	Sequence 6, Appli
C 278	20	10.7	45546	4	US-09-146-053-6	Sequence 6, Appli	351	19	10.2	7408	1	US-08-441-822-1	Sequence 1, Appli
C 279	20	10.7	72928	3	US-09-009-913-1	Sequence 1, Appli	352	19	10.2	7410	1	US-08-493-092-1	Sequence 1, Appli
C 280	20	10.7	112132	4	US-09-741-150-3	Sequence 3, Appli	353	19	10.2	7410	1	US-08-508-836A-1	Sequence 1, Appli
C 281	20	10.7	162450	4	US-09-345-882-1	Sequence 1, Appli	354	19	10.2	7680	4	US-09-210-748A-3	Sequence 3, Appli
C 282	19	10.2	20	1	US-08-222-177A-274	Sequence 274, App	355	19	10.2	7720	4	US-09-318-448-5	Sequence 5, Appli
C 283	19	10.2	20	1	US-09-435-296-74	Sequence 74, Appli	356	19	10.2	8056	3	US-09-136-605-14	Sequence 14, Appli
C 284	19	10.2	345	4	US-09-385-982-145	Sequence 145, App	357	19	10.2	8082	1	US-08-306-691B-41	Sequence 41, Appli
C 285	19	10.2	421	2	US-08-332-766A-25	Sequence 25, Appli	358	19	10.2	8082	1	US-08-187-785-1	Sequence 1, Appli
C 286	19	10.2	451	4	US-09-404-879A-43	Sequence 43, Appli	359	19	10.2	8082	4	US-09-167-322-11	Sequence 11, Appli
C 287	19	10.2	459	2	US-08-852-807-19	Sequence 19, Appli	360	19	10.2	8082	5	PCT-US93-06251-28	Sequence 28, Appli
C 288	19	10.2	591	4	US-09-385-982-406	Sequence 406, App	361	19	10.2	8224	2	US-09-010-398-14	Sequence 14, Appli
C 289	19	10.2	619	4	US-09-152-060-17	Sequence 17, Appli	362	19	10.2	8224	4	US-09-366-260-14	Sequence 14, Appli
C 290	19	10.2	863	4	US-08-943-731-171	Sequence 171, App	363	19	10.2	8342	3	US-08-545-860B-63	Sequence 63, Appli
C 291	19	10.2	897	3	US-09-058-389A-17	Sequence 17, Appli	364	19	10.2	8342	5	PCT-US94-04496-63	Sequence 63, Appli
C 292	19	10.2	897	4	US-09-611-781-17	Sequence 17, Appli	365	19	10.2	8392	1	US-08-080-255-6	Sequence 6, Appli
C 293	19	10.2	1272	3	US-09-058-389A-7	Sequence 7, Appli	366	19	10.2	8392	3	US-08-465-713-6	Sequence 6, Appli
C 294	19	10.2	1272	4	US-09-611-781-7	Sequence 7, Appli	367	19	10.2	8392	5	PCT-US93-05857-6	Sequence 6, Appli
C 295	19	10.2	1289	4	US-09-247-155-138	Sequence 138, App	368	19	10.2	9870	1	US-08-508-836A-9	Sequence 9, Appli
C 296	19	10.2	1371	3	US-08-884-324-11	Sequence 11, Appli	369	19	10.2	10380	4	US-09-077-354B-3	Sequence 3, Appli
C 297	19	10.2	1624	4	US-08-430-225A-19	Sequence 19, Appli	370	19	10.2	11298	1	US-07-869-933-31	Sequence 31, Appli
C 298	19	10.2	1645	2	US-08-724-394A-14	Sequence 14, Appli	371	19	10.2	11298	4	US-08-201-879A-2	Sequence 2, Appli
C 299	19	10.2	1763	4	US-09-449-437A-3	Sequence 3, Appli	372	19	10.2	11298	4	US-09-103-663-31	Sequence 31, Appli
C 300	19	10.2	1847	3	US-09-058-389A-9	Sequence 9, Appli	373	19	10.2	11464	3	US-08-884-324-13	Sequence 13, Appli
C 301	19	10.2	2181	4	US-09-611-781-9	Sequence 9, Appli	374	19	10.2	11811	4	US-09-078-294-7	Sequence 7, Appli
C 302	19	10.2	2847	2	US-08-737-371A-1	Sequence 1, Appli	375	19	10.2	12394	4	US-09-488-856A-10	Sequence 10, Appli
C 303	19	10.2	2181	5	PCT-US95-05853-1	Sequence 1, Appli	376	19	10.2	12597	4	US-09-705-299-12	Sequence 12, Appli
C 304	19	10.2	2309	4	US-09-449-437A-5	Sequence 5, Appli	377	19	10.2	16053	4	US-09-801-052-3	Sequence 3, Appli
C 305	19	10.2	2309	4	US-09-195-106-1	Sequence 1, Appli	378	19	10.2	16595	4	US-09-146-053-7	Sequence 7, Appli
C 306	19	10.2	2334	4	US-09-493-565-1	Sequence 1, Appli	379	19	10.2	17606	4	US-08-943-731-4	Sequence 4, Appli
C 307	19	10.2	2503	4	US-09-198-122-7	Sequence 7, Appli	380	19	10.2	18443	4	US-09-078-294-6	Sequence 6, Appli
C 308	19	10.2	2598	4	US-09-026-033-18	Sequence 18, Appli	381	19	10.2	19011	5	PCT-US92-06300-1	Sequence 1, Appli
C 309	19	10.2	3101	4	US-09-602-877A-97	Sequence 97, Appli	382	19	10.2	19557	5	PCT-US92-06300-1	Sequence 1, Appli
C 310	19	10.2	3480	1	US-07-657-769B-68	Sequence 68, Appli	383	19	10.2	19736	4	US-09-740-035-3	Sequence 3, Appli
C 311	19	10.2	3480	1	US-07-789-184-219	Sequence 219, App	384	19	10.2	28720	4	US-09-341-587-7	Sequence 7, Appli
C 312	19	10.2	3480	1	US-08-475-263-219	Sequence 219, App	385	19	10.2	28994	3	US-08-884-324-14	Sequence 14, Appli
C 313	19	10.2	3480	1	US-08-485-886-219	Sequence 219, App	386	19	10.2	29629	4	US-09-729-995-3	Sequence 3, Appli
C 314	19	10.2	3480	2	US-08-477-362-219	Sequence 219, App	387	19	10.2	29629	4	US-09-729-995-3	Sequence 3, Appli
C 315	19	10.2	3480	2	US-08-477-134-219	Sequence 219, App	388	19	10.2	36741	4	US-09-301-665-3	Sequence 3, Appli
C 316	19	10.2	3480	3	US-08-473-489A-219	Sequence 219, App	389	19	10.2	50000	4	US-09-146-053-3	Sequence 3, Appli
C 317	19	10.2	3480	3	US-08-485-695-219	Sequence 219, App	390	19	10.2	50000	4	US-09-146-053-4	Sequence 4, Appli
C 318	19	10.2	3480	4	US-08-018-760-219	Sequence 219, App	391	19	10.2	50000	4	US-09-146-053-4	Sequence 4, Appli
C 319	19	10.2	3494	4	US-09-334-601-5	Sequence 5, Appli	392	19	10.2	55827	4	US-09-813-133A-3	Sequence 3, Appli

C 393	19	10.2	56516	2	US-08-996-306-1	Sequence 1, Appl	C 466	18	9.6	1000	4	US-09-018-584A-40	Sequence 40, Appl
C 394	19	10.2	56516	4	US-09-338-907-1	Sequence 1, Appl	467	18	9.6	1002	4	US-09-641-638-578	Sequence 578, App
C 395	19	10.2	56516	4	US-09-218-207-1	Sequence 1, Appl	468	18	9.6	1116	1	US-08-672-569-1	Sequence 1, Appl
C 396	19	10.2	56520	4	US-09-338-907-179	Sequence 179, App	469	18	9.6	1260	4	US-08-943-731-169	Sequence 169, App
C 397	19	10.2	56520	4	US-09-800-960-3	Sequence 3, Appl	C 470	18	9.6	1334	3	US-08-884-324-8	Sequence 8, Appl
C 398	19	10.2	62804	4	US-09-851-896-3	Sequence 3, Appl	C 471	18	9.6	1361	1	US-08-530-529-1	Sequence 1, Appl
C 399	19	10.2	70000	4	US-09-268-992-7	Sequence 7, Appl	C 472	18	9.6	1371	4	US-09-119-264-1	Sequence 1, Appl
C 400	19	10.2	72604	4	US-09-268-992-7	Sequence 7, Appl	C 473	18	9.6	1361	3	US-08-884-324-11	Sequence 11, Appl
C 401	19	10.2	72604	4	US-09-268-992-7	Sequence 7, Appl	474	18	9.6	1418	5	PCT-US95-17111A-120	Sequence 120, App
C 402	19	10.2	72604	4	US-09-657-474-7	Sequence 7, Appl	475	18	9.6	1442	2	US-08-454-557C-120	Sequence 120, App
C 403	19	10.2	72604	4	US-09-657-474-7	Sequence 7, Appl	476	18	9.6	1442	2	US-08-340-426D-120	Sequence 120, App
C 404	19	10.2	80246	4	US-09-078-294-4	Sequence 4, Appl	477	18	9.6	1442	2	US-08-450-673C-120	Sequence 120, App
C 405	19	10.2	80246	4	US-09-078-294-4	Sequence 4, Appl	C 478	18	9.6	1561	5	PCT-US92-00282-25	Sequence 25, Appl
C 406	19	10.2	80595	4	US-09-078-294-3	Sequence 3, Appl	479	18	9.6	1618	1	US-08-236-918A-3	Sequence 3, Appl
C 407	19	10.2	80595	4	US-09-078-294-3	Sequence 3, Appl	480	18	9.6	1618	4	US-09-150-864A-3	Sequence 3, Appl
C 408	19	10.2	11282	4	US-09-754-250-3	Sequence 3, Appl	481	18	9.6	1624	2	US-08-852-807-10	Sequence 10, Appl
C 409	19	10.2	112132	4	US-09-741-150-3	Sequence 3, Appl	C 482	18	9.6	1742	4	US-08-477-928A-44	Sequence 44, Appl
C 410	19	10.2	152331	3	US-09-128-155-16	Sequence 16, Appl	C 483	18	9.6	1825	4	US-09-461-697-75	Sequence 75, Appl
C 411	19	10.2	168575	4	US-09-426-290-1	Sequence 1, Appl	484	18	9.6	1838	4	US-09-227-357-32	Sequence 32, Appl
C 412	19	10.2	169998	4	US-09-676-610B-24	Sequence 24, Appl	C 485	18	9.6	1883	2	US-08-967-101-10	Sequence 10, Appl
C 413	18	9.6	212	2	US-08-602-716A-10	Sequence 10, Appl	C 486	18	9.6	1883	2	US-08-967-101-153	Sequence 153, App
C 414	18	9.6	214	4	US-08-477-928A-45	Sequence 45, Appl	C 487	18	9.6	1883	2	US-08-592-541-10	Sequence 10, Appl
C 415	18	9.6	298	2	US-08-481-658B-64	Sequence 64, Appl	C 488	18	9.6	1883	2	US-08-592-541-153	Sequence 153, App
C 416	18	9.6	298	2	US-08-477-504A-64	Sequence 64, Appl	C 489	18	9.6	1883	3	US-08-888-077A-8	Sequence 8, Appl
C 417	18	9.6	298	2	US-08-486-756A-64	Sequence 64, Appl	C 490	18	9.6	1883	3	US-09-124-698-10	Sequence 10, Appl
C 418	18	9.6	298	2	US-08-485-862B-64	Sequence 64, Appl	C 491	18	9.6	1883	3	US-09-124-698-153	Sequence 153, App
C 419	18	9.6	298	3	US-08-787-739-64	Sequence 64, Appl	C 492	18	9.6	1883	4	US-09-127-480-10	Sequence 10, Appl
C 420	18	9.6	298	3	US-08-487-077A-64	Sequence 64, Appl	C 493	18	9.6	1883	4	US-09-127-480-153	Sequence 153, App
C 421	18	9.6	298	3	US-08-485-863A-64	Sequence 64, Appl	C 494	18	9.6	1883	4	US-08-496-841C-10	Sequence 10, Appl
C 422	18	9.6	298	4	US-08-485-049D-64	Sequence 64, Appl	C 495	18	9.6	1883	4	US-08-496-841C-153	Sequence 153, App
C 423	18	9.6	298	4	US-09-178-115-64	Sequence 64, Appl	C 496	18	9.6	1883	4	US-09-124-523-10	Sequence 10, Appl
C 424	18	9.6	298	4	US-09-177-776-64	Sequence 64, Appl	C 497	18	9.6	1883	4	US-09-124-523-153	Sequence 153, App
C 425	18	9.6	331	4	US-09-085-199B-21	Sequence 21, Appl	C 498	18	9.6	1988	2	US-08-257-963B-11	Sequence 11, Appl
C 426	18	9.6	445	2	US-08-967-101-78	Sequence 78, Appl	C 499	18	9.6	1988	5	PCT-US95-07201-11	Sequence 11, Appl
C 427	18	9.6	445	2	US-08-592-541-78	Sequence 78, Appl	500	18	9.6	1988	5	PCT-US95-07201-11	Sequence 11, Appl
C 428	18	9.6	445	3	US-09-124-698-78	Sequence 78, Appl	C 501	18	9.6	2051	2	US-08-530-569B-13	Sequence 13, Appl
C 429	18	9.6	445	4	US-09-127-480-78	Sequence 78, Appl	C 502	18	9.6	2076	2	US-08-979-095-3	Sequence 3, Appl
C 430	18	9.6	445	4	US-08-496-841C-78	Sequence 78, Appl	C 503	18	9.6	2119	2	US-09-227-357-48	Sequence 48, Appl
C 431	18	9.6	445	4	US-09-124-523-78	Sequence 78, Appl	C 504	18	9.6	2129	2	US-08-979-095-1	Sequence 1, Appl
C 432	18	9.6	451	4	US-09-404-879A-101	Sequence 101, App	C 505	18	9.6	2417	4	US-09-605-785-334	Sequence 334, App
C 433	18	9.6	500	2	US-08-967-101-86	Sequence 86, Appl	C 506	18	9.6	2417	4	US-09-439-313-334	Sequence 334, App
C 434	18	9.6	500	2	US-08-967-101-93	Sequence 93, Appl	C 507	18	9.6	2417	4	US-09-352-616A-334	Sequence 334, App
C 435	18	9.6	500	2	US-08-592-541-86	Sequence 86, Appl	C 508	18	9.6	2417	4	US-09-232-149A-334	Sequence 334, App
C 436	18	9.6	500	2	US-08-592-541-93	Sequence 93, Appl	C 509	18	9.6	2630	3	US-08-669-286-6	Sequence 6, Appl
C 437	18	9.6	500	3	US-09-124-698-86	Sequence 86, Appl	C 510	18	9.6	2630	4	US-09-469-253-6	Sequence 6, Appl
C 438	18	9.6	500	3	US-09-124-698-93	Sequence 93, Appl	C 511	18	9.6	2630	4	US-09-642-146-6	Sequence 6, Appl
C 439	18	9.6	500	4	US-09-127-480-86	Sequence 86, Appl	C 512	18	9.6	2813	4	US-09-689-255C-3	Sequence 3, Appl
C 440	18	9.6	500	4	US-09-127-480-93	Sequence 93, Appl	C 513	18	9.6	2961	4	US-09-177-437-1	Sequence 1, Appl
C 441	18	9.6	500	4	US-08-496-841C-86	Sequence 86, Appl	514	18	9.6	3117	4	US-09-146-580-6	Sequence 6, Appl
C 442	18	9.6	500	4	US-08-496-841C-93	Sequence 93, Appl	515	18	9.6	3158	2	US-08-464-517-36	Sequence 36, Appl
C 443	18	9.6	500	4	US-09-124-523-86	Sequence 86, Appl	516	18	9.6	3158	3	US-08-246-361A-36	Sequence 36, Appl
C 444	18	9.6	500	4	US-09-124-523-93	Sequence 93, Appl	517	18	9.6	3158	3	US-08-463-772-36	Sequence 36, Appl
C 445	18	9.6	512	2	US-08-481-658B-45	Sequence 45, Appl	518	18	9.6	3350	3	US-09-110-116-2	Sequence 2, Appl
C 446	18	9.6	512	2	US-08-477-504A-45	Sequence 45, Appl	C 519	18	9.6	3364	2	US-08-735-609-9	Sequence 9, Appl
C 447	18	9.6	512	2	US-08-486-756A-45	Sequence 45, Appl	C 520	18	9.6	3364	2	US-08-735-609-9	Sequence 9, Appl
C 448	18	9.6	512	2	US-08-485-862B-45	Sequence 45, Appl	C 521	18	9.6	3364	3	US-09-315-372-9	Sequence 9, Appl
C 449	18	9.6	512	3	US-08-787-739-45	Sequence 45, Appl	C 522	18	9.6	3364	3	US-09-244-752-9	Sequence 9, Appl
C 450	18	9.6	512	3	US-08-487-077A-45	Sequence 45, Appl	C 523	18	9.6	3364	3	US-09-245-497-9	Sequence 9, Appl
C 451	18	9.6	512	3	US-08-485-863A-45	Sequence 45, Appl	C 524	18	9.6	3674	4	US-09-562-919-9	Sequence 9, Appl
C 452	18	9.6	512	4	US-08-485-049D-45	Sequence 45, Appl	C 525	18	9.6	3674	4	US-09-605-785-698	Sequence 698, App
C 453	18	9.6	512	4	US-09-178-115-45	Sequence 45, Appl	C 526	18	9.6	4866	1	US-08-110-158-5	Sequence 5, Appl
C 454	18	9.6	512	4	US-09-177-776-45	Sequence 45, Appl	C 527	18	9.6	5092	4	US-09-412-545-1	Sequence 1, Appl
C 455	18	9.6	548	4	US-08-901-789A-15	Sequence 15, Appl	C 528	18	9.6	5137	5	PCT-US96-01314-39	Sequence 39, Appl
C 456	18	9.6	548	4	US-09-062-451-15	Sequence 15, Appl	C 529	18	9.6	5138	2	US-08-476-062A-39	Sequence 39, Appl
C 457	18	9.6	548	4	US-09-598-326-15	Sequence 15, Appl	C 530	18	9.6	5622	4	US-08-520-373D-5	Sequence 5, Appl
C 458	18	9.6	553	4	US-09-227-357-94	Sequence 94, Appl	531	18	9.6	6669	3	US-09-212-971-5	Sequence 5, Appl
C 459	18	9.6	602	4	US-09-078-294-27	Sequence 27, Appl	532	18	9.6	6669	3	US-08-800-929A-5	Sequence 5, Appl
C 460	18	9.6	624	4	US-09-385-982-414	Sequence 414, App	533	18	9.6	6669	4	US-09-617-053A-5	Sequence 5, Appl
C 461	18	9.6	685	4	US-09-227-357-100	Sequence 100, App	534	18	9.6	8133	3	US-09-659-791A-10	Sequence 10, Appl
C 462	18	9.6	690	4	US-08-328-111-74	Sequence 74, Appl	C 535	18	9.6	8353	4	US-08-611-587-1	Sequence 1, Appl
C 463	18	9.6	817	1	US-08-672-569-2	Sequence 2, Appl	C 536	18	9.6	8982	3	US-08-976-255-5	Sequence 5, Appl
C 464	18	9.6	949	4	US-09-247-155A-148	Sequence 148, App	C 537	18	9.6	9704	4	US-09-814-951A-3	Sequence 3, Appl
C 465	18	9.6	1000	4	US-09-018-584A-33	Sequence 33, Appl	538	18	9.6	9734	4	US-09-347-114A-80	Sequence 80, Appl

c 539	18	9.6	10684	3	US-08-618-100B-3	Sequence 3, Appli	c 612	17	9.1	1043	4	US-09-165-868-4	Sequence 4, Appli
c 540	18	9.6	10898	2	US-08-481-658B-5	Sequence 5, Appli	613	17	9.1	1048	4	US-09-227-357-145	Sequence 145, App
c 541	18	9.6	10898	2	US-08-477-504A-5	Sequence 5, Appli	614	17	9.1	1247	4	US-09-178-115-110	Sequence 110, App
c 542	18	9.6	10898	2	US-08-486-756A-5	Sequence 5, Appli	615	17	9.1	1247	4	US-09-177-776-110	Sequence 110, App
c 543	18	9.6	10898	2	US-08-485-862B-5	Sequence 5, Appli	616	17	9.1	1287	4	US-09-564-805-217	Sequence 217, App
c 544	18	9.6	10898	3	US-08-787-739-5	Sequence 5, Appli	c 617	17	9.1	1320	1	US-08-599-252-84	Sequence 84, Appl
c 545	18	9.6	10898	3	US-08-487-077A-5	Sequence 5, Appli	618	17	9.1	1320	1	US-08-436-074-57	Sequence 57, Appl
c 546	18	9.6	10898	3	US-08-485-863A-5	Sequence 5, Appli	619	17	9.1	1320	1	PCT-US96-06352-84	Sequence 84, Appl
c 547	18	9.6	10898	4	US-08-485-049D-5	Sequence 5, Appli	620	17	9.1	1320	5	PCT-US96-06583-84	Sequence 84, Appl
c 548	18	9.6	10898	4	US-09-178-115-5	Sequence 5, Appli	621	17	9.1	1407	4	US-09-153-804-6	Sequence 6, Appli
c 549	18	9.6	10898	4	US-08-177-776-5	Sequence 5, Appli	622	17	9.1	1526	1	US-08-694-915-3	Sequence 3, Appli
c 550	18	9.6	10952	1	US-08-602-036A-1	Sequence 1, Appli	c 623	17	9.1	1600	2	US-08-487-113B-117	Sequence 117, App
c 551	18	9.6	10952	2	US-08-602-374A-1	Sequence 1, Appli	624	17	9.1	1600	2	US-08-720-420A-117	Sequence 117, App
c 552	18	9.6	10952	2	US-08-642-407A-1	Sequence 1, Appli	c 625	17	9.1	1640	1	US-08-068-945A-32	Sequence 32, Appl
c 553	18	9.6	11298	2	US-07-869-933-31	Sequence 31, Appl	c 626	17	9.1	1640	1	US-08-442-806-32	Sequence 32, Appl
c 554	18	9.6	11298	1	US-08-201-879A-2	Sequence 2, Appli	627	17	9.1	2178	3	US-08-781-891-72	Sequence 72, Appl
c 555	18	9.6	11298	4	US-09-103-663-31	Sequence 31, Appl	c 628	17	9.1	2201	1	US-08-580-401-1	Sequence 1, Appli
c 556	18	9.6	12565	4	US-08-345-217-3	Sequence 3, Appli	c 629	17	9.1	2316	1	US-08-135-511-34	Sequence 34, Appl
c 557	18	9.6	12847	1	US-08-550-715-1	Sequence 1, Appli	c 630	17	9.1	2316	1	US-08-483-852-11	Sequence 11, Appl
c 558	18	9.6	13158	2	US-08-687-080-105	Sequence 105, App	c 631	17	9.1	2316	1	US-08-361-458-6	Sequence 6, Appli
c 559	18	9.6	14581	4	US-08-520-373D-4	Sequence 4, Appli	c 632	17	9.1	2316	1	US-08-477-953-11	Sequence 11, Appl
c 560	18	9.6	15297	4	US-08-817-180-3	Sequence 3, Appli	c 633	17	9.1	2316	1	US-08-187-453-34	Sequence 34, Appl
c 561	18	9.6	15977	4	US-08-608-285A-59	Sequence 59, Appl	c 634	17	9.1	2316	2	US-08-477-952-11	Sequence 11, Appl
c 562	18	9.6	18073	4	US-08-078-294-12	Sequence 12, Appl	c 635	17	9.1	2501	3	US-08-787-739-58	Sequence 58, Appl
c 563	18	9.6	20674	4	US-08-641-638-651	Sequence 651, App	c 636	17	9.1	2501	4	US-09-178-115-58	Sequence 58, Appl
c 564	18	9.6	22481	4	US-08-367-841A-43	Sequence 43, Appl	c 637	17	9.1	2501	4	US-09-177-776-58	Sequence 58, Appl
c 565	18	9.6	22481	5	PCT-US95-07201-43	Sequence 43, Appl	c 638	17	9.1	2688	2	US-08-909-965C-1	Sequence 1, Appli
c 566	18	9.6	22484	4	US-08-875-223-2	Sequence 2, Appli	c 639	17	9.1	2964	2	US-08-846-790A-2	Sequence 2, Appli
c 567	18	9.6	28001	4	US-08-819-993-3	Sequence 3, Appli	c 640	17	9.1	2964	3	US-08-935-333-2	Sequence 2, Appli
c 568	18	9.6	35060	3	US-08-814-095-7	Sequence 7, Appli	c 641	17	9.1	3373	1	US-08-273-411-2	Sequence 2, Appli
c 569	18	9.6	35828	4	US-09-449-218D-17	Sequence 17, Appl	c 642	17	9.1	3532	3	US-08-787-739-90	Sequence 90, Appl
c 570	18	9.6	40328	3	US-08-742-185-102	Sequence 102, App	c 643	17	9.1	3532	4	US-09-178-115-90	Sequence 90, Appl
c 571	18	9.6	43795	3	US-08-742-185-101	Sequence 101, App	c 644	17	9.1	3532	4	US-09-177-776-90	Sequence 90, Appl
c 572	18	9.6	45546	4	US-09-146-053-5	Sequence 6, Appli	c 645	17	9.1	3601	3	US-09-017-631-23	Sequence 23, Appl
c 573	18	9.6	45716	4	US-08-965-048-5	Sequence 5, Appli	c 646	17	9.1	3602	2	US-08-883-795A-33	Sequence 33, Appl
c 574	18	9.6	45989	4	US-08-965-048-6	Sequence 6, Appli	c 647	17	9.1	3602	4	US-09-018-138-1	Sequence 1, Appli
c 575	18	9.6	55827	4	US-08-813-133A-3	Sequence 3, Appli	c 648	17	9.1	3609	4	US-09-705-299-11	Sequence 11, Appl
c 576	18	9.6	98844	4	US-09-791-211-10	Sequence 10, Appl	c 649	17	9.1	3683	4	US-08-450-962-1	Sequence 1, Appli
c 577	18	9.6	111282	4	US-09-754-250-3	Sequence 3, Appli	c 650	17	9.1	3848	4	US-09-112-096-28	Sequence 28, Appl
c 578	18	9.6	169998	4	US-09-676-610B-24	Sequence 24, Appl	c 651	17	9.1	3865	2	US-08-832-883-48	Sequence 48, Appl
c 579	17	9.1	98	4	US-08-991-789A-282	Sequence 282, App	c 652	17	9.1	3865	2	US-08-832-877-48	Sequence 48, Appl
c 580	17	9.1	98	4	US-08-062-451A-282	Sequence 282, App	c 653	17	9.1	4233	4	US-09-056-105-27	Sequence 27, Appl
c 581	17	9.1	191	4	US-09-276-531-36	Sequence 36, Appl	c 654	17	9.1	4550	4	US-09-103-663-35	Sequence 35, Appl
c 582	17	9.1	211	2	US-08-332-766A-34	Sequence 34, Appl	c 655	17	9.1	4793	4	US-09-561-497-10	Sequence 10, Appl
c 583	17	9.1	262	2	US-08-481-658B-57	Sequence 57, Appl	c 656	17	9.1	5037	4	US-09-705-299-13	Sequence 13, Appl
c 584	17	9.1	262	2	US-08-481-658B-60	Sequence 60, Appl	c 657	17	9.1	5543	2	US-08-687-080-101	Sequence 101, App
c 585	17	9.1	262	2	US-08-477-504A-57	Sequence 57, Appl	c 658	17	9.1	5668	4	US-09-112-096-14	Sequence 14, Appl
c 586	17	9.1	262	2	US-08-477-504A-57	Sequence 57, Appl	c 659	17	9.1	5668	4	US-09-605-785-777	Sequence 777, App
c 587	17	9.1	262	2	US-08-477-504A-57	Sequence 57, Appl	c 660	17	9.1	5892	3	US-08-755-587-27	Sequence 27, Appl
c 588	17	9.1	262	2	US-08-486-756A-57	Sequence 57, Appl	c 661	17	9.1	6769	1	US-08-480-784-20	Sequence 20, Appl
c 589	17	9.1	262	2	US-08-486-756A-60	Sequence 60, Appl	c 662	17	9.1	6769	1	US-08-483-553-20	Sequence 20, Appl
c 590	17	9.1	262	2	US-08-485-862B-57	Sequence 57, Appl	c 663	17	9.1	6769	1	US-08-487-002-20	Sequence 20, Appl
c 591	17	9.1	262	2	US-08-485-862B-60	Sequence 60, Appl	c 664	17	9.1	6769	1	US-08-483-554B-20	Sequence 20, Appl
c 592	17	9.1	262	3	US-08-787-739-60	Sequence 60, Appl	c 665	17	9.1	6769	1	US-08-488-011B-20	Sequence 20, Appl
c 593	17	9.1	262	3	US-08-487-077A-57	Sequence 57, Appl	c 666	17	9.1	6769	4	US-08-850-727-20	Sequence 20, Appl
c 594	17	9.1	262	3	US-08-487-077A-60	Sequence 60, Appl	c 667	17	9.1	6769	5	PCT-US95-10203-20	Sequence 20, Appl
c 595	17	9.1	262	3	US-08-485-863A-57	Sequence 57, Appl	c 668	17	9.1	6769	5	PCT-US95-10203-20	Sequence 20, Appl
c 596	17	9.1	262	3	US-08-485-863A-60	Sequence 60, Appl	c 669	17	9.1	6769	5	PCT-US95-10220-20	Sequence 20, Appl
c 597	17	9.1	262	4	US-08-485-049D-60	Sequence 60, Appl	c 670	17	9.1	7152	4	US-09-167-681-29	Sequence 29, Appl
c 598	17	9.1	262	4	US-08-178-115-57	Sequence 57, Appl	c 671	17	9.1	8174	1	US-07-914-281-5	Sequence 5, Appli
c 599	17	9.1	262	4	US-09-178-115-60	Sequence 60, Appl	c 672	17	9.1	8174	1	US-08-393-246-5	Sequence 5, Appli
c 600	17	9.1	262	4	US-09-177-776-57	Sequence 57, Appl	c 673	17	9.1	8174	2	US-08-525-058A-5	Sequence 5, Appli
c 601	17	9.1	262	4	US-09-177-776-60	Sequence 60, Appl	c 674	17	9.1	8174	2	US-08-696-731-5	Sequence 5, Appli
c 602	17	9.1	461	4	US-09-404-879A-47	Sequence 47, Appl	c 675	17	9.1	8174	5	US-09-042-531-5	Sequence 5, Appli
c 603	17	9.1	490	4	US-09-328-111-41	Sequence 41, Appl	c 676	17	9.1	8174	5	PCT-US91-00899-3	Sequence 3, Appli
c 604	17	9.1	529	4	US-08-222-575-100	Sequence 100, App	c 677	17	9.1	8396	4	US-09-328-174A-1	Sequence 37, Appl
c 605	17	9.1	688	6	US-08-991-789A-282	Sequence 282, App	c 678	17	9.1	8409	4	US-09-167-681-37	Sequence 37, Appl
c 606	17	9.1	799	4	US-08-166-350-11	Sequence 11, Appl	c 679	17	9.1	8453	3	US-09-167-681-45	Sequence 45, Appl
c 607	17	9.1	1000	4	US-09-018-584A-30	Sequence 30, Appl	c 680	17	9.1	8835	3	US-08-884-324-10	Sequence 10, Appl
c 608	17	9.1	1000	4	US-09-018-584A-31	Sequence 31, Appl	c 681	17	9.1	9365	4	US-09-608-285A-8	Sequence 8, Appli
c 609	17	9.1	1000	4	US-09-641-638-647	Sequence 647, App	c 682	17	9.1	9365	4	US-09-350-836B-8	Sequence 8, Appli
c 610	17	9.1	1001	4	US-09-641-638-113	Sequence 113, App	c 683	17	9.1	9365	4	US-09-370-265-8	Sequence 8, Appli
c 611	17	9.1	1001	4	US-09-641-638-381	Sequence 381, App	c 684	17	9.1	10642	4	US-09-934-551-3	Sequence 3, Appli

c 685	17	9.1	11531	1	US-08-068-945A-1	Sequence 1, Appl	c 758	16	8.6	411	4	US-09-385-982-5	Sequence 5, Appl
c 686	17	9.1	11531	1	US-08-442-805A-1	Sequence 1, Appl	759	16	8.6	418	4	US-08-642-274D-46	Sequence 46, Appl
c 687	17	9.1	14747	4	US-09-608-285A-42	Sequence 42, Appl	760	16	8.6	418	4	US-08-952-014C-45	Sequence 46, Appl
c 688	17	9.1	14753	4	US-08-821-736-3	Sequence 3, Appl	c 761	16	8.6	443	4	US-09-385-982-28	Sequence 28, Appl
c 689	17	9.1	15328	2	US-08-888-497-33	Sequence 33, Appl	c 762	16	8.6	456	4	US-09-227-357-110	Sequence 110, App
c 690	17	9.1	15328	4	US-09-362-230-33	Sequence 33, Appl	c 763	16	8.6	471	4	US-09-018-584A-6	Sequence 6, Appl
c 691	17	9.1	15328	5	PCT-US94-07926-33	Sequence 33, Appl	c 764	16	8.6	476	4	US-09-020-956-80	Sequence 80, Appl
c 692	17	9.1	15581	3	US-08-646-538-35	Sequence 35, Appl	765	16	8.6	476	4	US-09-030-607-80	Sequence 80, Appl
c 693	17	9.1	15581	4	US-08-503-222-35	Sequence 35, Appl	766	16	8.6	476	4	US-09-605-785-80	Sequence 80, Appl
c 694	17	9.1	17949	4	US-09-087-465-3	Sequence 3, Appl	767	16	8.6	476	4	US-09-439-313-80	Sequence 80, Appl
c 695	17	9.1	32042	4	US-09-245-281-44	Sequence 44, Appl	768	16	8.6	476	4	US-09-352-616A-80	Sequence 80, Appl
c 696	17	9.1	40000	4	US-09-780-049-18	Sequence 18, Appl	769	16	8.6	476	4	US-09-232-149A-80	Sequence 80, Appl
c 697	17	9.1	56516	2	US-08-996-306-1	Sequence 1, Appl	770	16	8.6	479	4	US-09-030-607-182	Sequence 182, App
c 698	17	9.1	56516	4	US-09-338-907-1	Sequence 1, Appl	771	16	8.6	479	4	US-09-605-785-182	Sequence 182, App
c 699	17	9.1	56516	4	US-09-218-207-1	Sequence 1, Appl	772	16	8.6	479	4	US-09-439-313-182	Sequence 182, App
c 700	17	9.1	56520	4	US-09-338-207-179	Sequence 179, App	773	16	8.6	479	4	US-09-352-616A-182	Sequence 182, App
c 701	17	9.1	56520	4	US-09-218-207-179	Sequence 179, App	774	16	8.6	479	4	US-09-232-149A-182	Sequence 182, App
c 702	17	9.1	90050	4	US-09-245-041-5	Sequence 5, Appl	c 775	16	8.6	485	2	US-08-332-766A-18	Sequence 18, Appl
c 703	17	9.1	168575	4	US-09-426-290-1	Sequence 1, Appl	c 776	16	8.6	492	4	US-09-280-116-208	Sequence 208, App
c 704	16	8.6	20	4	US-08-286-959B-12	Sequence 12, Appl	777	16	8.6	504	4	US-09-328-111-123	Sequence 123, App
c 705	16	8.6	60	3	US-08-545-860D-71	Sequence 71, Appl	c 778	16	8.6	520	4	US-08-642-274D-57	Sequence 57, Appl
c 706	16	8.6	60	3	US-08-545-860D-72	Sequence 72, Appl	c 779	16	8.6	520	4	US-08-952-014C-57	Sequence 57, Appl
c 707	16	8.6	60	5	PCT-US94-04496-71	Sequence 71, Appl	c 780	16	8.6	534	1	US-08-599-252-101	Sequence 101, App
c 708	16	8.6	66	5	PCT-US94-04496-72	Sequence 72, Appl	c 781	16	8.6	534	5	PCT-US96-06352-101	Sequence 101, App
c 709	16	8.6	66	2	US-08-454-557C-67	Sequence 67, Appl	c 782	16	8.6	534	5	PCT-US96-06583-101	Sequence 101, App
c 710	16	8.6	66	2	US-08-340-426D-67	Sequence 67, Appl	c 783	16	8.6	542	4	US-09-305-639-5	Sequence 5, Appl
c 711	16	8.6	66	2	US-08-450-673C-67	Sequence 67, Appl	c 784	16	8.6	542	4	US-09-385-982-11	Sequence 11, Appl
c 712	16	8.6	66	5	PCT-US95-17111A-67	Sequence 67, Appl	c 785	16	8.6	585	4	US-08-991-789A-39	Sequence 39, Appl
c 713	16	8.6	141	4	US-09-404-879A-58	Sequence 58, Appl	c 786	16	8.6	585	4	US-09-062-451-39	Sequence 39, Appl
c 714	16	8.6	167	2	US-08-454-557C-90	Sequence 90, Appl	c 787	16	8.6	585	4	US-09-598-326-39	Sequence 39, Appl
c 715	16	8.6	167	2	US-08-340-426D-90	Sequence 90, Appl	c 788	16	8.6	588	4	US-09-385-982-128	Sequence 128, App
c 716	16	8.6	167	2	US-08-450-673C-90	Sequence 90, Appl	c 789	16	8.6	610	1	US-08-661-168-5	Sequence 5, Appl
c 717	16	8.6	167	5	PCT-US95-17111A-90	Sequence 90, Appl	c 790	16	8.6	618	4	US-09-385-982-373	Sequence 373, App
c 718	16	8.6	200	1	US-08-438-500-1	Sequence 1, Appl	c 791	16	8.6	629	4	US-09-385-982-204	Sequence 204, App
c 719	16	8.6	200	1	US-08-477-442-1	Sequence 1, Appl	c 792	16	8.6	633	4	US-09-328-111-358	Sequence 2, Appl
c 720	16	8.6	200	5	PCT-US94-05910-1	Sequence 1, Appl	793	16	8.6	640	4	US-09-385-982-2	Sequence 2, Appl
c 721	16	8.6	201	2	US-08-849-701-5	Sequence 5, Appl	794	16	8.6	657	4	US-09-385-982-326	Sequence 326, App
c 722	16	8.6	231	4	US-09-605-785-464	Sequence 464, App	c 795	16	8.6	719	4	US-09-227-357-74	Sequence 74, Appl
c 723	16	8.6	231	4	US-09-439-313-464	Sequence 464, App	c 796	16	8.6	719	4	US-09-227-357-74	Sequence 74, Appl
c 724	16	8.6	231	4	US-09-352-616A-464	Sequence 464, App	c 797	16	8.6	719	4	US-09-227-357-74	Sequence 74, Appl
c 725	16	8.6	292	2	US-08-481-658B-56	Sequence 56, Appl	c 798	16	8.6	798	4	US-09-288-143-21	Sequence 21, Appl
c 726	16	8.6	292	2	US-08-481-658B-59	Sequence 59, Appl	c 799	16	8.6	811	4	US-09-404-879A-55	Sequence 55, Appl
c 727	16	8.6	292	2	US-08-477-504A-56	Sequence 56, Appl	c 800	16	8.6	856	4	US-09-288-143-47	Sequence 47, Appl
c 728	16	8.6	292	2	US-08-477-504A-59	Sequence 59, Appl	c 801	16	8.6	859	4	US-09-535-008-58	Sequence 58, Appl
c 729	16	8.6	292	2	US-08-486-756A-56	Sequence 56, Appl	c 802	16	8.6	922	1	US-08-480-784-27	Sequence 27, Appl
c 730	16	8.6	292	2	US-08-486-756A-59	Sequence 59, Appl	c 803	16	8.6	922	1	US-08-483-553-27	Sequence 27, Appl
c 731	16	8.6	292	2	US-08-485-862B-56	Sequence 56, Appl	c 804	16	8.6	922	1	US-08-487-002-27	Sequence 27, Appl
c 732	16	8.6	292	2	US-08-485-862B-59	Sequence 59, Appl	c 805	16	8.6	922	1	US-08-483-554B-27	Sequence 27, Appl
c 733	16	8.6	292	3	US-08-787-739-56	Sequence 56, Appl	c 806	16	8.6	922	1	US-08-488-011B-27	Sequence 27, Appl
c 734	16	8.6	292	3	US-08-787-739-59	Sequence 59, Appl	c 807	16	8.6	922	4	US-08-850-727-27	Sequence 27, Appl
c 735	16	8.6	292	3	US-08-487-077A-56	Sequence 56, Appl	c 808	16	8.6	922	5	PCT-US95-10202-27	Sequence 27, Appl
c 736	16	8.6	292	3	US-08-487-077A-59	Sequence 59, Appl	c 809	16	8.6	922	5	PCT-US95-10203-27	Sequence 27, Appl
c 737	16	8.6	292	3	US-08-485-863A-56	Sequence 56, Appl	c 810	16	8.6	922	5	PCT-US95-10220-27	Sequence 27, Appl
c 738	16	8.6	292	3	US-08-485-863A-59	Sequence 59, Appl	c 811	16	8.6	940	4	US-09-659-791A-11	Sequence 11, Appl
c 739	16	8.6	292	4	US-08-485-049D-59	Sequence 59, Appl	c 812	16	8.6	951	4	US-09-605-785-570	Sequence 570, App
c 740	16	8.6	292	4	US-09-178-115-56	Sequence 56, Appl	c 813	16	8.6	955	4	US-09-641-638-4	Sequence 4, Appl
c 741	16	8.6	292	4	US-09-178-115-59	Sequence 59, Appl	c 814	16	8.6	955	4	US-09-641-638-5	Sequence 5, Appl
c 742	16	8.6	292	4	US-09-177-776-56	Sequence 56, Appl	c 815	16	8.6	955	4	US-09-641-638-7	Sequence 7, Appl
c 743	16	8.6	292	4	US-09-177-776-59	Sequence 59, Appl	c 816	16	8.6	956	4	US-09-641-638-41	Sequence 41, Appl
c 744	16	8.6	295	2	US-08-849-701-8	Sequence 8, Appl	c 817	16	8.6	1000	2	US-08-747-121-20	Sequence 20, Appl
c 745	16	8.6	301	4	US-09-605-785-233	Sequence 233, App	c 818	16	8.6	1000	4	US-09-018-584A-32	Sequence 32, Appl
c 746	16	8.6	301	4	US-09-439-313-233	Sequence 233, App	c 819	16	8.6	1000	4	US-09-641-638-590	Sequence 590, App
c 747	16	8.6	301	4	US-09-352-616A-233	Sequence 233, App	c 820	16	8.6	1000	4	US-09-641-638-650	Sequence 650, App
c 748	16	8.6	301	4	US-09-232-149A-233	Sequence 233, App	c 821	16	8.6	1001	4	US-09-641-638-319	Sequence 319, App
c 749	16	8.6	308	4	US-09-222-575-88	Sequence 88, Appl	c 822	16	8.6	1001	4	US-09-641-638-365	Sequence 365, App
c 750	16	8.6	320	1	US-08-629-939-5	Sequence 5, Appl	c 823	16	8.6	1001	4	US-09-641-638-366	Sequence 366, App
c 751	16	8.6	320	1	US-08-759-873-5	Sequence 5, Appl	c 824	16	8.6	1001	4	US-09-641-638-376	Sequence 376, App
c 752	16	8.6	321	4	US-09-385-982-366	Sequence 366, App	c 825	16	8.6	1001	4	US-09-641-638-448	Sequence 448, App
c 753	16	8.6	371	4	US-09-221-988-96	Sequence 96, Appl	c 826	16	8.6	1002	4	US-09-641-638-581	Sequence 581, App
c 754	16	8.6	374	4	US-09-385-982-135	Sequence 135, App	c 827	16	8.6	1014	4	US-09-257-179-32	Sequence 32, Appl
c 755	16	8.6	380	1	US-08-126-587C-5	Sequence 5, Appl	c 828	16	8.6	1037	4	US-09-257-179-16	Sequence 16, Appl
c 756	16	8.6	410	2	US-08-475-844-16	Sequence 16, Appl	c 829	16	8.6	1050	3	US-08-755-587-21	Sequence 21, Appl
c 757	16	8.6	410	5	PCT-US95-08429-16	Sequence 16, Appl	830	16	8.6	1078	2	US-08-728-521-2	Sequence 2, Appl

831	16	8.6	1078	4	US-09-212-146-2	Sequence 2, Appli	c 904	16	8.6	2343	4	US-09-610-417-1	Sequence 1, Appli
832	16	8.6	1081	1	US-08-832-887-57	Sequence 57, Appl	c 905	16	8.6	2394	4	US-09-414-010-3	Sequence 3, Appli
833	16	8.6	1081	2	US-08-832-887-57	Sequence 57, Appl	c 906	16	8.6	2409	1	US-07-911-531-18	Sequence 18, Appl
834	16	8.6	1182	4	US-09-469-242-1	Sequence 1, Appli	c 907	16	8.6	2409	1	US-07-911-531-18	Sequence 18, Appl
835	16	8.6	1182	1	US-08-451-947-9	Sequence 9, Appli	c 908	16	8.6	2415	3	US-09-019-689-1	Sequence 1, Appli
836	16	8.6	1190	1	US-08-451-947-9	Sequence 9, Appli	c 909	16	8.6	2415	3	US-09-019-689-1	Sequence 1, Appli
837	16	8.6	1190	3	US-08-424-826A-9	Sequence 9, Appli	c 910	16	8.6	2480	4	US-09-534-638-3	Sequence 3, Appli
838	16	8.6	1190	5	PCT-US91-06950-9	Sequence 9, Appli	c 911	16	8.6	2555	2	US-08-960-022-15	Sequence 15, Appl
839	16	8.6	1212	4	US-08-943-731-98	Sequence 98, Appl	c 912	16	8.6	2619	5	US-08-983-502-17	Sequence 17, Appl
840	16	8.6	1237	4	US-09-535-008-56	Sequence 56, Appl	c 913	16	8.6	2619	5	PCT-US96-10521-17	Sequence 17, Appl
841	16	8.6	1260	1	US-08-599-252-83	Sequence 83, Appl	c 914	16	8.6	2649	2	US-08-718-964-1	Sequence 1, Appli
842	16	8.6	1260	1	US-08-436-074-56	Sequence 56, Appl	c 915	16	8.6	2649	2	US-09-059-964A-1	Sequence 1, Appli
843	16	8.6	1260	5	PCT-US96-06352-83	Sequence 83, Appl	c 916	16	8.6	2649	2	US-08-842-341-1	Sequence 1, Appli
844	16	8.6	1260	5	PCT-US96-06352-83	Sequence 83, Appl	c 917	16	8.6	2741	1	US-08-832-883-59	Sequence 59, Appl
845	16	8.6	1301	4	US-08-983-502-19	Sequence 19, Appl	c 918	16	8.6	2741	1	US-08-832-883-59	Sequence 59, Appl
846	16	8.6	1301	5	PCT-US96-10521-19	Sequence 19, Appl	c 919	16	8.6	2821	2	US-08-680-395-6	Sequence 6, Appli
847	16	8.6	1323	4	US-08-983-502-15	Sequence 15, Appl	c 920	16	8.6	2821	2	US-08-983-502-15	Sequence 14, Appl
848	16	8.6	1323	5	PCT-US96-10521-15	Sequence 15, Appl	c 921	16	8.6	2821	2	US-08-983-502-15	Sequence 14, Appl
849	16	8.6	1375	4	US-09-511-8258-55	Sequence 55, Appl	c 922	16	8.6	2896	2	US-08-874-186-44	Sequence 44, Appl
850	16	8.6	1443	4	US-08-983-502-33	Sequence 33, Appl	c 923	16	8.6	2896	2	US-08-709-923-1	Sequence 1, Appli
851	16	8.6	1443	5	PCT-US96-10521-33	Sequence 33, Appl	c 924	16	8.6	2907	3	US-09-018-628-17	Sequence 17, Appl
852	16	8.6	1521	1	US-08-670-354-3	Sequence 3, Appli	c 925	16	8.6	2907	3	US-09-273-378-17	Sequence 17, Appl
853	16	8.6	1521	4	US-09-320-424-3	Sequence 3, Appli	c 926	16	8.6	2907	4	US-09-018-635-26	Sequence 26, Appl
854	16	8.6	1521	5	PCT-US96-10895-3	Sequence 3, Appli	c 927	16	8.6	2907	4	US-09-467-642-3	Sequence 3, Appli
855	16	8.6	1650	4	US-09-693-146-1	Sequence 1, Appli	c 928	16	8.6	2923	1	US-08-480-449-1	Sequence 1, Appli
856	16	8.6	1656	4	US-09-522-217-106	Sequence 106, App	c 929	16	8.6	2923	2	US-08-660-542-1	Sequence 1, Appli
857	16	8.6	1664	1	US-08-250-740-34	Sequence 34, Appl	c 930	16	8.6	2927	4	US-08-479-603-1	Sequence 5, Appli
858	16	8.6	1664	1	US-07-695-472B-3	Sequence 3, Appli	c 931	16	8.6	2927	4	US-09-232-878-5	Sequence 5, Appli
859	16	8.6	1677	4	US-09-154-750A-74	Sequence 74, Appl	c 932	16	8.6	2957	2	US-08-394-152A-48	Sequence 48, Appl
860	16	8.6	1688	2	US-08-439-814-2	Sequence 2, Appli	c 933	16	8.6	3017	2	US-08-394-152A-48	Sequence 38, Appl
861	16	8.6	1712	3	US-09-058-389A-12	Sequence 12, Appl	c 934	16	8.6	3158	2	US-08-464-517-36	Sequence 36, Appl
862	16	8.6	1712	4	US-09-611-781-12	Sequence 12, Appl	c 935	16	8.6	3158	2	US-08-464-517-36	Sequence 36, Appl
863	16	8.6	1751	1	US-08-670-354-1	Sequence 1, Appli	c 936	16	8.6	3158	3	US-08-463-772-36	Sequence 36, Appl
864	16	8.6	1751	4	US-09-320-424-1	Sequence 1, Appli	c 937	16	8.6	3233	3	US-08-755-587-43	Sequence 43, Appl
865	16	8.6	1751	5	PCT-US96-10895-1	Sequence 1, Appli	c 938	16	8.6	3266	1	US-08-369-043-3	Sequence 3, Appli
866	16	8.6	1769	4	US-09-333-593A-5	Sequence 5, Appli	c 939	16	8.6	3267	2	US-08-257-963B-12	Sequence 12, Appl
867	16	8.6	1769	4	US-09-505-250A-5	Sequence 5, Appli	c 940	16	8.6	3267	4	US-08-367-841A-12	Sequence 12, Appl
868	16	8.6	1792	2	US-08-386-198A-18	Sequence 18, Appl	c 941	16	8.6	3286	4	PCT-US95-07201-12	Sequence 12, Appl
869	16	8.6	1853	4	US-09-605-785-369	Sequence 369, App	c 942	16	8.6	3366	4	US-09-211-417-2	Sequence 2, Appli
870	16	8.6	1853	4	US-09-439-313-369	Sequence 369, App	c 943	16	8.6	3441	4	US-09-345-650-2	Sequence 2, Appli
871	16	8.6	1853	4	US-09-062-451-295	Sequence 295, App	c 944	16	8.6	3441	4	US-09-026-033-17	Sequence 17, Appl
872	16	8.6	1853	4	US-09-352-616A-369	Sequence 369, App	c 945	16	8.6	3535	2	US-09-118-448-30	Sequence 30, Appl
873	16	8.6	1856	1	US-08-157-171-3	Sequence 3, Appli	c 946	16	8.6	3569	4	US-08-618-408B-1	Sequence 1, Appli
874	16	8.6	1856	4	US-09-050-159-128	Sequence 128, App	c 947	16	8.6	3602	4	US-09-130-491-5	Sequence 5, Appli
875	16	8.6	1864	3	US-09-221-235-10	Sequence 10, Appl	c 948	16	8.6	3602	3	US-08-820-170A-30	Sequence 30, Appl
876	16	8.6	1864	3	US-09-221-235-10	Sequence 10, Appl	c 949	16	8.6	3602	3	US-09-055-699-30	Sequence 30, Appl
877	16	8.6	1864	3	US-09-221-527-10	Sequence 10, Appl	c 950	16	8.6	3602	4	US-09-273-565-30	Sequence 30, Appl
878	16	8.6	1864	3	US-09-221-236-10	Sequence 10, Appl	c 951	16	8.6	3602	4	US-09-565-538-30	Sequence 30, Appl
879	16	8.6	1864	3	US-09-221-416-10	Sequence 10, Appl	c 952	16	8.6	3607	2	US-09-661-468-30	Sequence 30, Appl
880	16	8.6	1864	4	US-09-221-245-10	Sequence 10, Appl	c 953	16	8.6	3607	4	US-08-629-001A-8	Sequence 8, Appli
881	16	8.6	1864	4	US-09-163-115-10	Sequence 10, Appl	c 954	16	8.6	3607	4	US-08-642-274D-8	Sequence 8, Appli
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885	16	8.6	1901	5	PCT-US93-05000-32	Sequence 32, Appl	c 958	16	8.6	3647	1	US-08-393-246-7	Sequence 7, Appli
886	16	8.6	1950	1	US-08-592-126-93	Sequence 93, Appl	c 959	16	8.6	3647	2	US-08-525-058A-7	Sequence 7, Appli
887	16	8.6	2002	2	US-08-747-121-32	Sequence 32, Appl	c 960	16	8.6	3647	2	US-08-696-731-7	Sequence 7, Appli
888	16	8.6	2022	2	US-08-464-517-32	Sequence 32, Appl	c 961	16	8.6	3647	5	PCT-US91-00899-4	Sequence 4, Appli
889	16	8.6	2022	2	US-08-246-361A-32	Sequence 32, Appl	c 962	16	8.6	3742	1	US-08-694-915-5	Sequence 5, Appli
890	16	8.6	2022	3	US-08-463-772-32	Sequence 32, Appl	c 963	16	8.6	3748	2	US-08-958-240-1	Sequence 1, Appli
891	16	8.6	2086	2	US-08-655-640-5	Sequence 5, Appli	c 964	16	8.6	3877	2	US-08-599-895-1	Sequence 1, Appli
892	16	8.6	2090	2	US-08-439-814-1	Sequence 1, Appli	c 965	16	8.6	3877	3	US-09-211-290-1	Sequence 1, Appli
893	16	8.6	2099	4	US-08-938-669A-5	Sequence 5, Appli	c 966	16	8.6	3877	3	US-09-322-676-1	Sequence 1, Appli
894	16	8.6	2119	2	US-08-381-691-17	Sequence 17, Appl	c 967	16	8.6	3877	4	US-09-466-036A-1	Sequence 1, Appli
895	16	8.6	2119	2	US-08-381-691-17	Sequence 17, Appl	c 968	16	8.6	3952	2	US-08-381-691-16	Sequence 16, Appl
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897	16	8.6	2184	4	US-09-439-313-370	Sequence 370, App	c 970	16	8.6	4036	3	US-08-866-340-1	Sequence 1, Appli
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899	16	8.6	2184	4	US-09-352-616A-370	Sequence 370, App	c 972	16	8.6	4136	4	US-09-103-875-2	Sequence 2, Appli
900	16	8.6	2322	1	US-08-618-164-1	Sequence 1, Appli	c 973	16	8.6	4285	4	US-09-460-145-1	Sequence 1, Appli
901	16	8.6	2329	4	US-08-927-219-80	Sequence 80, Appl	c 974	16	8.6	4335	3	US-09-058-489-19	Sequence 1, Appli
902	16	8.6	2343	2	US-09-031-392-1	Sequence 1, Appli	c 975	16	8.6	4415	4	US-09-486-580A-1	Sequence 1, Appli
903	16	8.6	2343	3	US-09-299-549-1	Sequence 1, Appli	c 976	16	8.6	4421	2	US-08-257-963B-9	Sequence 9, Appli

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977 16 8.6 4421 4 US-08-367-841A-9 Sequence 9, Appli
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979 16 8.6 4421 5 PCT-US95-07201-9 Sequence 9, Appli
980 16 8.6 4441 4 US-09-641-999-2 Sequence 2, Appli
981 16 8.6 4460 4 US-09-103-975-4 Sequence 4, Appli
982 16 8.6 4543 2 US-08-519-547A-5 Sequence 5, Appli
983 16 8.6 4545 6 5183884-3 Patent No. 5183884
984 16 8.6 4576 1 US-08-832-883-49 Sequence 49, Appli
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986 16 8.6 4668 4 US-09-045-301-1 Sequence 1, Appli
987 16 8.6 4698 4 US-09-439-261-34 Sequence 34, Appli
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989 16 8.6 4704 2 US-08-476-062A-52 Sequence 52, Appli
990 16 8.6 4741 1 US-07-695-472B-4 Sequence 4, Appli
991 16 8.6 4742 1 US-08-250-740-35 Sequence 35, Appli
992 16 8.6 4895 3 US-09-053-866-1 Sequence 1, Appli
993 16 8.6 4895 4 US-09-479-130-1 Sequence 1, Appli
994 16 8.6 4905 1 US-07-978-895-3 Sequence 3, Appli
995 16 8.6 4905 1 US-08-473-119-3 Sequence 3, Appli
996 16 8.6 4905 2 US-08-475-352-3 Sequence 3, Appli
997 16 8.6 4922 2 US-08-330-272-5 Sequence 5, Appli
998 16 8.6 4922 5 PCT-US95-13663-5 Sequence 5, Appli
999 16 8.6 4975 4 US-09-630-706-3 Sequence 3, Appli
1000 16 8.6 5035 2 US-08-616-392C-3 Sequence 3, Appli

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ALIGNMENTS

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RESULT 1
US-09-797-906-3
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO0151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

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Query Match 21.4%; Score 40; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 27 ACTCCTGGCTCAAGCAATCTCTGCTCAGCCTTCAA 66
Db 9295 ACTCCTGGCTCAAGCAATCTCTGCTCAGCCTTCAA 9334

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RESULT 2
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric

```

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; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89.US2.CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
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; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
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; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
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OTHER INFORMATION: 17-42.rp complement
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NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
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NAME/KEY: primer_bind
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NAME/KEY: primer_bind
LOCATION: 12348..12366
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OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
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OTHER INFORMATION: 17-41-250.mis complement
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NAME/KEY: misc binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe

NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
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Best Local Similarity 100.0%; Pred. No. 2.3e-08;
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Db 3410 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 3376
RESULT 3
US-09-128-155-17
Sequence 17, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Par. Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(176373)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
Query Match 18.7%; Score 35; DB 3; Length 176373;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 86219 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 86253
RESULT 4
US-08-482-728A-3
Sequence 3, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1652
US-08-482-728A-3

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Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-08-247-946A-2/c
Sequence 2, Application US/08247946A
Patent No. 5792838
GENERAL INFORMATION:
APPLICANT: AARONSON, S.A.; CHAN, A.;
APPLICANT: MIKI, T.
TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED
TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA
TITLE OF INVENTION: CLONING
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,946A
FILING DATE: 24-MAY-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 3350
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: Human R-ras gene
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: exons 2-6.
US-08-247-946A-2

Query Match 18.2%; Score 34; DB 1; Length 3350;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2764 CTCCTGGGCTCAAGCAATCTCTGCTCAGCCT 2731
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RESULT 6
PCT-US95-06420-2/c
Sequence 2, Application PC/TUS9506420
GENERAL INFORMATION:
APPLICANT: AARONSON, S.A.; CHAN, A.;
APPLICANT: MIKI, T.
TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED
TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA
TITLE OF INVENTION: CLONING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06420
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,946
FILING DATE: 24-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4150PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3350
TYPE: Nucleic acid


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; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY: Human R-ras gene
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: exons 2-6.
PCT-US95-06420-2

Query Match      18.2%; Score 34; DB 5; Length 3350;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db 2764 CTCTGGGCTCAAGCAATCTCTGCTCAGCCT 2731

RESULT 7
US-09-851-896-3/c
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-DEPENDENT)
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGC 59
Db 35591 ACTCTGGGCTCAAGCAATCTCTGCTCAGC 35559

RESULT 8
US-09-797-906-3/c
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianghe Yan, Karen A. Ketchum, Valentina DiFrancesco, Ellen M. Brasley
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: US95/097906
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match      17.6%; Score 33; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
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Qy 29 TCCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db 45348 TCCTGGGCTCAAGCAATCTCTGCTCAGCCT 45316

RESULT 9
US-09-328-111-76
; Sequence 76, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(674)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-76

Query Match      16.0%; Score 30; DB 4; Length 674;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTC 56
Db 93 ACTCTGGGCTCAAGCAATCTCTGCTC 122

RESULT 10
US-09-367-750-1
; Sequence 1, Application US/09367750
; Patent No. 6436639
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Ossina, Natalya K.
; TITLE OF INVENTION: Bak PROMOTER EXPRESSION SYSTEM
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;
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LXR BIOTECHNOLOGY INC.
; STREET: 3095 Richmond Parkway, Suite 213
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/367,750
; FILING DATE: 07-DEC-1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-14-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4066 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4022..4066
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 4022
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; US-09-367-750-1
;
; Query Match 16.0%; Score 30; DB 4; Length 4066;
; Best Local Similarity 100.0%; Pred. No. 6.7e-06;
; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 47 CTCCTGCTCAGCTTCCAACTAGCTGGGA 76
; DB 955 CTCCTGCTCAGCTTCCAACTAGCTGGGA 984
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; RESULT 11
; US-08-284-941-3/c
; Sequence 3, Application US/08284941
; Patent No. 5863756
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,941
; FILING DATE: 2 August 1994
;
; US-08-284-941-3
; Sequence 3, Application US/08447642
; Patent No. 5989890
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,642
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,941
; FILING DATE: 2 August 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; QY 29 TCCTGGGCTCAAGCAATCTCTGCTCA 57
; DB 414 TCCTGGGCTCAAGCAATCTCTGCTCA 386
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; RESULT 12
; US-08-447-642-3/c
; Sequence 3, Application US/08447642
; Patent No. 5989890
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,642
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,941
; FILING DATE: 2 August 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 29 TCCTGGGCTCAAGCAATCTCTGCTCA 57
; DB 414 TCCTGGGCTCAAGCAATCTCTGCTCA 386
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..58
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; US-08-284-941-3
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; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..58
US-08-447-642-3

Query Match          15.5%; Score 29; DB 2; Length 636;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TCCTGGGCTCAAGCAATCCTCTGCTCTCA 57
Db 414 TCCTGGGCTCAAGCAATCCTCTGCTCTCA 386

RESULT 13
US-09-236-503-3/c
; Sequence 3, Application US/09236503
; Patent No. 6277590
; GENERAL INFORMATION:
; APPLICANT: Barr, Philip J
; APPLICANT: Kiefer, Michael C
; TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
; TITLE OF INVENTION: Polypeptides in Cells
; FILE REFERENCE: CHIR-009/0405
; CURRENT APPLICATION NUMBER: US/09/236,503
; CURRENT FILING DATE: 1999-01-25
; EARLIER APPLICATION NUMBER: 08/447,642
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: 08/284,941
; EARLIER FILING DATE: 1994-08-02
; EARLIER APPLICATION NUMBER: 07/848,629
; EARLIER FILING DATE: 1992-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(57)
US-09-236-503-3

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Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 414 TCCTGGGCTCAAGCAATCCTCTGCTCTCA 386

RESULT 14
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; Sequence 3, Application PC/TUS9302147A
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; APPLICANT: KIEFER, MICHAEL C
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
; TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02147A
; FILING DATE: 19930309
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,629
; FILING DATE: 09-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH D., RICHARD L
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-7622
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cdna)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..58
PCT-US93-02147A-3

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Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 414 TCCTGGGCTCAAGCAATCCTCTGCTCTCA 386

RESULT 15
US-09-791-211-10/c
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 98844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 24962
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 64383
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65468
; OTHER INFORMATION: unknown
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65470
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65471
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; LOCATION: 87130
; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
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; LOCATION: 89049
; OTHER INFORMATION: unknown
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; OTHER INFORMATION:
US-09-791-211-10

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Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 40870 ACTCCTGGGCTCAGCAATCCTCCTGCCT 40842

Search completed: June 17, 2003, 06:29:10
Job time : 21.3201 secs

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OM nucleic - nucleic search, using sw model

Run on: June.16, 2003, 20:04:56 ; Search time 19.7691 Seconds
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13697.491 Million cell updates/sec

Title: US-09-513-888C-1_COPY_6939_7125

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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	36	19.3	32250	9	US-09-764-891-9663
3	36	19.3	183337	9	US-10-020-141-5
4	35	18.7	359	10	US-09-867-701-7276
5	35	18.7	548	9	US-10-198-846-11037
6	35	18.7	602	9	US-09-764-891-9533
7	35	18.7	691	9	US-10-198-846-2835
8	35	18.7	893	9	US-10-198-846-1806
9	35	18.7	1716	10	US-09-822-830A-425
10	35	18.7	1942	9	US-10-091-438-25
11	35	18.7	1948	10	US-09-764-853-242
12	35	18.7	2308	9	US-10-161-803-50
13	35	18.7	2642	9	US-10-161-572-23
14	35	18.7	2744	9	US-10-161-572-26
15	35	18.7	2800	9	US-10-198-846-9985
16	35	18.7	3552	9	US-10-198-846-11479
17	35	18.7	6511	9	US-10-074-095-1066
18	35	18.7	6511	9	US-10-074-095-1072
19	35	18.7	6511	10	US-09-764-860-1066

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Sequence 3933, Ap
Sequence 18, Appl
Sequence 11884, A

C 93	30	16.0	455	9	US-09-918-995-12099	Sequence 12099, A	C 166	29	15.5	110096	10	US-09-880-107-1542	Sequence 1542, Ap
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C 95	30	16.0	674	10	US-09-879-536-76	Sequence 76, Appl	C 168	29	15.5	170834	10	US-09-835-232-7	Sequence 7, Appli
C 96	30	16.0	703	9	US-10-073-961-415	Sequence 415, App	C 169	28	15.0	401	9	US-09-946-807-1213	Sequence 1213, Ap
C 97	30	16.0	7703	9	US-10-073-961-415	Sequence 456, App	C 170	28	15.0	401	10	US-09-795-668-1213	Sequence 1213, Ap
C 98	30	16.0	7703	10	US-09-764-887-415	Sequence 415, App	C 171	28	15.0	401	10	US-09-795-668-1213	Sequence 1213, Ap
C 99	30	16.0	7703	10	US-09-764-887-456	Sequence 456, App	C 172	28	15.0	417	10	US-09-867-701-6779	Sequence 6779, Ap
C 100	30	16.0	10195	10	US-09-764-864-1500	Sequence 1600, Ap	C 173	28	15.0	1644	10	US-09-822-849A-191	Sequence 191, App
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C 110	30	16.0	21721	10	US-09-764-853-861	Sequence 861, App	C 183	28	15.0	1738	9	US-09-997-653-360	Sequence 360, App
C 111	30	16.0	33795	10	US-09-880-107-2184	Sequence 2184, Ap	C 184	28	15.0	1738	9	US-10-174-590-239	Sequence 239, App
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681	27	14.4	20565	9	US-09-764-891-6045	Sequence 6045, Ap	C 754	25	13.4	338	10	US-09-867-701-8221	Sequence 8221, Ap
682	27	14.4	20565	9	US-10-091-438-270	Sequence 270, App	C 755	25	13.4	340	9	US-09-764-891-8217	Sequence 8217, Ap
683	27	14.4	28818	10	US-09-764-877-2266	Sequence 2266, Ap	C 756	25	13.4	344	9	US-09-764-891-1609	Sequence 1609, Ap
684	27	14.4	31949	9	US-09-764-891-8098	Sequence 8098, Ap	C 757	25	13.4	373	9	US-09-918-995-29762	Sequence 29762, A
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686	27	14.4	32152	9	US-09-764-872-517	Sequence 517, App	C 759	25	13.4	409	10	US-09-867-701-6488	Sequence 6488, Ap
687	27	14.4	32152	10	US-10-072-349-328	Sequence 328, App	C 760	25	13.4	465	10	US-09-867-701-8313	Sequence 8313, Ap
688	27	14.4	32186	9	US-09-764-855-328	Sequence 328, App	C 761	25	13.4	467	10	US-10-015-219-979	Sequence 979, App
689	27	14.4	32187	9	US-09-764-891-8099	Sequence 8099, Ap	C 762	25	13.4	467	10	US-09-777-564-979	Sequence 979, App
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691	27	14.4	32188	9	US-10-074-095-799	Sequence 799, App	C 764	25	13.4	475	10	US-09-918-995-11466	Sequence 11466, A
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693	27	14.4	32204	9	US-09-764-872-517	Sequence 517, App	C 766	25	13.4	478	9	US-09-918-995-428	Sequence 428, App
694	27	14.4	32204	9	US-10-072-349-327	Sequence 327, App	C 767	25	13.4	480	9	US-09-918-995-27030	Sequence 27030, A
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697	27	14.4	174424	10	US-09-967-7688-314	Sequence 314, App	C 770	25	13.4	574	9	US-09-986-480-162	Sequence 162, App
698	27	14.4	174424	10	US-09-967-7688-314	Sequence 314, App	C 771	25	13.4	728	9	US-09-986-480-162	Sequence 162, App
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701	26	13.9	210	9	US-09-796-692-347	Sequence 347, Ap	C 774	25	13.4	1381	10	US-09-964-667-3	Sequence 3, Appli
702	26	13.9	210	9	US-10-040-862-347	Sequence 347, Ap	C 775	25	13.4	1381	10	US-09-964-667-3	Sequence 3, Appli
703	26	13.9	258	9	US-10-040-739-1194	Sequence 1194, Ap	C 776	25	13.4	1381	10	US-09-964-667-3	Sequence 3, Appli
704	26	13.9	346	10	US-09-962-436-94	Sequence 94, Appli	C 777	25	13.4	1588	9	US-10-097-065-111	Sequence 111, App
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707	26	13.9	401	9	US-09-946-807-908	Sequence 908, App	C 780	25	13.4	1984	10	US-09-864-761-2811	Sequence 2811, Ap
708	26	13.9	401	10	US-09-795-668-907	Sequence 907, App	C 781	25	13.4	2071	9	US-09-956-993-1	Sequence 1, Appli
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710	26	13.9	401	10	US-09-795-686-907	Sequence 907, App	C 783	25	13.4	3116	9	US-09-764-872-585	Sequence 585, App
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712	26	13.9	412	10	US-09-867-701-1948	Sequence 1948, Ap	C 785	25	13.4	3585	9	US-09-764-868-1415	Sequence 1415, Ap
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727	26	13.9	6149	9	US-10-073-961-437	Sequence 437, App	C 800	25	13.4	7042	10	US-09-876-667-1	Sequence 1, Appli
728	26	13.9	6149	10	US-09-764-887-436	Sequence 436, App	C 801	25	13.4	7075	10	US-09-876-667-15	Sequence 15, Appli
729	26	13.9	6149	10	US-09-764-887-437	Sequence 437, App	C 802	25	13.4	7301	9	US-09-956-993-3	Sequence 3, Appli
730	26	13.9	7099	9	US-09-764-891-7570	Sequence 7570, Ap	C 803	25	13.4	8121	9	US-10-091-504-1689	Sequence 1689, Ap
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735	26	13.9	14796	10	US-09-954-456-1636	Sequence 1636, App	C 808	25	13.4	9192	9	US-10-092-154-1246	Sequence 1246, Ap
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ALIGNMENTS

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2928
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2928
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
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; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
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; Sequence 5, Application US/10020141
; Publication No. US20030092013A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; APPLICANT: Adelson, Allen
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-002
; CURRENT APPLICATION NUMBER: US/10/020,141
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/313,097
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/327,485
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 21
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US-10-020-141-5
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RESULT 4
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; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
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; ORGANISM: Homo sapien
US-09-867-701-7276
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; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11037
; LENGTH: 548
; TYPE: DNA
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; FEATURE:
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; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11037

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Best Local Similarity 100.0%; Pred. No. 6.1e-09;
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
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US-09-764-891-9533

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; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
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; SEQ ID NO 2835
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; LOCATION: 313, 342, 349, 383, 389, 390, 417, 441, 478, 509, 588, 590,
; LOCATION: 623, 636, 645, 648
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2835

Query Match 18.7%; Score 35; DB 9; Length 691;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
|||||
DB 191 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 225
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RESULT 8

US-10-198-846-1806/c
; Sequence 1806, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1806
; LENGTH: 893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 19, 20, 24, 290, 291, 292, 580, 589, 590, 591, 592, 593,
; LOCATION: 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605,
; LOCATION: 606, 612, 613, 614, 615, 623, 624, 625, 626, 627, 628, 629,
; LOCATION: 630, 631, 632, 633, 638, 640, 641, 642, 643, 644, 645
; OTHER INFORMATION: n = A,T,C or G

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; NAME/KEY: misc_feature
; LOCATION: 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 660,
; LOCATION: 674, 682, 694, 709, 719, 720, 721, 723, 727, 731, 732, 739,
; LOCATION: 748, 750, 754, 758, 767, 770, 777, 778, 784, 790, 794, 796,
; LOCATION: 798, 799, 804, 809, 814, 815, 816, 819, 829, 831, 838
; OTHER INFORMATION: n = A,T,C or G
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; NAME/KEY: misc_feature
; LOCATION: 843, 845, 846, 849, 851, 852, 853, 854, 859, 864, 875, 876,
; LOCATION: 877, 892
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-1806

Query Match      18.7%; Score 35; DB 9; Length 893;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
US-09-822-830A-425/c
; Sequence 425, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 425
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-425

Query Match      18.7%; Score 35; DB 10; Length 1716;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db      1159 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 1125

RESULT 10
US-10-091-438-25
; Sequence 25, Application US/10091438
; Publication No. US20030077606A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT217C1
; CURRENT APPLICATION NUMBER: US/10/091,438
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,879
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
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; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
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; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
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; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
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; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match      18.7%  Score 35;  DB 9;  Length 1942;
Best Local Similarity 100.0%;  Pred. No. 6.1e-09;
Matches 35;  Conservative 0;  Mismatches 0;  Indels

QY      27  ACTCTGGGGCTCAAGCAATCTCTGCTCAGCCT 61
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Db      1827  ACTCTGGGGCTCAAGCAATCTCTGCTCAGCCT 1861

RESULT 11
US-09-764-853-242
; Sequence 242, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 242
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-242

Query Match      18.7%  Score 35;  DB 10;  Length 1948

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18.78; Score 35; DB 10; Length 1948;

Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTAAGCAATCTCTCGCTCAGCCT 61
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Db 1834 ACTCTGGGCTAAGCAATCTCTCGCTCAGCCT 1868

RESULT 12

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US-10-161-803-50/C
; Sequence 50, Application US/10161803
; Publication No. US20030092028A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Yuanhong
; APPLICANT: Lih, Chih-Jian
; APPLICANT: Chen, Fan
; APPLICANT: Fairman, Jeffery
; APPLICANT: Chen, Yii-Der I
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS AND
; TITL OF INVENTION: TREATMENT OF INSULIN RESISTANCE AND RELATED CONDITIONS
; FILE REFERENCE: 421452000300
; CURRENT APPLICATION NUMBER: US/10/161,803
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/295,264
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 2308
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-803-50

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RESULT 13

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US-10-161-572-23
; Sequence 23, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 2642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-572-23

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RESULT 14

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US-10-161-572-26
; Sequence 26, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2744
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-572-26

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RESULT 15

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US-10-198-846-9985/c
; Sequence 9985, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Scheimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 9985
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2800_
; OTHER INFORMATION: n = A, T, C or G
US-10-198-846-9985

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-513-888c-1_COPY_6939_7125

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9: gb_est1:**

10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: gb_gss:**

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19: em_gss_inv:**

20: em_gss_pln:**

21: em_gss_vrt:**

22: em_gss_fun:**

23: em_gss_mam:**

24: em_gss_mus:**

25: em_gss_other:**

26: em_gss_pro:**

27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	40	21.4	433	9 A1140075	A1140075 qab7c12.x
6	40	21.4	458	9 A1077461	A1077461 oz37d07.x

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411	17	AQ599298
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243	9	A1611961
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434	9	A1874136
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302	12	BF908113
344	10	AW051154
358	10	BE155425
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331	14	H90192
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348	9	AA907764
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354	14	R53296
356	9	AA659653
356	17	AQ102785
359	9	AA826006
374	14	H62147
374	17	AZ933517
381	10	AW473113
383	14	BQ321093
394	14	BQ022124
395	17	AQ104087
405	12	BF848442
410	10	AW469976
411	17	AQ177185
414	9	AA148713
418	10	AW118248
422	14	BQ022626
422	14	R77818
427	10	AW084190
429	17	B65293
438	17	AQ308830
443	9	AA436603
445	14	R81229
448	9	AA722194
449	17	B36505
456	14	BQ082506
465	9	A1039436
465	17	AQ232167
465	17	AQ270374
469	14	H40451
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482	17	AQ037501
485	10	AW861577
487	17	AQ196431
487	17	AQ307966
492	9	AQ077826
499	17	AU158717
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A1874136	wm49f02.x
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BF908113	RC1-UT008
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AQ119174	HS 3032 A
AQ878841	HS 3144_B
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AQ427713	CITBI-El-
A1420264	tf06b09.x
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BF849602	IL5-ENO08
AQ028593	CIT-HSP-2
AA635310	nt67e12.s
BF738700	PM4-KT004
BQ22510	UI-1-BB1p
BF738700	PM4-KT004
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AA705040	zj83c02.s
R53296	Y82e03.r1
AA659653	ru84c02.s
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AZ933517	UP 335-11
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BQ022124	UI-1-BB1p
AQ104087	HS 3110 B
BF848442	PM4-ENO06
AW469976	xt37a08.x
AQ177185	HS 3223 A
AA148713	zl26g12.s
AW118248	xe12c12.x
BQ022626	UI-1-BB1p
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B65293	CIT-HSP-202
AQ308830	CITBI-El-
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R81229	yj03c11.r1
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B36505	HS-1041-A1-
BQ082506	K-EST0125
A1039436	ox35g04.s
AQ232167	HS_2021_B
AQ270374	HS_2052_B
H40451	yp60d10.r1
A1247506	qhs6f02.x
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C 83	35	18.7	543	12	BF989856	QV4-GN012	C 156	34	18.2	514	9	AA525205	AA525205 n152b03.s
C 84	35	18.7	548	17	AQ432974	HS 2208.A	C 157	34	18.2	514	14	QV677500	QV677500 HS 5529.A
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C 86	35	18.7	569	17	AQ534033	RPCI-11-3	C 159	34	18.2	549	17	AQ319730	AQ319730 RPCI11-10
C 87	35	18.7	572	14	BM671944	UT-E-EOO-	C 160	34	18.2	549	17	AQ552057	AQ552057 RPCI-11-4
C 88	35	18.7	582	17	AQ052781	RPCI11-49	C 161	34	18.2	549	17	AQ584340	AQ584340 RPCI-11-4
C 89	35	18.7	588	14	BQ348243	CM3-HT019	C 162	34	18.2	598	17	AQ552064	AQ552064 RPCI-11-4
C 90	35	18.7	594	9	AI114454	HA1036.Hu	C 163	34	18.2	604	17	AQ890397	AQ890397 HS 3131.A
C 91	35	18.7	600	17	AQ038706	CIT-HSP-2	C 164	34	18.2	610	17	AV727065	AV727065 AV727065
C 92	35	18.7	604	10	AW938867	PMO-DT006	C 165	34	18.2	627	17	AQ552075	AQ552075 RPCI-11-4
C 93	35	18.7	613	12	BF935736	MR2-NT013	C 166	34	18.2	629	10	AV707276	AV707276 AV707276
C 94	35	18.7	615	10	AW861568	RC4-CT032	C 167	34	18.2	648	17	AG042997	AG042997 Pan trogl
C 95	35	18.7	615	14	BQ777823	1137d12.Y	C 168	34	18.2	663	17	AQ535539	AQ535539 RPCI-11-3
C 96	35	18.7	622	14	BM978805	UT-CF-DUI	C 169	34	18.2	679	17	AG115659	AG115659 Pan trogl
C 97	35	18.7	626	17	AQ416377	RPCI-11-1	C 170	34	18.2	684	17	AG129727	AG129727 Pan trogl
C 98	35	18.7	634	14	BM679621	UT-E-EOO-	C 171	34	18.2	691	17	AG115645	AG115645 Pan trogl
C 99	35	18.7	640	9	AL704247	DKFZp686M	C 172	34	18.2	718	17	AG085965	AG085965 Pan trogl
C 100	35	18.7	655	17	AG131162	Pan trogl	C 173	34	18.2	717	17	AG030820	AG030820 Pan trogl
C 101	35	18.7	671	17	AG093536	Pan trogl	C 174	34	18.2	769	17	AG099959	AG099959 Pan trogl
C 102	35	18.7	678	17	AG157581	Pan trogl	C 175	34	18.2	782	17	AG091502	AG091502 HS 3131.A
C 103	35	18.7	688	17	AQ037643	CIT-HSP-2	C 176	34	18.2	846	14	BQ689051	BQ689051 AGENCOURT
C 104	35	18.7	719	17	AG171172	Pan trogl	C 177	34	18.2	860	13	BI861930	BI861930 603391476
C 105	35	18.7	723	17	AQ424250	CITBI-EI-	C 178	34	18.2	867	14	BQ687953	BQ687953 AGENCOURT
C 106	35	18.7	734	14	EQ025166	UT-1-BBIP	C 179	34	18.2	869	14	BQ688301	BQ688301 AGENCOURT
C 107	35	18.7	737	14	BM971245	UT-CF-DUI	C 180	34	18.2	873	14	BQ898023	BQ898023 AGENCOURT
C 108	35	18.7	746	14	BM679680	UT-E-EOO-	C 181	34	18.2	880	14	BQ687265	BQ687265 AGENCOURT
C 109	35	18.7	755	9	AL572352	AL572352	C 182	34	18.2	887	12	BG387775	BG387775 602412656
C 110	35	18.7	760	12	BG741015	602634742	C 183	34	18.2	899	12	BG506453	BG506453 6018610329
C 111	35	18.7	775	9	AL596490	DKFZp761D	C 184	34	18.2	914	13	BM006829	BM006829 603615279
C 112	35	18.7	782	12	BE856643	601508847	C 185	34	18.2	920	14	BQ641632	BQ641632 AGENCOURT
C 113	35	18.7	831	9	AL538354	AL538354	C 186	34	18.2	927	14	BQ690195	BQ690195 AGENCOURT
C 114	35	18.7	832	17	AQ752359	HS 5565.B	C 187	34	18.2	928	14	BQ684796	BQ684796 AGENCOURT
C 115	35	18.7	834	14	BQ893749	AGENCOURT	C 188	34	18.2	938	14	BQ722797	BQ722797 AGENCOURT
C 116	35	18.7	835	12	BG681657	602627962	C 189	34	18.2	945	14	BQ711550	BQ711550 AGENCOURT
C 117	35	18.7	923	13	BI116411	602868828	C 190	34	18.2	949	14	BQ689618	BQ689618 AGENCOURT
C 118	35	18.7	934	12	BG255934	602367593	C 191	34	18.2	1018	13	BM550040	BM550040 AGENCOURT
C 119	35	18.7	937	14	BQ646637	AGENCOURT	C 192	34	18.2	1022	14	BQ052061	BQ052061 AGENCOURT
C 120	35	18.7	955	14	BQ644740	AGENCOURT	C 193	34	18.2	1058	14	BQ892421	BQ892421 AGENCOURT
C 121	35	18.7	976	14	BQ723342	AGENCOURT	C 194	34	18.2	1078	13	BM476430	BM476430 AGENCOURT
C 122	35	18.7	1038	13	BM557184	AGENCOURT	C 195	34	18.2	1119	14	BM918113	BM918113 AGENCOURT
C 123	35	18.7	1040	17	AQ091036	HS 3203.B	C 196	33	17.6	220	14	H72054	H72054 YR98C03.s1
C 124	35	18.7	1860	11	EC021283	Homo sapi	C 197	33	17.6	257	9	AA093988	AA093988 cl1521.se
C 125	35	18.7	2503	11	EC013892	Homo sapi	C 198	33	17.6	281	13	BI040057	BI040057 MR4-NT014
C 126	35	18.7	2931	17	AQ899828	260L13-C4	C 199	33	17.6	285	9	AA004640	AA004640 zh92b07.s
C 127	34	18.2	195	9	AA457186	aa88C04.r	C 200	33	17.6	286	12	BE765850	BE765850 IL3-NT010
C 128	34	18.2	235	9	AA310229	EST18106	C 201	33	17.6	309	14	R16796	R16796 yf33d03.s1
C 129	34	18.2	258	9	AA328095	EST31528	C 202	33	17.6	318	9	AA334237	AA334237 EST38445
C 130	34	18.2	279	10	BE045008	hm26a02.x	C 203	33	17.6	341	14	R05291	R05291 ye91e02.s1
C 131	34	18.2	280	14	R38238	yh94f09.r1	C 204	33	17.6	347	9	AA503446	AA503446 ng21f01.s
C 132	34	18.2	286	14	R97371	YQ52b10.s1	C 205	33	17.6	371	12	BF928726	BF928726 IL5-NT022
C 133	34	18.2	287	9	AA744060	ny50d03.s	C 206	33	17.6	375	9	AA847847	AA847847 od39a04.s
C 134	34	18.2	328	9	AA340852	EST46139	C 207	33	17.6	396	10	AA265752	AA265752 xg76f10.x
C 135	34	18.2	330	9	AL702757	DKFZp6860	C 208	33	17.6	398	9	AA777266	AA777266 zi96b02.s
C 136	34	18.2	342	13	BI023942	CM4-WT024	C 209	33	17.6	419	17	AQ392086	AQ392086 CITBI-E1-
C 137	34	18.2	369	17	AQ057630	CIT-HSP-2	C 210	33	17.6	427	14	BM703988	BM703988 UT-E-CK1-
C 138	34	18.2	373	9	AI016321	ct78b10.s	C 211	33	17.6	429	9	AA583390	AA583390 nm34d07.s
C 139	34	18.2	424	12	BF37203	PM4-KT004	C 212	33	17.6	431	17	AA004239	AA004239 zh32b07.r
C 140	34	18.2	426	14	BQ357586	PM1-HT035	C 213	33	17.6	457	17	AQ202084	AQ202084 RPCI11-48
C 141	34	18.2	432	17	B98853	CIT-HSP-228	C 214	33	17.6	458	17	AQ151340	AQ151340 HS 2202.B
C 142	34	18.2	433	12	BF812241	QV1-CI017	C 215	33	17.6	458	17	AQ242344	AQ242344 HS 2061.A
C 143	34	18.2	435	14	N20833	yx49a06.s1	C 216	33	17.6	464	17	AQ770658	AQ770658 HS 5365.B
C 144	34	18.2	436	10	BE045159	hm28g10.x	C 217	33	17.6	473	9	AA847846	AA847846 od39a03.s
C 145	34	18.2	441	17	AQ082771	RPCI11-54	C 218	33	17.6	474	17	B49067	B49067 RPCI11-4J13
C 146	34	18.2	445	9	AL601967	DKFZp313F	C 219	33	17.6	482	17	AQ665949	AQ665949 HS 5372.B
C 147	34	18.2	445	12	BF811950	QV1-CI017	C 220	33	17.6	483	10	AW270081	AW270081 xv37g03.x
C 148	34	18.2	451	13	BM310143	in08d08.x	C 221	33	17.6	484	17	B89466	B89466 RPCI11-24H9
C 149	34	18.2	454	9	AI371165	ta09C02.x	C 222	33	17.6	491	17	AQ232072	AQ232072 HS 2021.A
C 150	34	18.2	457	13	BI321726	sat98C03	C 223	33	17.6	513	17	AQ148964	AQ148964 HS 3141.B
C 151	34	18.2	486	10	AW274699	xv32f11.x	C 224	33	17.6	514	14	BM823407	BM823407 K-EST0094
C 152	34	18.2	496	17	AQ278609	CITBI-EI-	C 225	33	17.6	547	17	AQ547374	AQ547374 RPCI-11-4

c 226	33	17.6	566	9	AA428410	AA428410 zw57g04.s	c 299	31	16.6	395	12	BG193212	BG193212 RST12339
227	33	17.6	576	14	BM729138	BM729138 UT-E-E01-	300	31	16.6	408	10	AW305124	AW305124 xv99h06.x
228	33	17.6	576	17	AQ419842	AQ419842 RPCI-11-1	301	31	16.6	411	10	AW084237	AW084237 xc53f08.x
c 229	33	17.6	586	12	BE931686	BE931686 QV4-HT053	302	31	16.6	412	14	R94177	R94177 y7f4f12.s1
c 230	33	17.6	590	14	W26920	W26920 17h6 Human	303	31	16.6	416	9	AI434126	AI434126 t136e01.x
c 231	33	17.6	605	17	AQ013403	AQ013403 RPCI11-24	304	31	16.6	416	12	BF738543	BF738543 PM3-KT003
c 232	33	17.6	647	17	AG152943	AG152943 Pan trogl	c 305	31	16.6	417	13	BG996748	BG996748 CM0-HT129
c 233	33	17.6	659	17	AG109493	AG109493 Pan trogl	306	31	16.6	419	17	B30683	B30683 HS-1003-A1-
234	33	17.6	668	10	AV723319	AV723319 AV723319	c 307	31	16.6	424	9	AI903485	AI903485 RC-BT029-
c 235	33	17.6	670	17	AG149798	AG149798 Pan trogl	308	31	16.6	433	17	AQ420463	AQ420463 RPCI-11-1
c 236	33	17.6	691	14	BM682065	BM682065 UT-E-E01-	c 309	31	16.6	435	12	BF841250	BF841250 RC4-HT088
c 237	33	17.6	722	17	AG183270	AG183270 Pan trogl	310	31	16.6	436	9	AA694572	AA694572 ah23f10.s
c 238	33	17.6	736	12	BE960663	BE960663 601647975	311	31	16.6	436	9	AA604118	AA604118 no72d12.s
239	33	17.6	745	13	BI038316	BI038316 IL3-NT028	c 312	31	16.6	438	14	N38889	N38889 yy81f11.s1
c 240	33	17.6	766	12	BG577057	BG577057 602599472	313	31	16.6	441	9	AI903483	AI903483 RC-BT029-
c 241	33	17.6	896	14	BQ212758	BQ212758 AGENCOURT	314	31	16.6	449	9	AI929235	AI929235 au58g06.x
c 242	33	17.6	938	10	BE622056	BE622056 601440917	315	31	16.6	443	9	AI903308	AI903308 RC-BT029-
c 243	33	17.6	1030	12	BG611194	BG611194 602612172	c 316	31	16.6	443	17	AQ042262	AQ042262 CIT-HSP-2
c 244	32	17.1	157	10	AW979448	AW979448 CM1-UM003	317	31	16.6	447	9	AI990175	AI990175 ws38b05.x
c 245	32	17.1	232	13	BM510001	BM510001 1g96f09.x	318	31	16.6	453	9	AA94437	AA94437 ne28d05.s
c 246	32	17.1	266	17	AQ281914	AQ281914 RPCI11-85	c 319	31	16.6	456	9	AA736944	AA736944 nwl3e03.s
c 247	32	17.1	321	9	AA579352	AA579352 nf29b05.s	320	31	16.6	459	9	AA568459	AA568459 nm25c10.s
c 248	32	17.1	362	9	AA526829	AA526829 ni92c05.s	321	31	16.6	460	10	AW973943	AW973943 EST386166
c 249	32	17.1	391	9	AA593553	AA593553 nf29b06.s	322	31	16.6	462	9	AI651362	AI651362 wd05c12.x
c 250	32	17.1	398	9	AA457510	AA457510 aa89b05.s	323	31	16.6	463	9	AI929425	AI929425 au60c09.x
c 251	32	17.1	422	9	AI732225	AI732225 nf18e09.x	324	31	16.6	466	14	H09534	H09534 y196a01.s1
c 252	32	17.1	424	9	AI089568	AI089568 qb06h02.x	325	31	16.6	467	13	BI712105	BI712105 ie01f08.x
c 253	32	17.1	433	9	AA573644	AA573644 nf18e09.s	326	31	16.6	471	12	BE223032	BE223032 7c27g11.x
c 254	32	17.1	433	9	AA579542	AA579542 nf17a09.s	327	31	16.6	474	10	BE677579	BE677579 7d87r08.x
c 255	32	17.1	453	14	R38004	R38004 ynf7h09.r1	328	31	16.6	474	17	AQ186283	AQ186283 HS_3083.B
c 256	32	17.1	455	12	BF725051	BF725051 bx11f09.x	329	31	16.6	477	9	AI804109	AI804109 tj99f06.s
c 257	32	17.1	467	14	H00780	H00780 yj30c08.r1	330	31	16.6	481	9	AA548300	AA548300 nc56d04.x
c 258	32	17.1	467	17	BH140946	BH140946 UP_392-15	331	31	16.6	483	10	AW516009	AW516009 xv04a07.x
c 259	32	17.1	468	14	R76692	R76692 y61f02.s1	332	31	16.6	485	13	BM351888	BM351888 iq83g07.x
c 260	32	17.1	474	10	AW972965	AW972965 EST385062	c 333	31	16.6	488	17	AQ544321	AQ544321 CITBI-E1-
c 261	32	17.1	516	10	AW857473	AW857473 CM3-CIT031	c 334	31	16.6	493	17	AQ582765	AQ582765 RPCI-11-4
c 262	32	17.1	528	17	AQ262571	AQ262571 CITBI-E1-	335	31	16.6	497	17	AQ591529	AQ591529 HS_2126.B
c 263	32	17.1	537	17	AQ787097	AQ787097 HS_5480.A	336	31	16.6	499	10	AW085628	AW085628 xb41e03.x
c 264	32	17.1	591	12	BF628555	BF628555 IL0-HN008	337	31	16.6	505	17	AQ505427	AQ505427 RPCI-11-3
c 265	32	17.1	629	12	BF576984	BF576984 602134437	c 338	31	16.6	510	14	R59249	R59249 y997c05.r1
c 266	32	17.1	645	17	AG144818	AG144818 Pan trogl	339	31	16.6	515	17	AQ701400	AQ701400 HS_2133.A
c 267	32	17.1	655	12	BG435771	BG435771 602506877	c 340	31	16.6	524	9	AA179303	AA179303 zp45c03.s
c 268	32	17.1	655	17	AG061496	AG061496 Pan trogl	c 341	31	16.6	524	17	AQ366587	AQ366587 HS_5037.B
c 269	32	17.1	663	17	AG046860	AG046860 Pan trogl	342	31	16.6	528	9	AI581141	AI581141 t133h08.x
c 270	32	17.1	675	17	AG167399	AG167399 Pan trogl	c 343	31	16.6	535	13	BI713058	BI713058 ie01f08.y
c 271	32	17.1	678	10	AV763666	AV763666 AV763666	344	31	16.6	555	9	AU146499	AU146499 AUI146499
c 272	32	17.1	682	17	AG046384	AG046384 Pan trogl	345	31	16.6	553	9	AL038960	AL038960 DKF2p566P
c 273	32	17.1	719	17	AG232640	AG232640 Pan trogl	c 346	31	16.6	579	17	AQ629104	AQ629104 RPCI-11-4
c 274	32	17.1	875	14	BQ222361	BQ222361 AGENCOURT	c 347	31	16.6	639	17	B80027	B80027 CIT-HSP-204
c 275	32	17.1	911	12	BF672382	BF672382 602150620	348	31	16.6	640	10	AV723883	AV723883 AV723883
c 276	32	17.1	912	10	BE617249	BE617249 601441943	349	31	16.6	647	10	AV705708	AV705708 AV705708
c 277	32	17.1	1022	13	BM556059	BM556059 AGENCOURT	350	31	16.6	649	10	BE513817	BE513817 601315658
c 278	31	16.6	174	13	BG989744	BG989744 PM3-HT092	351	31	16.6	689	17	AG046676	AG046676 Pan trogl
c 279	31	16.6	250	10	AW837863	AW837863 CM1-LT004	c 352	31	16.6	689	17	AG097968	AG097968 Pan trogl
c 280	31	16.6	267	12	BF807023	BF807023 QV4-CIT015	353	31	16.6	701	17	AQ531646	AQ531646 RPCI-11-3
c 281	31	16.6	274	12	BF807024	BF807024 QV4-CIT015	c 354	31	16.6	719	17	AG153387	AG153387 Pan trogl
c 282	31	16.6	280	17	AQ094824	AQ094824 HS_3028.B	c 355	31	16.6	731	9	AQ627605	AQ627605 CITBI-E1-
c 283	31	16.6	285	9	AI868487	AI868487 tc51f06.x	356	31	16.6	752	9	AI816245	AI816245 au46b02.x
c 284	31	16.6	292	17	AQ582699	AQ582699 RPCI-11-4	357	31	16.6	785	10	BE396566	BE396566 601288992
c 285	31	16.6	293	14	R12832	R12832 y5f1f09.r1	c 358	31	16.6	848	17	AQ752067	AQ752067 HS_55770.A
c 286	31	16.6	295	12	BF805606	BF805606 QV1-CIT017	359	31	16.6	859	17	AQ752067	AQ752067 HS_55770.A
c 287	31	16.6	304	12	BF834988	BF834988 PM3-HT092	c 360	31	16.6	911	12	BG432418	BG432418 602495449
c 288	31	16.6	326	9	AI240840	AI240840 qh54f07.x	361	31	16.6	958	13	BI829583	BI829583 603079319
c 289	31	16.6	325	12	BF833644	BF833644 PM3-HT092	362	31	16.6	1058	13	BM552320	BM552320 AGENCOURT
c 290	31	16.6	331	14	F07346	F07346 HSC22G051.n	c 363	30	16.0	103	10	AW818097	AW818097 CM4-ST027
c 291	31	16.6	336	17	AQ037232	AQ037232 CIT-HSP-2	c 364	30	16.0	113	10	BE155428	BE155428 PM1-HT035
c 292	31	16.6	337	9	AA470600	AA470600 nc69f12.x	365	30	16.0	123	14	T18553	T18553 hbc2055.Hum
c 293	31	16.6	348	9	AA836156	AA836156 odi16c07.s	c 366	30	16.0	129	17	AQ393826	AQ393826 CITBI-E1-
c 294	31	16.6	348	14	R07081	R07081 yf13e01.r1	367	30	16.0	166	12	BG236478	BG236478 nsf28g07.
c 295	31	16.6	355	14	T90895	T90895 yd48b11.s1	368	30	16.0	174	10	AW848983	AW848983 IL3-CT021
c 296	31	16.6	371	9	AA470609	AA470609 nc69h09.s	369	30	16.0	191	12	BF844107	BF844107 MR2-HT104
c 297	31	16.6	375	12	BF174954	BF174954 MYE4124a	370	31	16.0	212	12	BF843242	BF843242 MR2-HT104
c 298	31	16.6	394	14	R43081	R43081 ygl7e07.s1	371	30	16.0	262	9	AA533836	AA533836 nj94d03.s.

C 372	30	16.0	262	12	BF891514	BF891514 PM3-MT011	445	30	16.0	609	10	AW975001	AW975001 EST387106
C 373	30	16.0	274	9	AA281726	AA281726 zc07e04.s	446	30	16.0	623	17	AG157923	AG157923 Pan trogl
C 374	30	16.0	289	14	H63269	H63269 yf51n05.s1	C 447	30	16.0	626	10	AW962581	AW962581 EST374654
C 375	30	16.0	295	9	AA834690	AA834690 od99b03.s	C 448	30	16.0	633	17	AQ279400	AQ279400 CITBI-EI-
C 376	30	16.0	305	9	AA635295	AA635295 wt71d04.s	C 449	30	16.0	642	17	AQ336538	AQ336538 RPTBI-11-3
C 377	30	16.0	319	9	AI872352	AI872352 nm35c06.x	C 450	30	16.0	664	17	AQ309089	AQ309089 CITBI-EI-
C 378	30	16.0	319	10	BE145115	BE145115 CM4-HT019	C 451	30	16.0	671	17	AG057609	AG057609 Pan trogl
C 379	30	16.0	324	17	B82231	B82231 RPTBI-13M4	C 452	30	16.0	674	17	AG087269	AG087269 Pan trogl
C 380	30	16.0	333	9	AA846890	AA846890 oe08a01.s	C 453	30	16.0	679	9	AA715049	AA715049 nx94d12.s
C 381	30	16.0	337	9	AA584925	AA584925 nm33d04.s	C 454	30	16.0	685	17	AQ016886	AQ016886 CIT-HSP-2
C 382	30	16.0	337	14	N70409	N70409 za61a12.s1	C 455	30	16.0	689	17	AG125044	AG125044 Pan trogl
C 383	30	16.0	342	12	BF855008	BF855008 MR1-FN021	C 456	30	16.0	694	17	AG069532	AG069532 Pan trogl
C 384	30	16.0	343	14	H68086	H68086 yul5e04.s1	C 457	30	16.0	698	10	AV685392	AV685392 AV685392
C 385	30	16.0	357	9	AA094643	AA094643 cp0942.se	C 458	30	16.0	704	14	BM981128	BM981128 UT-CR-EN1
C 386	30	16.0	360	12	BF848352	BF848352 PM4-EN006	C 459	30	16.0	731	12	EG259843	EG259843 602371992
C 387	30	16.0	365	10	AW069667	AW069667 cf49h02.x	C 460	30	16.0	758	12	EG723353	EG723353 602694262
C 388	30	16.0	367	10	AW805877	AW805877 QV1-UM010	C 461	30	16.0	758	17	AG030513	AG030513 Pan trogl
C 389	30	16.0	372	9	AA283064	AA283064 zt14a11.r	C 462	30	16.0	761	17	AG186292	AG186292 Pan trogl
C 390	30	16.0	374	12	BF961453	BF961453 RC6-NN023	C 463	30	16.0	790	9	AL601348	AL601348 DKF2p313A
C 391	30	16.0	380	10	AW902186	AW902186 OV3-NN102	C 464	30	16.0	854	12	BG433829	BG433829 602497353
C 392	30	16.0	381	9	AA650145	AA650145 ns90g09.s	C 465	30	16.0	858	17	AQ741568	AQ741568 HS 5572.B
C 393	30	16.0	382	10	AW068977	AW068977 gr39f03.x	C 466	30	16.0	885	17	BF215212	BF215212 601846983
C 394	30	16.0	389	9	AA748026	AA748026 nx87d06.s	C 467	30	16.0	895	12	BQ213585	BQ213585 AGENCOURT
C 395	30	16.0	393	14	R43529	R43529 yf19d05.s1	C 468	30	16.0	919	12	BE788574	BE788574 601476093
C 396	30	16.0	395	9	AI095204	AI095204 ov83c10.s	C 469	30	16.0	940	12	BE893063	BE893063 601436548
C 397	30	16.0	395	9	AI381434	AI381434 td01b01.x	C 470	30	16.0	987	12	BE895584	BE895584 601438382
C 398	30	16.0	397	14	T89762	T89762 yd99c02.r1	C 471	30	16.0	987	13	BM471500	BM471500 AGENCOURT
C 399	30	16.0	398	12	BF961435	BF961435 RC6-NN023	C 472	30	16.0	1112	13	BM548235	BM548235 AGENCOURT
C 400	30	16.0	400	10	AW663330	AW663330 hh7602.y	C 473	29	15.5	126	9	AI312481	AI312481 ta91f02.x
C 401	30	16.0	413	9	AI285709	AI285709 qu81a02.x	C 474	29	15.5	162	9	AA347077	AA347077 EST53326
C 402	30	16.0	414	17	AQ323275	AQ323275 RPTBI-11-99	C 475	29	15.5	168	9	AA429130	AA429130 zw19b05.r
C 403	30	16.0	416	12	EG555296	EG555296 602582984	C 476	29	15.5	175	9	AQ263841	AQ263841 CITBI-EI-
C 404	30	16.0	417	17	AQ230188	AQ230188 HS 2041.B	C 477	29	15.5	238	17	AQ005651	AQ005651 CIT-HSP-2
C 405	30	16.0	419	14	BM721579	BM721579 UT-E-BOI-	C 478	29	15.5	259	9	AI625977	AI625977 ar91g02.x
C 406	30	16.0	423	17	AQ815322	AQ815322 HS 5014.A	C 479	29	15.5	273	12	BF929478	BF929478 IL2-NT020
C 407	30	16.0	437	17	AQ110019	AQ110019 CIT-HSP-2	C 480	29	15.5	275	9	AI933797	AI933797 wn92d08.x
C 408	30	16.0	439	17	AQ438712	AQ438712 HS 5141.A	C 481	29	15.5	312	14	BQ355605	BQ355605 MR4-HT126
C 409	30	16.0	441	9	AI821120	AI821120 ns90g09.y	C 482	29	15.5	316	10	AW613931	AW613931 hg71c08.x
C 410	30	16.0	443	9	AA489868	AA489868 ab01b08.r	C 483	29	15.5	316	10	AW613931	AW613931 hg71c08.x
C 411	30	16.0	447	9	AA648731	AA648731 ns34d07.s	C 484	29	15.5	337	13	BI045154	BI045154 RC6-FN020
C 412	30	16.0	453	12	BG059520	BG059520 nah62h04.	C 485	29	15.5	337	10	AW351985	AW351985 CM0-HT009
C 413	30	16.0	453	13	BI712813	BI712813 le09e11.y	C 486	29	15.5	337	10	AW196601	AW196601 xm35c06.x
C 414	30	16.0	454	9	AA813393	AA813393 aj33d02.s	C 487	29	15.5	337	10	AW196601	AW196601 xm35c06.x
C 415	30	16.0	458	17	AQ015673	AQ015673 CIT-HSP-2	C 488	29	15.5	338	14	BM672790	BM672790 UT-E-CQO-
C 416	30	16.0	472	9	AI972099	AI972099 wr52e02.x	C 489	29	15.5	338	14	M77904	M77904 EST01488.Fe
C 417	30	16.0	472	9	AA491444	AA491444 ab01b08.s	C 490	29	15.5	345	10	AV690340	AV690340 AV690340
C 418	30	16.0	485	9	AA028137	AA028137 zk07e03.s	C 491	29	15.5	348	10	AV685168	AV685168 AV685168
C 419	30	16.0	488	9	AA658935	AA658935 nt85g04.s	C 492	29	15.5	351	9	AA687547	AA687547 nu27e03.s
C 420	30	16.0	501	14	BM672958	BM672958 UT-E-CQO-	C 493	29	15.5	351	10	AV692604	AV692604 AV692604
C 421	30	16.0	505	14	BM686779	BM686779 UT-E-CQO-	C 494	29	15.5	351	17	B72993	B72993 RPTBI-11-10N1
C 422	30	16.0	513	9	AI950421	AI950421 wq35c04.x	C 495	29	15.5	355	17	B72993	B72993 RPTBI-11-10N1
C 423	30	16.0	523	13	EG993351	EG993351 MR3-HT099	C 500	29	15.5	355	10	AW613944	AW613944 hg71e08.x
C 424	30	16.0	524	12	BF924273	BF924273 MR2-NT013	C 501	29	15.5	358	10	AW105452	AW105452 xg52n07.x
C 425	30	16.0	525	9	AI821864	AI821864 ns90g09.x	C 502	29	15.5	359	10	AW105452	AW105452 xg52n07.x
C 426	30	16.0	538	12	BF854095	BF854095 MR2-EN009	C 503	29	15.5	361	9	AI376993	AI376993 tc34g07.x
C 427	30	16.0	538	12	BF956902	BF956902 RC1-NN023	C 504	29	15.5	361	9	AL710493	AL710493 DKF2p686H
C 428	30	16.0	541	10	AW979221	AW979221 EST391331	C 505	29	15.5	368	14	N62686	N62686 za15f10.s1
C 429	30	16.0	544	17	AQ349993	AQ349993 CITBI-EI-	C 506	29	15.5	370	14	BM706618	BM706618 UT-E-CQO-
C 430	30	16.0	545	17	AQ378718	AQ378718 RPTBI-11-1	C 507	29	15.5	372	12	BF766884	BF766884 CM3-CS000
C 431	30	16.0	547	17	B48233	B48233 RPTBI-11-6G2.	C 508	29	15.5	375	9	AI192587	AI192587 qe61f09.x
C 432	30	16.0	548	10	BE145625	BE145625 IL0-HT020	C 509	29	15.5	379	13	BI026468	BI026468 CM4-WT028
C 433	30	16.0	550	17	AQ455175	AQ455175 HS 5079.B	C 510	29	15.5	379	17	BI026468	BI026468 CM4-WT028
C 434	30	16.0	555	17	AQ435224	AQ435224 CITBI-EI-	C 511	29	15.5	382	10	AA287992	AA287992 z855d05.f
C 435	30	16.0	566	10	AW795447	AW795447 MR4-UM001	C 512	29	15.5	382	10	BE181661	BE181661 QV1-HT063
C 436	30	16.0	575	10	AW858657	AW858657 CM2-CT034	C 513	29	15.5	388	14	N48878	N48878 yf77b06.s1
C 437	30	16.0	578	17	AQ469734	AQ469734 CITBI-EI-	C 514	29	15.5	388	14	T96976	T96976 ye50h08.s1
C 438	30	16.0	580	17	AQ311112	AQ311112 CITBI-EI-	C 515	29	15.5	390	14	BQ694126	BQ694126 1000269.H
C 439	30	16.0	587	17	AQ275024	AQ275024 RPTBI-5-11	C 516	29	15.5	392	13	BI495581	BI495581 df119c03.
C 440	30	16.0	587	17	AG016809	AG016809 Homo sapi	C 517	29	15.5	392	13	BI495581	BI495581 df119c03.
C 441	30	16.0	595	17	AQ725304	AQ725304 HS 5404.A	C 518	29	15.5	392	13	BI495581	BI495581 df119c03.
C 442	30	16.0	595	17	AQ543268	AQ543268 RPTBI-11-3	C 519	29	15.5	392	13	BI495581	BI495581 df119c03.
C 443	30	16.0	602	12	BG617170	BG617170 602615566	C 520	29	15.5	392	13	BI495581	BI495581 df119c03.
C 444	30	16.0	609	9	AA121504	AA121504 zk88b09.s	C 521	29	15.5	392	13	BI495581	BI495581 df119c03.

c 518	29	15.5	393	13	BI495582	BI495582 df119c03.	c 591	29	15.5	529	12	BF668501
519	29	15.5	394	9	AA181902	AA181902 zp63d06.s	592	29	15.5	533	17	BI6189
520	29	15.5	395	9	AA640681	AA640681 nt70c10.s	593	29	15.5	535	14	T54095
521	29	15.5	403	9	AI453629	AI453629 tj45f08.x	594	29	15.5	536	9	AI732594
c 522	29	15.5	405	17	AQ112829	AQ112829 CIT-HSP-2	595	29	15.5	536	10	BE170274
523	29	15.5	410	10	AW65069	AW65069 xg60h07.x	c 596	29	15.5	537	10	AW846932
524	29	15.5	411	10	AW238203	AW238203 xp21e08.x	c 597	29	15.5	537	10	AW846932
525	29	15.5	413	10	AW471153	AW471153 xu08e02.x	c 598	29	15.5	541	9	AI809122
526	29	15.5	413	14	T50387	T50387 yb30a08.s1	c 599	29	15.5	541	17	AQ533134
c 527	29	15.5	414	13	BM021066	BM021066 ief5d02.x	600	29	15.5	544	17	B73164
c 528	29	15.5	414	17	AQ603768	AQ603768 HS.2126.A	c 601	29	15.5	546	14	BQ673038
529	29	15.5	417	9	AI839943	AI839943 wj88e04.x	602	29	15.5	551	17	AQ309709
530	29	15.5	418	9	AA635412	AA635412 nt68c07.s	c 603	29	15.5	552	17	AZ518780
531	29	15.5	420	9	AA054219	AA054219 wf52e02.s	604	29	15.5	555	17	AQ074924
532	29	15.5	422	9	AI984473	AI984473 fr83d10.x	c 605	29	15.5	555	17	AQ072759
533	29	15.5	425	9	AI050020	AI050020 an22d03.x	c 606	29	15.5	561	12	BF736316
534	29	15.5	428	17	AQ671819	AQ671819 HS.5458.B	c 607	29	15.5	561	12	BF736316
535	29	15.5	430	9	AA639076	AA639076 nb03a06.F	c 608	29	15.5	561	17	AQ381485
536	29	15.5	430	17	AQ168926	AQ168926 HS.3174.A	609	29	15.5	570	17	AQ381485
537	29	15.5	430	17	AQ168946	AQ168946 HS.3174.A	610	29	15.5	571	17	AQ381485
538	29	15.5	434	9	AI809829	AI809829 wh77f12.x	c 611	29	15.5	571	17	AQ371948
c 539	29	15.5	434	9	AA430262	AA430262 zw65h04.x	612	29	15.5	581	9	AI341559
540	29	15.5	441	9	AA700314	AA700314 zj73h09.s	613	29	15.5	592	9	AA614340
c 541	29	15.5	443	9	AI734103	AI734103 zj19b05.y	614	29	15.5	620	14	BQ776015
542	29	15.5	443	9	AA583227	AA583227 nm33f11.s	c 615	29	15.5	621	14	BM686415
543	29	15.5	444	10	AW265068	AW265068 xg60g07.x	c 616	29	15.5	626	17	BQ6951
544	29	15.5	445	9	AA132735	AA132735 zo18g06.s	c 617	29	15.5	629	10	AW937743
545	29	15.5	445	9	AA568308	AA568308 nf15b04.s	618	29	15.5	632	10	AW722208
546	29	15.5	445	17	AQ166168	AQ166168 HS.3070.B	c 619	29	15.5	633	10	AV711379
547	29	15.5	446	14	H66848	H66848 yr71c04.s1	c 620	29	15.5	633	17	AQ003147
548	29	15.5	448	9	AA021090	AA021090 ze67c12.x	c 621	29	15.5	639	17	AG089588
549	29	15.5	451	9	AI025850	AI025850 ow12c06.s	622	29	15.5	641	17	AG147536
550	29	15.5	451	14	H61877	H61877 yr02c08.r1	623	29	15.5	643	13	BM044552
c 551	29	15.5	453	10	AW819579	AW819579 RC5-ST029	624	29	15.5	646	12	BF718626
c 552	29	15.5	454	12	BF854518	BF854518 MR2-EN009	c 625	29	15.5	647	10	AW962846
c 553	29	15.5	457	12	BF996660	BF996660 PM4-GN006	c 626	29	15.5	666	17	AG147431
554	29	15.5	458	12	BF116111	BF116111 7132b05.x	c 627	29	15.5	679	17	AG147935
555	29	15.5	459	17	AQ786548	AQ786548 HS.3086.B	c 628	29	15.5	683	17	AG165239
556	29	15.5	460	9	AI469824	AI469824 tj87e04.x	c 629	29	15.5	686	12	BG427545
c 557	29	15.5	461	9	AA179446	AA179446 zp45c03.x	c 630	29	15.5	689	17	AQ386353
558	29	15.5	468	9	AI034073	AI034073 cx12b07.x	c 631	29	15.5	691	17	AQ780061
559	29	15.5	468	9	AI478300	AI478300 tm39e01.x	c 632	29	15.5	696	17	B81466
560	29	15.5	468	10	AW264320	AW264320 xq98c06.x	633	29	15.5	707	17	AQ415514
c 561	29	15.5	468	12	BG007192	BG007192 PM2-GN001	634	29	15.5	713	17	AQ267177
c 562	29	15.5	473	10	AW819581	AW819581 RC5-ST029	c 635	29	15.5	717	17	AG177031
c 563	29	15.5	475	9	AI361719	AI361719 qz18h03.x	c 636	29	15.5	725	13	BI916155
c 564	29	15.5	486	12	BF853957	BF853957 MR2-EN009	c 637	29	15.5	727	10	AW850586
c 565	29	15.5	487	14	BM689148	BM689148 UI-E-CQ1-	c 638	29	15.5	737	14	W28851
c 566	29	15.5	487	14	H74185	H74185 yu02b03.s1	c 639	29	15.5	789	12	BG565408
c 567	29	15.5	488	17	AQ812921	AQ812921 HS.5300.B	640	29	15.5	822	13	BM012392
568	29	15.5	490	12	BF436024	BF436024 nab34a07.	641	29	15.5	825	12	BF665467
569	29	15.5	491	9	AI708321	AI708321 at04b03.x	642	29	15.5	843	12	BG499230
570	29	15.5	495	9	AI416956	AI416956 th02a05.x	643	29	15.5	871	14	BQ889198
571	29	15.5	496	17	AQ411061	AQ411061 HS.5064.B	c 644	29	15.5	886	12	BF967751
572	29	15.5	499	17	AQ245993	AQ245993 HS.2059.A	c 645	29	15.5	887	17	AG180245
573	29	15.5	503	13	BM662910	BM662910 UI-E-CKO-	646	29	15.5	897	14	BQ884289
c 574	29	15.5	505	9	AA234699	AA234699 z839g05.x	c 647	29	15.5	912	14	BQ876665
575	29	15.5	506	9	AI400709	AI400709 tg93g05.x	648	29	15.5	944	12	BG121050
576	29	15.5	506	17	AQ372034	AQ372034 RPC11-15	649	29	15.5	947	12	BG290621
c 577	29	15.5	509	17	AQ189357	AQ189357 HS.3199.B	650	29	15.5	957	12	BE878431
578	29	15.5	511	9	AA978266	AA978266 op46b10.s	651	29	15.5	977	14	BQ950224
579	29	15.5	514	14	BQ183977	BQ183977 UI-E-EUO-	652	28	15.0	124	9	AA489088
580	29	15.5	515	17	AQ169206	AQ169206 HS.3175.B	c 653	28	15.0	156	12	BF929895
581	29	15.5	517	9	AA703833	AA703833 ag78g09.x	654	28	15.0	178	14	BM718789
c 582	29	15.5	517	17	AQ186702	AQ186702 HS.3115.A	c 655	28	15.0	223	9	AA558078
c 583	29	15.5	517	17	AQ534213	AQ534213 RPC11-11-3	c 656	28	15.0	224	12	BF854944
584	29	15.5	518	17	AQ244095	AQ244095 HS.2063.B	c 657	28	15.0	233	17	AA248704
c 585	29	15.5	520	10	BE069849	BE069849 CM4-BT039	c 658	28	15.0	236	10	BE152023
c 586	29	15.5	520	17	AQ554188	AQ554188 RPC11-11-4	659	28	15.0	239	10	BE067838
c 587	29	15.5	521	17	AQ827518	AQ827518 HS.5304.A	660	28	15.0	240	10	BE152096
c 588	29	15.5	523	9	AA017574	AA017574 ze37e04.F	661	28	15.0	242	10	BE152096
c 589	29	15.5	528	10	BE166317	BE166317 QV4-HT049	662	28	15.0	247	10	AW083681
590	29	15.5	529	9	AA020904	AA020904 ze64h09.x	c 663	28	15.0	253	10	AW886174

C 664	28	15.0	297	14	R34029	R34029 yH83d06.r1	C 737	28	15.0	552	12	BGI89114	BI89114 RST8153 A
C 665	28	15.0	308	9	AA584677	AA584677 n09b07.s	738	28	15.0	558	17	AQ562775	AQ562775 HS 2079 B
C 666	28	15.0	311	14	R67777	R67777 y128h06.r1	C 739	28	15.0	561	17	AQ267549	AQ267549 RPCI11-73
C 667	28	15.0	309	14	R67756	R67756 y128e07.r1	740	28	15.0	563	9	AA482037	AA482037 z198h06.s
C 668	28	15.0	324	12	BB4904	BB4904 RPCI11-28M3	C 741	28	15.0	567	17	AQ421424	AQ421424 RPCI-11-1
C 669	28	15.0	328	12	BF817311	BF817311 PM3-CI011	C 742	28	15.0	576	17	AQ245110	AQ245110 HS 2059 A
C 670	28	15.0	338	10	AW009059	AW009059 w875g03.x	C 743	28	15.0	592	17	AQ120007	AQ120007 HS 3022 B
C 671	28	15.0	344	14	F35325	F35325 HSPD31385.H	C 744	28	15.0	622	17	AG161008	AG161008 Pan trogl
C 672	28	15.0	344	14	T83216	T83216 yd48b011.r1	C 745	28	15.0	640	10	AW971457	AW971457 RST38356
C 673	28	15.0	345	9	AA757872	AA757872 z940c11.s	C 746	28	15.0	643	17	AG154460	AG154460 Pan trogl
C 674	28	15.0	349	17	AQ839629	AQ839629 HS 4707 A	C 747	28	15.0	644	17	AG154268	AG154268 Pan trogl
C 675	28	15.0	361	17	B70512	B70512 CIT-HSP-205	C 748	28	15.0	654	17	AG053415	AG053415 Pan trogl
C 676	28	15.0	362	9	AA993968	AA993968 ou34c08.s	C 749	28	15.0	658	17	AZ520093	AZ520093 RPCI-11-2
C 677	28	15.0	362	9	AA508640	AA508640 nm66g12.s	C 750	28	15.0	659	17	AG086436	AG086436 Pan trogl
C 678	28	15.0	367	14	H23683	H23683 ym72c11.r1	C 751	28	15.0	661	17	AG160937	AG160937 Pan trogl
C 679	28	15.0	368	17	B88097	B88097 RPCI11-18G1	C 752	28	15.0	664	14	BM982678	BM982678 UI-CF-EN1
C 680	28	15.0	371	10	AW857889	AW857889 RC4-CT032	C 753	28	15.0	666	17	AQ395356	AQ395356 CITBI-EI-
C 681	28	15.0	371	14	R00488	R00488 ye74a05.s1	C 754	28	15.0	672	17	AG073268	AG073268 Pan trogl
C 682	28	15.0	375	9	AA634936	AA634936 ab28h07.r	C 755	28	15.0	673	17	AG137583	AG137583 Pan trogl
C 683	28	15.0	381	12	BG014646	BG014646 IL5-GN023	C 756	28	15.0	674	17	AG056575	AG056575 Pan trogl
C 684	28	15.0	383	17	AQ223300	AQ223300 HS 2016.A	C 757	28	15.0	674	17	AG070745	AG070745 Pan trogl
C 685	28	15.0	389	17	AQ036470	AQ036470 CIT-HSP-2	C 758	28	15.0	676	10	AW978209	AW978209 RST390318
C 686	28	15.0	395	9	AA954475	AA954475 on73d07.s	C 759	28	15.0	689	17	AG096816	AG096816 Pan trogl
C 687	28	15.0	395	12	BF805575	BF805575 QV1-CI017	C 760	28	15.0	694	12	BF344600	BF344600 602015221
C 688	28	15.0	395	14	H46876	H46876 vo19e01.r1	C 761	28	15.0	703	17	AG002669	AG002669 Homo sapi
C 689	28	15.0	396	9	AA600325	AA600325 ag04d01.s	C 762	28	15.0	706	13	BI086004	BI086004 602870228
C 690	28	15.0	400	14	BQ354138	BQ354138 RC0-HI095	C 763	28	15.0	708	17	B02898	B02898 CSRL-162D12
C 691	28	15.0	400	17	AQ219704	AQ219704 HS 3243.B	C 764	28	15.0	712	10	AW836579	AW836579 PM3-LT003
C 692	28	15.0	405	9	AA527830	AA527830 nm25d08.s	C 765	28	15.0	713	13	BI226587	BI226587 602951569
C 693	28	15.0	407	9	AA807588	AA807588 nm26e06.s	C 766	28	15.0	721	17	AG128838	AG128838 Pan trogl
C 694	28	15.0	408	9	AA745017	AA745017 nv43d09.r	C 767	28	15.0	724	14	BM976958	BM976958 UI-CF-EN1
C 695	28	15.0	417	9	AA526420	AA526420 n160b09.s	C 768	28	15.0	736	13	BG928574	BG928574 HNC58-1-E
C 696	28	15.0	420	14	T96200	T96200 ye48b04.r1	C 769	28	15.0	741	17	AZ081513	AZ081513 104282Sp6
C 697	28	15.0	426	9	AA504788	AA504788 ab02g07.r	C 770	28	15.0	779	14	W28662	W28662 49h10 Human
C 698	28	15.0	426	14	H47417	H47417 yp74f03.r1	C 771	28	15.0	786	10	AW733736	AW733736 AV733736
C 699	28	15.0	439	17	AQ839625	AQ839625 HS 4707 A	C 772	28	15.0	817	17	AQ741307	AQ741307 HS 5570 B
C 700	28	15.0	440	10	AM663053	AM663053 h164c02.x	C 773	28	15.0	870	14	BQ425754	BQ425754 AGENCECOURT
C 701	28	15.0	441	14	N66928	N66928 za47g12.s1	C 774	28	15.0	885	9	AA203378	AA203378 zx57d10.x
C 702	28	15.0	445	14	H49368	H49368 yq18h10.s1	C 775	28	15.0	885	17	AQ738816	AQ738816 HS 5386 B
C 703	28	15.0	447	14	H68100	H68100 yu15g04.s1	C 776	28	15.0	893	14	BQ711984	BQ711984 AGENCECOURT
C 704	28	15.0	448	14	R83638	R83638 yq12e09.r1	C 777	28	15.0	903	12	BG257392	BG257392 602377722
C 705	28	15.0	449	17	B58109	B58109 CIT-HSP-201	C 778	28	15.0	956	12	BE887869	BE887869 601511256
C 706	28	15.0	451	17	B45784	B45784 HS-1062-A2-	C 779	28	15.0	973	12	BG260789	BG260789 602372374
C 707	28	15.0	452	14	BQ581338	BQ581338 i107e10.y	C 780	28	15.0	1033	14	BM907862	BM907862 AGENCECOURT
C 708	28	15.0	455	9	AI623365	AI623365 ts18d07.x	C 781	28	15.0	1059	13	BM454445	BM454445 AGENCECOURT
C 709	28	15.0	460	17	AQ705348	AQ705348 HS 5526.B	C 782	28	15.0	1070	12	BF982751	BF982751 602304963
C 710	28	15.0	462	10	AM104300	AM104300 xg77a04.x	C 783	28	15.0	1077	14	BQ224082	BQ224082 AGENCECOURT
C 711	28	15.0	463	12	BF110245	BF110245 7n51d07.x	C 784	28	15.0	1087	14	BQ707212	BQ707212 AGENCECOURT
C 712	28	15.0	475	12	BF921230	BF921230 MR2-NT013	C 785	28	15.0	1097	14	BQ054355	BQ054355 AGENCECOURT
C 713	28	15.0	475	12	BF921393	BF921393 MR2-NT013	C 786	28	15.0	1098	14	BM920573	BM920573 AGENCECOURT
C 714	28	15.0	475	17	AQ280338	AQ280338 CITBI-EI-	C 787	28	15.0	1116	14	BM914723	BM914723 AGENCECOURT
C 715	28	15.0	476	9	AA553438	AA553438 nk77d03.s	C 788	28	15.0	1117	14	BM918691	BM918691 AGENCECOURT
C 716	28	15.0	483	9	AA559121	AA559121 nj33d10.s	C 789	28	15.0	1175	12	BF343846	BF343846 602015521
C 717	28	15.0	486	12	BG460082	BG460082 RST42526	C 790	28	15.0	1247	13	BM476900	BM476900 AGENCECOURT
C 718	28	15.0	488	17	AQ285465	AQ285465 RPCI11-77	C 791	27	14.4	151	14	T84393	T84393 yd45f08.r1
C 719	28	15.0	489	12	BG220463	BG220463 RST40248	C 792	27	14.4	161	9	AA738169	AA738169 nx12d01.s
C 720	28	15.0	489	14	N54550	N54550 yv37h03.s1	C 793	27	14.4	174	9	AI569391	AI569391 to98h12.x
C 721	28	15.0	491	17	B85360	B85360 RPCI11-16G2	C 794	27	14.4	176	14	R62345	R62345 y120a09.s1
C 722	28	15.0	493	10	AV748729	AV748729 AV748729	C 795	27	14.4	189	14	BQ024100	BQ024100 UI-1-BB1P
C 723	28	15.0	495	17	AQ682862	AQ682862 HS 5522.B	C 796	27	14.4	192	10	AW275667	AW275667 xp39e07.x
C 724	28	15.0	497	9	AI624339	AI624339 ts67h02.x	C 797	27	14.4	193	10	AW168653	AW168653 xi92d03.x
C 725	28	15.0	497	14	H66244	H66244 yu18e03.r1	C 798	27	14.4	223	10	BE141309	BE141309 MR0-HT007
C 726	28	15.0	498	12	BG212650	BG212650 RST32245	C 799	27	14.4	227	13	BG991487	BG991487 MR1-HT105
C 727	28	15.0	508	13	BM504781	BM504781 i990d07.x	C 800	27	14.4	231	9	AA372669	AA372669 EST84799
C 728	28	15.0	520	17	AQ252670	AQ252670 HS 3202.B	C 801	27	14.4	232	9	AI648410	AI648410 tx11g05.x
C 729	28	15.0	520	17	AQ607988	AQ607988 HS 2128.B	C 802	27	14.4	239	14	M85702	M85702 EST02220 Fe
C 730	28	15.0	527	17	AQ357477	AQ357477 CITBI-EI-	C 803	27	14.4	246	14	R81816	R81816 vj03f08.s1
C 731	28	15.0	528	12	BF930856	BF930856 MR2-NT013	C 804	27	14.4	246	9	AA299208	AA299208 EST11695
C 732	28	15.0	533	9	AA805354	AA805354 oc15e06.s	C 805	27	14.4	246	17	AO017368	AO017368 CIT-HSP-2
C 733	28	15.0	535	17	AQ475997	AQ475997 CITBI-EI-	C 806	27	14.4	248	9	AI832399	AI832399 at68e02.x
C 734	28	15.0	540	17	AQ469801	AQ469801 CITBI-EI-	C 807	27	14.4	257	10	AW816404	AW816404 QV4-ST023
C 735	28	15.0	541	17	AZ521007	AZ521007 RPCI-11-2	C 808	27	14.4	262	14	N46698	N46698 yv50g02.r1
C 736	28	15.0	548	17	AQ532706	AQ532706 RPCI-11-3	C 809	27	14.4	268	9	AA847742	AA847742 oe20g06.s

c 810	27	14.4	272	14	T04979	T04979 EST02867.Fe	883	27	14.4	433	9	AA775190	AA775190 ac79b07.s
c 811	27	14.4	280	17	AQ416201	AQ416201 RPECI-11-1	884	27	14.4	434	9	AA088661	AA088661 z183a04.s
c 812	27	14.4	295	9	AA568991	AA568991 nm08e12.s	c 885	27	14.4	435	17	AQ589030	AQ589030 CITBI-E1-
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c 814	27	14.4	300	12	BG206762	BG206762 RST26213	887	27	14.4	442	9	AI873103	AI873103 w152g09.x
c 815	27	14.4	300	14	T05319	T05319 EST03208.Fe	c 888	27	14.4	442	12	BF111659	BF111659 7132g09.x
c 816	27	14.4	304	17	AQ094252	AQ094252 HS_3022.B	c 889	27	14.4	444	17	AQ825212	AQ825212 HS_5305.A
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c 818	27	14.4	314	17	AQ491051	AQ491051 RPECI-11-2	891	27	14.4	445	14	N73819	N73819 za56a05.s1
c 819	27	14.4	318	17	AQ386081	AQ386081 RPECI11-13	892	27	14.4	446	14	H38847	H38847 yp48e06.s1
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c 821	27	14.4	320	17	AA720722	AA720722 nv93c01.x	894	27	14.4	448	9	AI807636	AI807636 wf49c09.x
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c 824	27	14.4	332	10	AV743385	AV743385 AV743385	897	27	14.4	449	17	AQ516670	AQ516670 HS_5123.A
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c 826	27	14.4	339	9	AA352045	AA352045 EST59978	c 899	27	14.4	454	10	AW809470	AW809470 M41-ST012
c 827	27	14.4	342	10	AW802066	AW802066 IL5-UW007	900	27	14.4	455	9	AA017083	AA017083 ze33e11.s
c 828	27	14.4	344	9	AI536790	AI536790 to80e07.x	c 901	27	14.4	456	17	AQ089605	AQ089605 HS_3008.A
c 829	27	14.4	345	9	AA904926	AA904926 oj79c05.s	c 902	27	14.4	457	12	BF528591	BF528591 602043591
c 830	27	14.4	347	17	AQ323257	AQ323257 RPECI11-99	903	27	14.4	459	9	AI939607	AI939607 tg30a03.x
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c 833	27	14.4	350	17	AQ078062	AQ078062 CIT-HSP-2	906	27	14.4	461	17	AQ523401	AQ523401 HS_5194.A
c 834	27	14.4	351	17	AQ238123	AQ238123 RPECI11-65	c 907	27	14.4	461	17	AQ527289	AQ527289 CITBI-E1-
c 835	27	14.4	353	17	AQ013833	AQ013833 RPECI11-23	c 908	27	14.4	462	14	C15968	C15968 C15968 Clon
c 836	27	14.4	357	9	AA605258	AA605258 no83b05.s	909	27	14.4	465	9	AA480674	AA480674 ne24e02.s
c 837	27	14.4	357	10	BE139358	BE139358 xt69d09.x	910	27	14.4	467	9	AI571245	AI571245 tn43h05.x
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c 848	27	14.4	372	10	AW674188	AW674188 ba34c05.x	921	27	14.4	487	17	AQ475722	AQ475722 CITBI-E1-
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c 851	27	14.4	374	13	EG993565	EG993565 PM0-HT091	c 924	27	14.4	490	9	AL586304	AL586304 DKZp313D
c 852	27	14.4	377	9	AA837023	AA837023 og90c05.s	c 925	27	14.4	492	17	AQ567286	AQ567286 HS_2110.B
c 853	27	14.4	379	9	AI760985	AI760985 wh97a10.x	c 926	27	14.4	496	10	BE062258	BE062258 RCI-BT025
c 854	27	14.4	380	17	AQ393311	AQ393311 CITBI-E1-	927	27	14.4	501	17	AI498212	AI498212 tm85a10.x
c 855	27	14.4	383	10	BE139267	BE139267 xt68a06.x	c 928	27	14.4	501	17	AQ627334	AQ627334 CITBI-E1-
c 856	27	14.4	385	9	AI023115	AI023115 ow53d01.s	c 929	27	14.4	503	9	AA577748	AA577748 nm23e05.s
c 857	27	14.4	396	9	AA309414	AA309414 EST180315	c 930	27	14.4	503	17	AQ313545	AQ313545 RPECI11-10
c 858	27	14.4	398	10	BE000773	BE000773 RC2-BN007	c 931	27	14.4	509	17	AZ912610	AZ912610 RPECI-24-1
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c 860	27	14.4	398	17	AQ493275	AQ493275 HS_5214.B	933	27	14.4	513	17	AQ347924	AQ347924 RPECI11-10
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c 862	27	14.4	402	14	R06860	R06860 yf11d11.s1	c 935	27	14.4	514	17	AQ209217	AQ209217 HS_3236.B
c 863	27	14.4	403	14	R26768	R26768 ym44d06.s1	936	27	14.4	514	17	AQ347370	AQ347370 RPECI11-10
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c 865	27	14.4	406	9	AI253501	AI253501 qo43c02.x	c 938	27	14.4	520	17	AZ446630	AZ446630 1M0243F08
c 866	27	14.4	406	13	BI262393	BI262393 602953827	939	27	14.4	522	17	AI732542	AI732542 ni36g03.x
c 867	27	14.4	407	14	W96202	W96202 ze42h02.s1	c 940	27	14.4	524	17	AQ784935	AQ784935 HS_3251.A
c 868	27	14.4	409	9	AA554511	AA554511 ni36g03.s	c 941	27	14.4	525	17	AQ580791	AQ580791 RPECI-11-4
c 869	27	14.4	413	17	AQ884144	AQ884144 HS_5499.B	942	27	14.4	526	9	AI732401	AI732401 z178b12.x
c 870	27	14.4	417	9	AA707767	AA707767 zh24d06.s	943	27	14.4	527	17	AQ585764	AQ585764 RPECI-11-4
c 871	27	14.4	418	9	AA829147	AA829147 od78e06.s	944	27	14.4	530	17	AQ759573	AQ759573 HS_3124.A
c 872	27	14.4	420	9	AA682912	AA682912 ae88g09.s	c 945	27	14.4	534	17	AQ712742	AQ712742 HS_5383.A
c 873	27	14.4	420	17	AQ093875	AQ093875 HS_3025.A	c 946	27	14.4	535	10	AW747974	AW747974 QV0-BT004
c 874	27	14.4	421	17	AQ202300	AQ202300 RPECI11-61	947	27	14.4	535	10	AW748969	AW748969 RCI-BT031
c 875	27	14.4	423	9	AA053088	AA053088 z173d04.s	948	27	14.4	542	9	AU154910	AU154910 AU154910
c 876	27	14.4	423	10	AV750133	AV750133 AV750133	c 949	27	14.4	543	14	BQ268193	BQ268193 1J96d10.Y
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c 878	27	14.4	429	10	AA474181	AA474181 xy12c03.x	c 951	27	14.4	553	12	BF699333	BF699333 DKZp686E
c 879	27	14.4	430	9	AA720706	AA720706 nv93a01.x	952	27	14.4	554	12	BF732246	BF732246 nae08c10.
c 880	27	14.4	430	12	BF821854	BF821854 MR0-RT003	c 953	27	14.4	554	17	AQ373406	AQ373406 RPECI11-15
c 881	27	14.4	431	17	AQ684045	AQ684045 HS_2162.B	c 954	27	14.4	554	17	AQ483611	AQ483611 RPECI-11-2
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 c 996 27 14.4 675 17 AG046145
 c 997 27 14.4 675 12 BG218374
 c 998 27 14.4 676 12 BG218374
 c 999 27 14.4 676 17 AG148657
 c1000 27 14.4 676 17 AG148657

ALIGNMENTS

RESULT 1
 AQ785529
 LOCUS
 DEFINITION HS_3063_A2_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=12 Row=O, DNA sequence.
 ACCESSION AQ785529
 VERSION AQ785529.1 GI:5693153
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 459)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 JOURNAL 99380589
 MEDLINE Contact: Mahairas GG, Wallace JC, Hood L
 COMMENT High Throughput Sequencing Center
 University of Washington

BASE COUNT 118 a 114 c 89 g 138 t
 ORIGIN
 Query Match 22.5%; Score 42; DB 17; Length 459;
 Best Local Similarity 100.0%; Pred. No. 6.8e-09;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ATCATAGCTACCTGACGCTCATCTCTGGGCTCAAGCAAT 45
 Db 229 ATCATAGCTACCTGACGCTCATCTCTGGGCTCAAGCAAT 270
 RESULT 2
 AA864787
 LOCUS
 DEFINITION AA864787.1 166 bp mRNA linear EST 13-MAY-1998
 similar to contains Alu repetitive element; contains element LTR7
 repetitive element ;, mRNA sequence.
 ACCESSION AA864787
 VERSION AA864787.1 GI:2959100
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 166)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 644 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 129.
 Location/Qualifiers
 1. 166
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1456643"
 /clone_lib="NCI_CGAP_Kid3"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site:1: Not 1; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors

401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3063 row: O column: 12
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 459.
 Location/Qualifiers
 1. 459
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=3063 Col=12 Row=O"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
 BASE COUNT 118 a 114 c 89 g 138 t
 ORIGIN
 Query Match 22.5%; Score 42; DB 17; Length 459;
 Best Local Similarity 100.0%; Pred. No. 6.8e-09;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ATCATAGCTACCTGACGCTCATCTCTGGGCTCAAGCAAT 45
 Db 229 ATCATAGCTACCTGACGCTCATCTCTGGGCTCAAGCAAT 270
 RESULT 2
 AA864787
 LOCUS
 DEFINITION AA864787.1 166 bp mRNA linear EST 13-MAY-1998
 similar to contains Alu repetitive element; contains element LTR7
 repetitive element ;, mRNA sequence.
 ACCESSION AA864787
 VERSION AA864787.1 GI:2959100
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 166)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 644 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 129.
 Location/Qualifiers
 1. 166
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1456643"
 /clone_lib="NCI_CGAP_Kid3"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site:1: Not 1; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 47 a 38 c 38 g 43 t

ORIGIN
Query Match 21.4%; Score 40; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCCAA 66
|||||
Db 39 ACTCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCCAA 78
|||||

RESULT 3
B49276/c
DEFINITION
RPC111-5L13.TP RPC1-11 Homo sapiens genomic clone RPC1-11-5L13, DNA sequence.

ACCESSION B49276.1 GI:2601513
VERSION B49276
KEYWORDS GSS.
SOURCE human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 252)
AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter
J.C.

TITLE
Use of BAC End Sequences for Sequence-Ready Map Building
JOURNAL
Unpublished (1997)
COMMENT
Other_GSSs: RPC111-5L13.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: mdadams@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..252
/organism="Homo sapiens"
/db_xref="GDB:7501812"
/db_xref="taxon:9606"
/clone="RPC1-11-5L13"
/clone_lib="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; RPC111 Human Male BAC Library"
71 a 53 c 68 g 60 t

Query Match 21.4%; Score 40; DB 17; Length 252;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCCAA 66
|||||
Db 94 ACTCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCCAA 55
|||||

RESULT 4
A1139009
LOCUS
DEFINITION

A1139009 388 bp mRNA linear EST 28-OCT-1998
q883g09.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1736128
2' similar to contains Alu repetitive element; contains element LTR7
LTR7 repetitive element ; mRNA sequence.

ACCESSION A1139009
VERSION A1139009.1 GI:3644981
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 388)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 665 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 363.

FEATURES
source
Location/Qualifiers
1..388
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1736128"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
Inc., and primed with a Not I - oligo(dT) primer [5'.
TGTTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 109 a 73 c 110 g 96 t

ORIGIN

Query Match 21.4%; Score 40; DB 9; Length 388;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCCAA 66
|||||
Db 42 ACTCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCCAA 81
|||||

RESULT 5
A1140075
LOCUS
DEFINITION

A1140075 433 bp mRNA linear EST 13-APR-1999
qa87cl2.x1 Soares fetal heart NDHH19W Homo sapiens cDNA clone
IMAGE:1693750 3' similar to contains Alu repetitive element
; contains element LTR7 repetitive element ; mRNA sequence.

ACCESSION A1140075
VERSION A1140075.1 GI:3647532
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 433)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1086 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 427.
Location/Qualifiers
FEATURES
source
1..433
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatina Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHH19W."
BASE COUNT 121 a 81 c 122 g 109 t
ORIGIN
Query Match 21.4%; Score 40; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 66
|||||
Db 39 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 78
|||||
RESULT 6
LOCUS
DEFINITION
0z37d07.x1 Soares NhMPu.S1 Homo sapiens cDNA clone IMAGE:1677517
3' similar to contains Alu repetitive element/contains element LTR7
repetitive element ;, mRNA sequence.
ACCESSION
AI077461
VERSION
AI077461.1 GI:3411869
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 458)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 984 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
FEATURES
source
1..458
/organism="Homo sapiens"

```

```

/db_xref="taxon:9606"
/clone_lib="Soares_NhMPu_S1"
/tissue_type="pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/notes="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 128 a 86 c 130 g 114 t
ORIGIN
Query Match 21.4%; Score 40; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 66
|||||
Db 39 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 78
|||||
RESULT 7
LOCUS
DEFINITION
BQ182580 629 bp mRNA linear EST 30-APR-2002
UI-H-EU0-arj-n-01-0-UI.s1 NCI-CGAP_Carl Homo sapiens cDNA clone
IMAGE: 5849664 3', mRNA sequence.
ACCESSION
BQ182580
VERSION
BQ182580.1 GI:20358130
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 629)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 18-215, >LIM4_5 (matched complement) 224-394, >ALU
(matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
FEATURES
source
1..629
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI-CGAP_Carl"
/tissue_type="Osteoarthritic Cartilage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI-CGAP_Carl is a cDNA library containing the following
tissue(s): Osteoarthritic Cartilage The library was
constructed according to Bonaldo, Lennon and Soares,

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Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCAGCT.

TAG LIB=UI-H-EUO
TAG TISSUE=osteochondritic cartilage
TAG_SEQ=TGATCAGCT"

BASE COUNT 128 a 114 c 118 g 269 t

ORIGIN

Query Match 21.4%; Score 40; DB 14; Length 629;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66
|||||
Db 302 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 341
|||||

RESULT 8
AG172545 682 bp DNA linear GSS 09-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-042D19.T7, genomic survey
DEFINITION sequence.

ACCESSION AG172545
VERSION AG172545.1 GI:16702225
KEYWORDS GSS; (genome survey sequence).
SOURCE Pan troglodytes male lymphocytes DNA, clone lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-042D19.T7.

ORGANISM Pan troglodytes

REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS
Sequencing: T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI

Location/Qualifiers

1. 682
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-042D19.T7"
/sex="male"
/cell_type="lymphocytes"
/clone lib="RPCI-43 Chimpanzee Male BAC Library"

BASE COUNT 200 a 143 c 141 g 197 t

ORIGIN

Query Match 21.4%; Score 40; DB 17; Length 682;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66
|||||
Db 587 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 626
|||||

RESULT 9
AQ599298 411 bp DNA linear GSS 08-JUN-1999
LOCUS HS 5343_B2_B02_T7A RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=919 Col=4 Row=D, DNA sequence.

ACCESSION AQ599298
VERSION AQ599298.1 GI:5030391
KEYWORDS GSS.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 411)
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 919 row: D column: 4
Seq primer: T7
Class: BAC ends
High quality sequence stop: 411.

FEATURES Location/Qualifiers

1..411
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="plate=919 Col=4 Row=D"

/clone lib="RPCI-11 Human Male BAC Library"

/sex="male"

/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

BASE COUNT 103 a 87 c 94 g 122 t

ORIGIN

Query Match 20.9%; Score 39; DB 17; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66
|||||

Db 265 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 303
|||||

RESULT 10

AQ685901

LOCUS

DEFINITION

genomic clone Plate=1126 Col=19 Row=1, DNA sequence.

Query Match 21.4%; Score 40; DB 17; Length 682;

Best Local Similarity 100.0%; Pred. No. 5.1e-08;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66

Db 265 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 303

RESULT 10

AQ685901

LOCUS

DEFINITION

genomic clone Plate=1126 Col=19 Row=1, DNA sequence.

Query Match 21.4%; Score 40; DB 17; Length 682;

Best Local Similarity 100.0%; Pred. No. 5.1e-08;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66

Db 265 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 303

RESULT 10

AQ685901

LOCUS

DEFINITION

genomic clone Plate=1126 Col=19 Row=1, DNA sequence.

Query Match 21.4%; Score 40; DB 17; Length 682;

Best Local Similarity 100.0%; Pred. No. 5.1e-08;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66

Db 265 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 303

RESULT 10

AQ685901

LOCUS

DEFINITION

genomic clone Plate=1126 Col=19 Row=1, DNA sequence.

ACCESSION AQ685901
 VERSION AQ685901.1 GI:5261972
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 446)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallaceu.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 Plate: 1126 row: 1 column: 19
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 446.
 Location/Qualifiers
 1..446
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACE3.6 vector at EcoRI sites"
 BASE COUNT 126 a 82 c 97 g 139 t 2 others
 ORIGIN
 Query Match 20.9%; Score 39; DB 17; Length 446;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GATCATAGCTCACTGCAGCCTCATCTCTGGGCTCAAG 41
 DB 379 GATCATAGCTCACTGCAGCCTCATCTCTGGGCTCAAG 417
 RESULT 11
 AQ426550/c
 LOCUS
 DEFINITION CITBI-EI-2574H6.TR CITBI-EI Homo sapiens genomic clone 2574H6, DNA
 sequence.
 ACCESSION AQ426550
 VERSION AQ426550.1 GI:4499318
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 463)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
 Map Building

JOURNAL Unpublished (1997)
 COMMENT Other GSSs: CITBI-EI-2574H6.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.
 Location/Qualifiers
 1..463
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="2574H6"
 /clone_lib="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 115 a 126 c 103 g 119 t
 ORIGIN
 Query Match 20.3%; Score 38; DB 17; Length 463;
 Best Local Similarity 100.0%; Pred. No. 4.5e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCC 64
 DB 155 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCC 118
 RESULT 12
 AI611434/c
 LOCUS
 DEFINITION AI611434 239 bp mRNA linear EST 14-DEC-1999
 similar to contains Alu repetitive element;; mRNA sequence.
 ACCESSION AI611434
 VERSION AI611434.1 GI:4620601
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 239)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert length: 293 Std Error: 0.00
 Seq primer: -40UP from Gibco
 POLYA-No.
 Location/Qualifiers
 1..239
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:2245244"
 /tissue_type="CD34+, CD38- from normal bone marrow donor"

132 CTCCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCC 96

RESULT 14
 A1280214
 LOCUS
 DEFINITION
 qm65g11.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION
 A1280214
 VERSION
 A1280214.1 GI:3918447
 KEYWORDS
 EST.
 SOURCE
 human.

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 415)

REFERENCE
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.lml.gov) for further information.
 Insert Length: 658 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 367.
 Location/Qualifiers
 1. .415
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1893668"
 /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9w"
 /dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTCAAGTCGGAGCGCGCGATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 93 a 122 c 87 g 113 t
 ORIGIN

Query Match 19.8%; Score 37; DB 9; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCC 64
 |||||
 76 CTCCTGGGCTCAAGCAATCTCTCGCTCAGCCTTCC 112
 |||||

RESULT 15
 A1874136
 LOCUS
 DEFINITION
 wm49f02.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2439291 3' similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION
 A1874136
 VERSION
 A1874136.1 GI:5548185
 KEYWORDS
 EST.
 SOURCE
 human.

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 434)

REFERENCE
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

JOURNAL COMMENT

Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 377;
 Location/Qualifiers
 1..434
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2439291"
 /clone_lib="NCI-CCAP_Ut4"
 /tissue_types="serous papillary carcinoma, high grade, 2 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
 BASE COUNT 108 a 108 c 95 g 122 t 1 others
 ORIGIN
 Query Match 19.8%; Score 37; DB 9; Length 434;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTC 63
 ||||||||||||||||||||||||||||||||||
 Db 81 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTC 117

Search completed: June 17, 2003, 06:25:42
 Job time : 256.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using gap model

Run on: June 16, 2003, 11:19:02 ; Search time 895.527 Seconds
(without alignments)
15794.017 Million cell updates/sec

Title: US-09-513-888c-1_COPY_7148_7633

Perfect score: 486

Sequence: 1 agattgcagatgtgagccac.....cattgtcttagtcccaagc 486

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_man:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	486	100.0	5492	9	AF123659	Homo sapi
2	486	100.0	9108	9	AF123653	Homo sapi
3	366	75.3	173264	2	AC025853	Homo sapi
C 4	38	7.8	97430	9	AL391334	Human DNA
C 5	31	6.4	137845	2	AC010367	Homo sapi
C 6	31	6.4	152786	9	AL135778	Human DNA
C 7	31	6.4	179959	9	AL160395	Human DNA
C 8	31	6.4	186415	9	AC008675	Homo sapi
9	31	6.4	186418	9	AC018757	Homo sapi
10	31	6.4	197456	2	AC005054	Homo sapi
11	30	6.2	161013	9	AC018709	Homo sapi
C 12	30	6.2	240000	2	AC012525	Homo sapi
C 13	29	6.0	150336	9	HSJ395C13	Human DNA
C 14	29	6.0	153234	2	AC026947	Homo sapi
C 15	29	6.0	182208	9	AC113193	Homo sapi
C 16	29	6.0	185102	9	AC113139	Homo sapi
C 17	29	6.0	186072	2	AC018960	Homo sapi
C 18	29	6.0	193281	2	AC079376	Homo sapi
C 19	29	6.0	200823	9	AC009652	Homo sapi
C 20	28	5.8	93974	9	AC084421	Homo sapi
21	28	5.8	97146	9	AL135929	Human DNA
C 22	28	5.8	124102	9	AC021148	Homo sapi
C 23	28	5.8	140966	9	AC023058	Homo sapi
C 24	28	5.8	157750	9	AL512599	Human DNA
C 25	28	5.8	158977	9	AP002469	Homo sapi
C 26	28	5.8	159887	2	AC067823	Homo sapi
C 27	28	5.8	175609	2	AC024663	Homo sapi
C 28	28	5.8	181598	9	AC026172	Homo sapi
C 29	28	5.8	181598	9	AC026194	Homo sapi
C 30	28	5.8	189994	9	AP002762	Homo sapi
C 31	28	5.8	191569	9	AC018506	Homo sapi
C 32	28	5.8	196852	9	AC084866	Homo sapi
C 33	28	5.8	213965	2	AL353721	Homo sapi
C 34	27	5.6	2702	9	HSICAMIAS	X84737 H. sapiens I
C 35	27	5.6	43761	9	HS597B2	AL031346 Human DNA
C 36	27	5.6	65244	2	AC124302	Homo sapi
C 37	27	5.6	127431	9	AC027796	Homo sapi
C 38	27	5.6	129305	2	AL355983	Homo sapi
C 39	27	5.6	143423	9	AL161932	Human DNA
C 40	27	5.6	143517	9	AC083783	Homo sapi
C 41	27	5.6	146127	9	AL391838	Human DNA
C 42	27	5.6	147767	2	AC105030	Homo sapi
C 43	27	5.6	148278	9	AC006101	citb 338
C 44	27	5.6	149320	2	AC126357	Homo sapi
C 45	27	5.6	154214	9	AC079753	Homo sapi
C 46	27	5.6	154604	2	AC104974	Homo sapi
C 47	27	5.6	156503	9	AC011511	Homo sapi
C 48	27	5.6	159122	2	AC025556	Homo sapi
C 49	27	5.6	159397	2	AC027040	Homo sapi
C 50	27	5.6	160846	9	AC124306	Homo sapi
C 51	27	5.6	162886	2	AC025542	Homo sapi
C 52	27	5.6	165201	9	AC107081	Homo sapi
C 53	27	5.6	168613	9	AC091133	Homo sapi
C 54	27	5.6	169897	9	AL353674	Human DNA
C 55	27	5.6	170543	9	AC021012	Homo sapi
C 56	27	5.6	170544	9	CNS05TCC	AL355093 Human chr
C 57	27	5.6	173987	9	AL450337	Human DNA
C 58	27	5.6	174311	2	AL365319	Homo sapi
C 59	27	5.6	178384	2	AL591026	Homo sapi
C 60	27	5.6	178825	2	AC074251	Homo sapi
C 61	27	5.6	179394	9	AC010619	Homo sapi
C 62	27	5.6	185854	2	AC027736	Homo sapi
C 63	27	5.6	197372	9	AC103592	Homo sapi
C 64	27	5.6	200418	9	AC074138	Homo sapi
C 65	27	5.6	200688	2	AC073266	Homo sapi

c 66	27	5.6	217657	9	HSMTW0	AL034384 Human chr	c 139	26	5.3	204485	2	AC114962	AC114962 Homo sapi
c 67	27	5.6	239697	2	AC084854	AC084854 Homo sapi	140	26	5.3	206710	2	AL844520	AL844520 Homo sapi
c 68	26	5.3	1523	9	AX054712	AX054712 Homo sapi	c 141	26	5.3	206909	9	AC016397	AC016397 Homo sapi
c 69	26	5.3	15862	9	AC114816	AC114816 Homo sapi	c 142	26	5.3	207256	9	AC010321	AC010321 Homo sapi
c 70	26	5.3	33931	9	AC022156	AC022156 Homo sapi	c 143	26	5.3	208813	2	AC092425	AC092425 Homo sapi
c 71	26	5.3	63684	9	AL357564	AL357564 Human DNA	c 144	26	5.3	210320	2	AC093873	AC093873 Homo sapi
c 72	26	5.3	67462	2	AC091595	AC091595 Homo sapi	c 145	26	5.3	211001	9	AC018695	AC018695 Homo sapi
c 73	26	5.3	67895	9	AL138807	AL138807 Human DNA	146	26	5.3	215441	9	AC005736	AC005736 Homo sapi
c 74	26	5.3	75761	9	AL359733	AL359733 Human DNA	147	26	5.3	240379	9	AC005077	AC005077 Homo sapi
c 75	26	5.3	76295	2	AC023542	AC023542 Homo sapi	148	26	5.3	242970	2	AC004803	AC004803 Homo sapi
c 76	26	5.3	87665	9	AL158840	AL158840 Human DNA	c 149	26	5.3	242970	2	AC004803	AC004803 Homo sapi
c 77	26	5.3	93418	9	AC008379	AC008379 Homo sapi	c 150	26	5.3	247924	2	AC080037	AC080037 Homo sapi
c 78	26	5.3	93714	2	AL161661	AL161661 Homo sapi	c 151	26	5.3	278524	2	AC074326	AC074326 Homo sapi
c 79	26	5.3	104660	9	AP000347	AP000347 Homo sapi	c 152	26	5.3	314989	2	AC009871	AC009871 Homo sapi
c 80	26	5.3	105362	9	AC012370	AC012370 Homo sapi	c 153	25	5.1	819	6	AX200941	AX200941 Sequence
c 81	26	5.3	106008	9	HS506	AL020993 Human DNA	c 154	25	5.1	819	6	AX267597	AX267597 Sequence
c 82	26	5.3	114084	2	AL445427	AL445427 Homo sapi	c 155	25	5.1	2455	6	AX201108	AX201108 Sequence
c 83	26	5.3	116131	9	AL139324	AL139324 Human DNA	c 156	25	5.1	2455	6	AX201109	AX201109 Sequence
c 84	26	5.3	120869	9	HSJ788L20	AL121722 Human DNA	c 157	25	5.1	2455	6	AX267907	AX267907 Sequence
c 85	26	5.3	121909	9	HSJ492P14	AL121977 Human DNA	c 158	25	5.1	2455	6	AX267908	AX267908 Sequence
c 86	26	5.3	124278	2	AC104618	AC104618 Homo sapi	c 159	25	5.1	5908	9	HSZ02TUP03	HSZ02TUP03
c 87	26	5.3	128398	9	AC004817	AC004817 Homo sapi	c 160	25	5.1	30826	9	AL807743	AL807743 Human DNA
c 88	26	5.3	132867	9	AC004601	AC004601 Homo sapi	c 161	25	5.1	36648	2	AF209069	AF209069 Homo sapi
c 89	26	5.3	136312	9	HSJ657D16	AL050343 Human DNA	c 162	25	5.1	36651	6	AX357904	AX357904 Sequence
c 90	26	5.3	137718	9	AL137066	AL137066 Human DNA	c 163	25	5.1	38703	9	AC119400	AC119400 Homo sapi
c 91	26	5.3	138969	9	AC104600	AC104600 Homo sapi	c 164	25	5.1	39601	9	AC005581	AC005581 Homo sapi
c 92	26	5.3	147815	9	HS998H6	AL031687 Human DNA	c 165	25	5.1	39935	9	AC093231	AC093231 Homo sapi
c 93	26	5.3	149271	2	AC112489	AC112489 Homo sapi	c 166	25	5.1	43780	2	AC068017	AC068017 Homo sapi
c 94	26	5.3	149856	2	AC021411	AC021411 Homo sapi	c 167	25	5.1	43780	2	AC068017	AC068017 Homo sapi
c 95	26	5.3	154218	9	AC020663	AC020663 Homo sapi	c 168	25	5.1	54099	2	AC079963	AC079963 Homo sapi
c 96	26	5.3	155405	9	AC009812	AC009812 Homo sapi	c 169	25	5.1	60761	2	AC068568	AC068568 Homo sapi
c 97	26	5.3	158587	9	AC074325	AC074325 Homo sapi	c 170	25	5.1	61513	9	AL353610	AL353610 Human DNA
c 98	26	5.3	159593	2	AC026302	AC026302 Homo sapi	c 171	25	5.1	63930	2	AC106017	AC106017 Homo sapi
c 99	26	5.3	159766	9	AC104942	AC104942 Homo sapi	c 172	25	5.1	64455	2	AC084134	AC084134 Homo sapi
c 100	26	5.3	160463	2	AC110607	AC110607 Homo sapi	c 173	25	5.1	66256	2	AC087454	AC087454 Homo sapi
c 101	26	5.3	161421	2	AC068114	AC068114 Homo sapi	c 174	25	5.1	66792	9	AC008754	AC008754 Homo sapi
c 102	26	5.3	161593	9	HSBA49G10	AL121901 Human DNA	c 175	25	5.1	68035	2	AC103699	AC103699 Homo sapi
c 103	26	5.3	161973	9	HUAC002038	AC002038 Homo sapi	c 176	25	5.1	68109	9	AP000315	AP000315 Homo sapi
c 104	26	5.3	162423	9	AL513304	AL513304 Human DNA	c 177	25	5.1	70203	2	AC024012	AC024012 Homo sapi
c 105	26	5.3	165139	9	AC010182	AC010182 Homo sapi	c 178	25	5.1	72273	2	AC090859	AC090859 Homo sapi
c 106	26	5.3	165196	9	AC007151	AC007151 Homo sapi	c 179	25	5.1	73396	9	AC008848	AC008848 Homo sapi
c 107	26	5.3	167185	9	AC093132	AC093132 Papio cyn	c 180	25	5.1	75120	9	AC004666	AC004666 Homo sapi
c 108	26	5.3	167557	2	AC079866	AC079866 Homo sapi	c 181	25	5.1	75386	2	AC027760	AC027760 Homo sapi
c 109	26	5.3	168085	9	AC027687	AC027687 Homo sapi	c 182	25	5.1	75657	9	HSB11L7C8	HSB11L7C8
c 110	26	5.3	169032	9	AC016931	AC016931 Homo sapi	c 183	25	5.1	77651	9	AC120118	AC120118 Homo sapi
c 111	26	5.3	169739	9	AC005082	AC005082 Homo sapi	c 184	25	5.1	79516	9	AC004834	AC004834 Homo sapi
c 112	26	5.3	169819	9	AC078991	AC078991 Homo sapi	c 185	25	5.1	81764	9	AL139080	AL139080 Human DNA
c 113	26	5.3	169844	2	AC025738	AL359372 Homo sapi	c 186	25	5.1	81831	9	AL365506	AL365506 Human DNA
c 114	26	5.3	170608	2	AL359372	AL359372 Homo sapi	c 187	25	5.1	85444	9	AP003900	AP003900 Homo sapi
c 115	26	5.3	170877	2	AC025610	AC025610 Homo sapi	c 188	25	5.1	86945	2	AC002490	AC002490 Homo sapi
c 116	26	5.3	171225	2	AC024431	AC024431 Homo sapi	c 189	25	5.1	87120	2	AC012225	AC012225 Homo sapi
c 117	26	5.3	171518	2	AL589697	AL589697 Homo sapi	c 190	25	5.1	90434	2	AC007952	AC007952 Homo sapi
c 118	26	5.3	175588	9	AL139326	AL139326 Human DNA	c 191	25	5.1	92118	9	AC074384	AC074384 Homo sapi
c 119	26	5.3	175620	2	AC127391	AC127391 Homo sapi	c 192	25	5.1	96120	9	AC093669	AC093669 Homo sapi
c 120	26	5.3	175789	2	AP000425	AP000425 Homo sapi	c 193	25	5.1	96874	9	AL138709	AL138709 Human DNA
c 121	26	5.3	177242	2	AC021923	AC021923 Homo sapi	c 194	25	5.1	97473	9	AC127165	AC127165 Homo sapi
c 122	26	5.3	179087	2	AC069489	AC069489 Homo sapi	c 195	25	5.1	97734	9	AC095066	AC095066 Homo sapi
c 123	26	5.3	179262	9	AL355343	AL355343 Human DNA	c 196	25	5.1	98274	9	HS714B7	HS714B7
c 124	26	5.3	183695	9	AC012450	AC012450 Homo sapi	c 197	25	5.1	98908	9	AL139279	AL139279 Human DNA
c 125	26	5.3	183797	9	AC022400	AC022400 Homo sapi	c 198	25	5.1	100000	9	AP000080	AP000080 Homo sapi
c 126	26	5.3	184778	2	AC023567	AC023567 Homo sapi	c 199	25	5.1	100000	9	AP000165	AP000165 Homo sapi
c 127	26	5.3	187349	9	AP003352	AP003352 Homo sapi	c 200	25	5.1	100000	17	AP000118	AP000118 Homo sapi
c 128	26	5.3	187394	2	AC104573	AC104573 Homo sapi	c 201	25	5.1	100521	2	AC119397	AC119397 Homo sapi
c 129	26	5.3	187530	2	AC096875	AC096875 Pan trogl	c 202	25	5.1	104061	2	AC16019	AC16019 Homo sapi
c 130	26	5.3	192440	9	CNS01DXH	AL139316 Human chr	c 203	25	5.1	106465	2	AC090156	AC090156 Homo sapi
c 131	26	5.3	194771	2	AC109912	AC109912 Homo sapi	c 204	25	5.1	110885	9	HS191E19	HS191E19 Human DNA
c 132	26	5.3	195293	2	AC112169	AC112169 Homo sapi	c 205	25	5.1	112846	9	AC004991	AC004991 Homo sapi
c 133	26	5.3	196756	2	AC121858	AC121858 Mus muscu	c 206	25	5.1	116506	9	AL160163	AL160163 Human DNA
c 134	26	5.3	197431	9	AL360157	AL360157 Human DNA	c 207	25	5.1	116664	9	HS1191N16	HS1191N16
c 135	26	5.3	197870	2	AC091075	AC091075 Homo sapi	c 208	25	5.1	120873	9	AL445986	AL445986 Human DNA
c 136	26	5.3	198218	2	AC037447	AC037447 Homo sapi	c 209	25	5.1	122888	9	AL022326	AL022326 Human DNA
c 137	26	5.3	198952	2	AP002016	AP002016 Homo sapi	c 210	25	5.1	123866	9	AC008603	AC008603 Homo sapi
c 138	26	5.3	199208	2	AC019236	AC019236 Homo sapi	c 211	25	5.1	125041	2	AC068693	AC068693 Homo sapi

212	25	5.1	125780	9	CNS01DWK	AL137229 Human chr	c	285	25	5.1	162763	9	AL359262	Human DNA
213	25	5.1	127148	2	AP002081	AP002081 Homo sapi	286	25	5.1	162810	9	AC083923	Homo sapi	
214	25	5.1	127413	9	AL137784	AL137784 Human DNA	287	25	5.1	163856	9	AC084797	Homo sapi	
c 215	25	5.1	127917	9	HS257A7	AL008729 Human DNA	c 288	25	5.1	163996	2	AL139116	Homo sapi	
216	25	5.1	129719	9	AL358113	AL358113 Human DNA	289	25	5.1	163997	2	AL773524	Homo sapi	
217	25	5.1	130077	9	AL353643	AL353643 Human DNA	c 290	25	5.1	164113	2	AC086128	Homo sapi	
218	25	5.1	130318	9	AC026979	AC026979 Homo sapi	c 291	25	5.1	164354	9	AP003785	Homo sapi	
219	25	5.1	130898	9	AL353770	AL353770 Human DNA	c 292	25	5.1	164598	2	AC093212	Homo sapi	
c 220	25	5.1	132937	2	AC115097	AC115097 Homo sapi	c 293	25	5.1	164801	9	AC133418	Homo sapi	
221	25	5.1	134210	9	AC005052	AC005052 Homo sapi	294	25	5.1	164857	9	AC110054	Homo sapi	
c 222	25	5.1	134896	9	AC006571	AC006571 Homo sapi	295	25	5.1	165007	9	AC019047	Homo sapi	
c 223	25	5.1	135300	9	AC008163	AC008163 Homo sapi	c 296	25	5.1	165007	9	AC019047	Homo sapi	
c 224	25	5.1	135331	9	AC008798	AC008798 Homo sapi	c 297	25	5.1	165183	2	AC010787	Homo sapi	
c 225	25	5.1	136931	9	HS1050C22	AL121888 Homo sapi	c 298	25	5.1	165570	2	AC015765	Homo sapi	
c 226	25	5.1	137347	9	AL354674	AL354674 Human DNA	c 299	25	5.1	166308	9	CNS01DX2	Human chr	
227	25	5.1	138021	9	AC090820	AC090820 Homo sapi	c 300	25	5.1	166549	2	AC025990	Homo sapi	
228	25	5.1	139388	9	AC007666	AC007666 Homo sapi	c 301	25	5.1	166595	9	AC109599	Homo sapi	
c 229	25	5.1	140827	9	AL451123	AL451123 Human DNA	c 302	25	5.1	166664	9	AL441992	Human DNA	
c 230	25	5.1	141790	9	AL590636	AL590636 Human DNA	c 303	25	5.1	167218	9	AC090461	Homo sapi	
c 231	25	5.1	142432	9	AC017074	AC017074 Homo sapi	c 304	25	5.1	167357	2	AC026264	Homo sapi	
c 232	25	5.1	142560	2	AC021906	AC021906 Homo sapi	c 305	25	5.1	167390	9	AC007263	Homo sapi	
c 233	25	5.1	142667	9	AC125387	AC125387 Homo sapi	c 306	25	5.1	167439	2	AC130273	Papio cyn	
234	25	5.1	142669	2	AC018912	AC018912 Homo sapi	c 307	25	5.1	167700	9	AC007036	Homo sapi	
c 235	25	5.1	142669	2	AC018912	AC018912 Homo sapi	c 307	25	5.1	167722	9	AC073548	Homo sapi	
c 236	25	5.1	142805	9	AL592525	AL592525 Human DNA	c 308	25	5.1	167888	2	AL731569	Homo sapi	
c 237	25	5.1	143067	2	AC099796	AC099796 Homo sapi	c 309	25	5.1	168068	9	AL445668	Human DNA	
c 238	25	5.1	143638	9	AL157698	AL157698 Human DNA	c 310	25	5.1	168283	2	AL844892	Homo sapi	
c 239	25	5.1	143785	2	AC092334	AC092334 Homo sapi	c 311	25	5.1	168367	9	AC104440	Homo sapi	
c 240	25	5.1	143804	2	AC012617	AC012617 Homo sapi	c 312	25	5.1	168995	2	AP002359	Homo sapi	
c 241	25	5.1	143839	9	AC004701	AC004701 Homo sapi	c 313	25	5.1	168995	9	AC126605	Homo sapi	
c 242	25	5.1	144079	2	AC024342	AC024342 Homo sapi	c 314	25	5.1	169125	9	AC136605	Homo sapi	
c 243	25	5.1	146463	2	AC068306	AC068306 Homo sapi	c 315	25	5.1	169552	9	AC015976	Homo sapi	
c 244	25	5.1	146578	9	AC012468	AC012468 Homo sapi	c 316	25	5.1	169565	2	AC113557	Homo sapi	
c 245	25	5.1	146578	9	AC012468	AC012468 Homo sapi	c 317	25	5.1	169616	9	AL355336	Human DNA	
c 246	25	5.1	146641	2	AC011140	AC011140 Homo sapi	c 318	25	5.1	170138	2	AC018794	Homo sapi	
c 247	25	5.1	146642	2	HSJ9617	AL7009617 Homo sapi	c 319	25	5.1	170216	9	AC008432	Homo sapi	
c 248	25	5.1	147122	9	AC090109	AC090109 Homo sapi	c 320	25	5.1	170274	2	AC016462	Homo sapi	
c 249	25	5.1	147519	2	AC079099	AC079099 Homo sapi	c 321	25	5.1	170490	2	AC022042	Homo sapi	
c 250	25	5.1	147587	2	AC055800	AC055800 Homo sapi	c 322	25	5.1	170507	9	AC087530	Homo sapi	
251	25	5.1	148835	2	AC011225	AC011225 Homo sapi	c 323	25	5.1	170533	9	AP003356	Homo sapi	
252	25	5.1	149089	9	AC090735	AC090735 Homo sapi	c 324	25	5.1	170586	2	HSBA536C5	Homo sapi	
c 253	25	5.1	149490	2	AL589985	AL589985 Homo sapi	c 325	25	5.1	170586	2	HSBA536C5	Homo sapi	
254	25	5.1	149901	2	AL356367	AL356367 Homo sapi	c 326	25	5.1	171056	2	AC026318	Homo sapi	
255	25	5.1	150526	2	AC092339	AC092339 Homo sapi	c 327	25	5.1	171200	9	AP000864	Homo sapi	
256	25	5.1	150817	2	AC021762	AC021762 Homo sapi	c 328	25	5.1	171386	2	AC130786	Papio cyn	
257	25	5.1	150918	2	AC027364	AC027364 Homo sapi	c 329	25	5.1	171386	2	AC130786	Papio cyn	
258	25	5.1	152185	2	AC012219	AC012219 Homo sapi	c 330	25	5.1	171483	9	AL162580	Human DNA	
c 259	25	5.1	152748	9	AC106730	AC106730 Homo sapi	c 331	25	5.1	171501	9	AL359704	Human DNA	
260	25	5.1	152798	9	AC004057	AC004057 Homo sapi	c 332	25	5.1	171523	9	AC010206	Homo sapi	
261	25	5.1	153231	9	AL161452	AL161452 Human DNA	c 333	25	5.1	171621	2	AC011961	Homo sapi	
c 262	25	5.1	153382	2	AL359996	AL359996 Homo sapi	c 334	25	5.1	171731	2	AC091659	Papio cyn	
263	25	5.1	153586	2	AC016316	AC016316 Homo sapi	335	25	5.1	171742	30	AC069495	Homo sapi	
264	25	5.1	153617	9	AC012306	AC012306 Homo sapi	336	25	5.1	172051	2	AC023493	Homo sapi	
c 265	25	5.1	153619	2	AC130430	AC130430 Homo sapi	337	25	5.1	172393	2	AC025740	Homo sapi	
c 266	25	5.1	154639	2	AC090175	AC090175 Homo sapi	338	25	5.1	172579	9	AL596385	Human DNA	
267	25	5.1	155146	2	AC025216	AC025216 Homo sapi	339	25	5.1	172883	2	AL391374	Human DNA	
c 268	25	5.1	155705	9	AC093823	AC093823 Homo sapi	340	25	5.1	172915	2	AC010160	Homo sapi	
269	25	5.1	155952	9	AC004534	AC004534 Homo sapi	c 341	25	5.1	173153	9	AC008119	Homo sapi	
c 270	25	5.1	156616	2	AC126566	AC126566 Homo sapi	c 342	25	5.1	173354	9	HS149A16	Human DNA	
c 271	25	5.1	157762	9	AP001893	AP001893 Homo sapi	c 343	25	5.1	173791	9	AC021035	Homo sapi	
c 272	25	5.1	157918	2	AC024252	AC024252 Homo sapi	c 344	25	5.1	173886	2	AC097007	Homo sapi	
c 273	25	5.1	157918	9	AL512422	AL512422 Human DNA	c 345	25	5.1	174239	2	AC073830	Homo sapi	
c 274	25	5.1	158060	2	AC024423	AC024423 Homo sapi	346	25	5.1	174366	9	AL590491	Human DNA	
c 275	25	5.1	158116	2	AL357622	AL357622 Homo sapi	347	25	5.1	174700	2	AC025344	Homo sapi	
c 276	25	5.1	158574	2	AC024895	AC024895 Homo sapi	348	25	5.1	175274	9	AP004286	Homo sapi	
277	25	5.1	158838	9	CNS05TDN	AL356805 Human chr	c 349	25	5.1	176287	9	HSBA12M9	Human DNA	
278	25	5.1	159285	2	AL354816	AL354816 Human DNA	c 350	25	5.1	176470	9	AL353626	Human DNA	
279	25	5.1	159582	2	AC015734	AC015734 Homo sapi	c 351	25	5.1	176473	2	AC090986	Homo sapi	
280	25	5.1	160069	2	AC023329	AC023329 Homo sapi	c 352	25	5.1	176562	2	AC130272	Papio cyn	
281	25	5.1	161422	2	AC021544	AC021544 Homo sapi	c 353	25	5.1	176562	2	AC130272	Papio cyn	
282	25	5.1	161549	9	AC044913	AC044913 Homo sapi	354	25	5.1	177750	9	AC067743	Homo sapi	
283	25	5.1	161610	2	AC011728	AC011728 Homo sapi	c 355	25	5.1	177795	9	AC067743	Homo sapi	
284	25	5.1	161699	9	AC107300	AC107300 Homo sapi	c 356	25	5.1	177941	9	AF134471	Homo sapi	
285	25	5.1	162478	9	AC125634	AC125634 Homo sapi	c 357	25	5.1	177993	9	AC093133	Papio cyn	
286	25	5.1	162478	9	AC125634	AC125634 Homo sapi	c 358	25	5.1	178338	2	AC125603	Homo sapi	
287	25	5.1	162478	9	AC125634	AC125634 Homo sapi	c 359	25	5.1	178344	2	AC067846	Homo sapi	

c 358	25	5.1	178611	2	AC024631	Homo sapi	AC024631	Homo sapi	c 431	25	5.1	227632	9	AC087382	Homo sapi	AC087382	Homo sapi
c 359	25	5.1	178796	2	AC020667	Homo sapi	AC020667	Homo sapi	432	25	5.1	231566	2	AL158811	Homo sapi	AL158811	Homo sapi
c 360	25	5.1	179919	2	AC007456	Homo sapi	AC007456	Homo sapi	c 433	25	5.1	231566	2	AL158811	Homo sapi	AL158811	Homo sapi
c 361	25	5.1	180269	9	AC016025	Homo sapi	AC016025	Homo sapi	c 434	25	5.1	233461	2	AC092978	Homo sapi	AC092978	Homo sapi
c 362	25	5.1	180368	2	AC024276	Homo sapi	AC024276	Homo sapi	c 435	25	5.1	233738	9	AC007956	Homo sapi	AC007956	Homo sapi
c 363	25	5.1	180818	9	AP000821	Homo sapi	AP000821	Homo sapi	c 436	25	5.1	260409	9	AC004019	Homo sapi	AC004019	Homo sapi
c 364	25	5.1	181054	2	AC025019	Homo sapi	AC025019	Homo sapi	c 437	25	5.1	270105	2	AC099650	Homo sapi	AC099650	Homo sapi
c 365	25	5.1	181182	2	AC084832	Homo sapi	AC084832	Homo sapi	c 438	25	5.1	270105	2	AC099650	Homo sapi	AC099650	Homo sapi
c 366	25	5.1	181191	9	AC117379	Homo sapi	AC117379	Homo sapi	c 439	25	5.1	271144	9	HSXDPB	Homo sapi	HSXDPB	Homo sapi
c 367	25	5.1	181254	2	AP000825	Homo sapi	AP000825	Homo sapi	440	25	5.1	281116	9	HS21C001	Homo sapi	HS21C001	Homo sapi
c 368	25	5.1	181589	9	AP000868	Homo sapi	AP000868	Homo sapi	441	25	5.1	304623	2	AC021052	Homo sapi	AC021052	Homo sapi
c 369	25	5.1	182105	9	AC009136	Homo sapi	AC009136	Homo sapi	442	25	5.1	340000	9	AP001719	Homo sapi	AP001719	Homo sapi
c 370	25	5.1	182496	2	AC011190	Homo sapi	AC011190	Homo sapi	443	24	4.9	644	9	HS342650	Homo sapi	HS342650	Homo sapi
c 371	25	5.1	184313	9	AL445584	Human DNA	AL445584	Human DNA	444	24	4.9	644	9	HS342650	Homo sapi	HS342650	Homo sapi
c 372	25	5.1	184477	2	AC026277	Homo sapi	AC026277	Homo sapi	445	24	4.9	725	9	HS343358	Homo sapi	HS343358	Homo sapi
c 373	25	5.1	185143	2	AC025861	Homo sapi	AC025861	Homo sapi	446	24	4.9	726	9	HS343358	Homo sapi	HS343358	Homo sapi
c 374	25	5.1	186147	9	AC020739	Homo sapi	AC020739	Homo sapi	c 447	24	4.9	730	9	HSU50463	Homo sapi	HSU50463	Homo sapi
c 375	25	5.1	186183	9	AC026827	Homo sapi	AC026827	Homo sapi	448	24	4.9	1516	9	AK024577	Human inter	AK024577	Human inter
c 376	25	5.1	186635	2	AC051645	Homo sapi	AC051645	Homo sapi	c 449	24	4.9	4993	9	HSY11341	Homo sapi	HSY11341	Homo sapi
c 377	25	5.1	186635	2	AC051645	Homo sapi	AC051645	Homo sapi	c 450	24	4.9	25094	9	AC003045	Human BAC	AC003045	Human BAC
c 378	25	5.1	187691	2	AL359982	Homo sapi	AL359982	Homo sapi	c 451	24	4.9	26040	9	AF217491	Homo sapi	AF217491	Homo sapi
c 379	25	5.1	187857	2	AC044850	Homo sapi	AC044850	Homo sapi	452	24	4.9	31325	9	AP000274	Homo sapi	AP000274	Homo sapi
c 380	25	5.1	188410	2	AC124073	Homo sapi	AC124073	Homo sapi	c 453	24	4.9	33458	9	HSU398F6	Human DNA	HSU398F6	Human DNA
c 381	25	5.1	188639	9	AC011236	Homo sapi	AC011236	Homo sapi	454	24	4.9	35476	9	HS398F6	Human DNA	HS398F6	Human DNA
c 382	25	5.1	188743	2	AC069195	Homo sapi	AC069195	Homo sapi	c 455	24	4.9	38653	6	AX244215	Sequence	AX244215	Sequence
c 383	25	5.1	188755	9	AC013562	Homo sapi	AC013562	Homo sapi	c 456	24	4.9	38897	9	AC021092	Homo sapi	AC021092	Homo sapi
c 384	25	5.1	188928	9	AC020612	Homo sapi	AC020612	Homo sapi	c 457	24	4.9	39608	9	AC009004	Homo sapi	AC009004	Homo sapi
c 385	25	5.1	189022	2	AC016270	Homo sapi	AC016270	Homo sapi	c 458	24	4.9	40883	9	AC005776	Homo sapi	AC005776	Homo sapi
c 386	25	5.1	189396	2	AL161418	Homo sapi	AL161418	Homo sapi	c 459	24	4.9	41911	9	AL139408	Human DNA	AL139408	Human DNA
c 387	25	5.1	190277	9	AF254983	Homo sapi	AF254983	Homo sapi	c 460	24	4.9	42497	9	AC004798	Homo sapi	AC004798	Homo sapi
c 388	25	5.1	190363	9	AC000052	Homo sapi	AC000052	Homo sapi	c 461	24	4.9	43104	9	AC004257	Homo sapi	AC004257	Homo sapi
c 389	25	5.1	190482	9	AC004106	Homo sapi	AC004106	Homo sapi	c 462	24	4.9	47542	9	HS162H14	Human DNA	HS162H14	Human DNA
c 390	25	5.1	191152	9	AC005722	Homo sapi	AC005722	Homo sapi	c 463	24	4.9	48723	9	AL645992	Human DNA	AL645992	Human DNA
c 391	25	5.1	191871	2	AC084133	Homo sapi	AC084133	Homo sapi	464	24	4.9	50150	2	AP001285	Homo sapi	AP001285	Homo sapi
c 392	25	5.1	191942	9	AC079951	Homo sapi	AC079951	Homo sapi	c 465	24	4.9	65814	9	HSJ202D23	Human DNA	HSJ202D23	Human DNA
c 393	25	5.1	192068	2	AC036208	Homo sapi	AC036208	Homo sapi	c 466	24	4.9	66374	2	AC013501	Homo sapi	AC013501	Homo sapi
c 394	25	5.1	192618	9	AC092811	Homo sapi	AC092811	Homo sapi	c 467	24	4.9	69096	2	AC124072	Homo sapi	AC124072	Homo sapi
c 395	25	5.1	192651	2	AC092406	Papio cyn	AC092406	Papio cyn	c 468	24	4.9	70834	9	AP005401	Homo sapi	AP005401	Homo sapi
c 396	25	5.1	193234	2	AC024293	Homo sapi	AC024293	Homo sapi	c 469	24	4.9	76428	9	AC005401	Homo sapi	AC005401	Homo sapi
c 397	25	5.1	193605	2	AC130472	Homo sapi	AC130472	Homo sapi	c 470	24	4.9	77538	9	AC004500	Homo sapi	AC004500	Homo sapi
c 398	25	5.1	193772	9	AC007073	Homo sapi	AC007073	Homo sapi	c 471	24	4.9	78242	2	AP000483	Homo sapi	AP000483	Homo sapi
c 399	25	5.1	194079	9	AC020559	Homo sapi	AC020559	Homo sapi	c 472	24	4.9	78958	2	AC114937	Homo sapi	AC114937	Homo sapi
c 400	25	5.1	194615	2	AC024190	Homo sapi	AC024190	Homo sapi	c 473	24	4.9	79829	2	AC036211	Homo sapi	AC036211	Homo sapi
c 401	25	5.1	194683	2	AC105344	Homo sapi	AC105344	Homo sapi	c 474	24	4.9	80398	9	AL513485	Human DNA	AL513485	Human DNA
c 402	25	5.1	195529	2	AC025612	Homo sapi	AC025612	Homo sapi	c 475	24	4.9	80589	2	AC107040	Pan trogl	AC107040	Pan trogl
c 403	25	5.1	195668	9	AL353729	Human DNA	AL353729	Human DNA	c 476	24	4.9	80589	2	AC107040	Pan trogl	AC107040	Pan trogl
c 404	25	5.1	197550	9	CNS01RHP	Human chr	AL162171	Human chr	c 477	24	4.9	81188	2	AP001128	Homo sapi	AP001128	Homo sapi
c 405	25	5.1	199036	9	AC025449	Homo sapi	AC025449	Homo sapi	c 478	24	4.9	81410	9	AP004715	Homo sapi	AP004715	Homo sapi
c 406	25	5.1	200379	9	AC098614	Homo sapi	AC098614	Homo sapi	c 479	24	4.9	83557	9	AL138735	Human DNA	AL138735	Human DNA
c 407	25	5.1	200542	2	CNS01RG3	Homo sapi	AL157736	Homo sapi	c 480	24	4.9	84684	2	AC023321	Homo sapi	AC023321	Homo sapi
c 408	25	5.1	200673	9	AC021396	Homo sapi	AC021396	Homo sapi	c 481	24	4.9	84684	2	AC023321	Homo sapi	AC023321	Homo sapi
c 409	25	5.1	202544	9	AC104447	Homo sapi	AC104447	Homo sapi	c 482	24	4.9	84902	9	AC021216	Homo sapi	AC021216	Homo sapi
c 410	25	5.1	203279	9	AL354826	Human DNA	AL354826	Human DNA	c 483	24	4.9	89507	9	AL357132	Human DNA	AL357132	Human DNA
c 411	25	5.1	203912	9	AC008755	Homo sapi	AC008755	Homo sapi	c 484	24	4.9	91692	9	AC084253	Homo sapi	AC084253	Homo sapi
c 412	25	5.1	204720	2	AC008052	Homo sapi	AC008052	Homo sapi	c 485	24	4.9	92203	2	AP001920	Homo sapi	AP001920	Homo sapi
c 413	25	5.1	205473	2	AC092554	Papio cyn	AC092554	Papio cyn	c 486	24	4.9	92998	9	AC092019	Homo sapi	AC092019	Homo sapi
c 414	25	5.1	205312	2	AC092725	Homo sapi	AC092725	Homo sapi	c 487	24	4.9	95484	2	AC015854	Homo sapi	AC015854	Homo sapi
c 415	25	5.1	207362	2	AL355484	Homo sapi	AL355484	Homo sapi	c 488	24	4.9	96075	9	AL590639	Human DNA	AL590639	Human DNA
c 416	25	5.1	207850	2	AC096510	Homo sapi	AC096510	Homo sapi	c 489	24	4.9	96678	9	HS477J10A	Human DNA	HS477J10A	Human DNA
c 417	25	5.1	209112	2	AC084146	Homo sapi	AC084146	Homo sapi	c 490	24	4.9	96948	2	AC084728	Homo sapi	AC084728	Homo sapi
c 418	25	5.1	209794	9	AL390878	Human DNA	AL390878	Human DNA	c 491	24	4.9	99014	6	AX410782	Sequence	AX410782	Sequence
c 419	25	5.1	210133	9	AC013564	Homo sapi	AC013564	Homo sapi	c 492	24	4.9	99014	9	HSU78027	Homo sapi	HSU78027	Homo sapi
c 420	25	5.1	210933	2	AC027394	Homo sapi	AC027394	Homo sapi	c 493	24	4.9	100000	9	AP000104	Homo sapi	AP000104	Homo sapi
c 421	25	5.1	211550	9	AC073912	Homo sapi	AC073912	Homo sapi	c 494	24	4.9	100000	9	AP000180	Homo sapi	AP000180	Homo sapi
c 422	25	5.1	214530	9	AC020916	Homo sapi	AC020916	Homo sapi	c 495	24	4.9	100000	9	AP000502	Homo sapi	AP000502	Homo sapi
c 423	25	5.1	214945	9	AC098588	Homo sapi	AC098588	Homo sapi	c 496	24	4.9	102259	9	AC015916	Homo sapi	AC015916	Homo sapi
c 424	25	5.1	215007	9	AC008507	Homo sapi	AC008507	Homo sapi	c 497	24	4.9	106317	9	AL136958	Human DNA	AL136958	Human DNA
c 425	25	5.1	215077	9	AC112504	Homo sapi	AC112504	Homo sapi	c 498	24	4.9	108408	2	AC022210	Homo sapi	AC022210	Homo sapi
c 426	25	5.1	215812	2	AC084037	Homo sapi	AC084037	Homo sapi	c 499	24	4.9	111763	9	AC092783	Homo sapi	AC092783	Homo sapi
c 427	25	5.1	215139	2	AC084418	Homo sapi	AC084418	Homo sapi	c 500	24	4.9	112417	9	AC006015	Homo sapi	AC006015	Homo sapi
c 428	25	5.1	223797	2	AC021978	Homo sapi	AC021978	Homo sapi	c 501	24	4.9	113546	2	HSAC000382	Homo sapi	HSAC000382	Homo sapi
c 429	25	5.1	224360	2	AC090670	Homo sapi	AC090670	Homo sapi	c 502	24	4.9	113996	2	AC026438	Homo sapi	AC026438	Homo sapi
c 430	25	5.1	224573	9	AC008758	Homo sapi	AC008758	Homo sapi	c 503	24	4.9	117145	9	AC011370	Homo sapi	AC011370	Homo sapi

504	24	4.9 119245	2	CNS08C8Q	AL731886	Oryza sat	c 577	24	4.9 163132	9	AC025038	Homo sapi
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506	24	4.9 120612	9	AC108518	AC108518	Homo sapi	c 579	24	4.9 163375	2	AC027777	Homo sapi
507	24	4.9 120857	9	AC116334	AC116334	Homo sapi	c 580	24	4.9 163819	2	AC022758	Homo sapi
508	24	4.9 122568	9	AF196972	AF196972	Homo sapi	c 581	24	4.9 163836	9	AC073917	Homo sapi
509	24	4.9 122764	9	HSJ831D17	AL109984	Human DNA	c 582	24	4.9 163970	2	AC115247	Rattus no
510	24	4.9 123817	9	AL713980	AL109984	Human DNA	c 583	24	4.9 164350	9	AC068919	Homo sapi
511	24	4.9 125698	9	HS692C8	AL034561	Human DNA	c 584	24	4.9 164482	9	AC092474	Homo sapi
512	24	4.9 126910	9	AC026794	AC026794	Homo sapi	c 585	24	4.9 164731	9	AC007485	Homo sapi
513	24	4.9 128152	9	AL136313	AL136313	Human DNA	c 586	24	4.9 164928	9	AC087752	Homo sapi
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515	24	4.9 130754	2	AC008508	AC008508	Homo sapi	c 588	24	4.9 165062	9	AC087834	Pan trogl
516	24	4.9 131098	9	AC010607	AC010607	Homo sapi	c 589	24	4.9 165385	2	AC093003	Homo sapi
517	24	4.9 131359	9	AC019068	AC019068	Homo sapi	c 590	24	4.9 165720	2	AC025524	Homo sapi
518	24	4.9 131378	9	AC112653	AC112653	Homo sapi	c 591	24	4.9 166049	2	AC037470	Homo sapi
519	24	4.9 132764	9	AC073842	AC073842	Homo sapi	c 592	24	4.9 166093	2	AC015462	Homo sapi
520	24	4.9 132424	9	AL607128	AL607128	Human DNA	c 593	24	4.9 166173	2	AC023060	Homo sapi
521	24	4.9 134474	9	HS33F8	AL022160	Human DNA	c 594	24	4.9 166174	2	AC009633	Homo sapi
522	24	4.9 135259	9	AC004590	AC004590	Homo sapi	c 595	24	4.9 167131	9	CNS01DST	Human chr
523	24	4.9 135664	2	AC016559	AC016559	Homo sapi	c 596	24	4.9 168108	9	AL445687	Human DNA
524	24	4.9 136693	9	HS164F3	AL033422	Human DNA	c 597	24	4.9 169594	9	AC025480	Homo sapi
525	24	4.9 138264	9	AC008722	AC008722	Homo sapi	c 598	24	4.9 169753	9	AC087506	Homo sapi
526	24	4.9 138350	9	AC010801	AC010801	Homo sapi	c 599	24	4.9 169980	2	AC023981	Homo sapi
527	24	4.9 138587	9	AC010363	AC010363	Homo sapi	c 600	24	4.9 170800	2	AC024411	Homo sapi
528	24	4.9 140476	10	AC116659	AC116659	Mus muscu	c 601	24	4.9 171140	9	AC090685	Homo sapi
529	24	4.9 140974	9	AC068533	AC068533	Homo sapi	c 602	24	4.9 171304	2	AC090297	Homo sapi
530	24	4.9 141492	2	AC093204	AC093204	Homo sapi	c 603	24	4.9 171656	9	AL136380	Human DNA
531	24	4.9 141832	9	AP000432	AP000432	Homo sapi	c 604	24	4.9 171813	2	AC022722	Homo sapi
532	24	4.9 141878	9	AC000004	AC000004	Genomic s	c 605	24	4.9 171985	2	AL445675	Human DNA
533	24	4.9 143009	9	AC022447	AC022447	Homo sapi	c 606	24	4.9 172335	2	AC104451	Homo sapi
534	24	4.9 143291	9	AL137792	AL137792	Human DNA	c 607	24	4.9 172816	9	AC093899	Homo sapi
535	24	4.9 143676	2	AC026435	AC026435	Homo sapi	c 608	24	4.9 173121	2	AC087831	Homo sapi
536	24	4.9 143759	9	AC073532	AC073532	Homo sapi	c 609	24	4.9 173131	2	AC099532	Homo sapi
537	24	4.9 144430	9	AC091155	AC091155	Homo sapi	c 610	24	4.9 173438	9	AP003967	Homo sapi
538	24	4.9 144967	2	AC008963	AC008963	Homo sapi	c 611	24	4.9 173864	9	AL365364	Human DNA
539	24	4.9 145100	2	AC024641	AC024641	Homo sapi	c 612	24	4.9 174327	2	AL672191	Homo sapi
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541	24	4.9 145540	9	AP001052	AP001052	Homo sapi	c 614	24	4.9 175262	9	AC021491	Homo sapi
542	24	4.9 146466	9	AL353637	AL353637	Human DNA	c 615	24	4.9 175691	2	AC007615	Homo sapi
543	24	4.9 147101	9	AC109134	AC109134	Homo sapi	c 616	24	4.9 176145	2	AL731550	Homo sapi
544	24	4.9 148293	9	AC087730	AC087730	Pan trogl	c 617	24	4.9 176512	9	AC012323	Homo sapi
545	24	4.9 149110	9	AP003692	AP003692	Homo sapi	c 618	24	4.9 176932	9	AC016772	Homo sapi
546	24	4.9 149394	2	AP000828	AP000828	Homo sapi	c 619	24	4.9 177273	9	AC074194	Homo sapi
547	24	4.9 150813	9	AC118758	AC118758	Homo sapi	c 620	24	4.9 177289	2	AC090176	Homo sapi
548	24	4.9 151041	8	AP003258	AP003258	Oryza sat	c 621	24	4.9 177319	2	AC098698	Papio cyn
549	24	4.9 151371	2	AC091889	AC091889	Homo sapi	c 622	24	4.9 177505	9	AC022276	Homo sapi
550	24	4.9 151801	9	AC008906	AC008906	Homo sapi	c 623	24	4.9 177731	2	AC018937	Homo sapi
551	24	4.9 152065	2	AL844853	AL844853	Homo sapi	c 624	24	4.9 178377	9	AC007685	Homo sapi
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553	24	4.9 153629	9	AC092325	AC092325	Homo sapi	c 626	24	4.9 178518	2	AC025332	Homo sapi
554	24	4.9 153788	2	AC023971	AC023971	Homo sapi	c 627	24	4.9 178653	2	AC090088	Homo sapi
555	24	4.9 154101	2	AL357565	AL357565	Homo sapi	c 628	24	4.9 178980	9	AP001591	Homo sapi
556	24	4.9 154147	2	AL356487	AL356487	Homo sapi	c 629	24	4.9 179090	2	AC011014	Homo sapi
557	24	4.9 154325	2	AC008452	AC008452	Homo sapi	c 630	24	4.9 179272	2	AC022659	Homo sapi
558	24	4.9 154616	2	AC067772	AC067772	Homo sapi	c 631	24	4.9 179310	9	AC006160	Homo sapi
559	24	4.9 154904	9	AL162272	AL162272	Human DNA	c 632	24	4.9 179562	2	AP001323	Homo sapi
560	24	4.9 155064	9	CNS01DUP	AL133312	Human chr	c 633	24	4.9 179894	9	AL662834	Human DNA
561	24	4.9 155385	2	AL357552	AL357552	Homo sapi	c 634	24	4.9 180283	9	AF134726	Homo sapi
562	24	4.9 155770	2	AC092381	AC092381	Homo sapi	c 635	24	4.9 180365	9	AC046143	Homo sapi
563	24	4.9 156442	9	AL354915	AL354915	Human DNA	c 636	24	4.9 180419	2	AC108691	Homo sapi
564	24	4.9 156705	2	AC027270	AC027270	Homo sapi	c 637	24	4.9 180559	2	AL645922	Human DNA
565	24	4.9 157013	2	AP001778	AP001778	Homo sapi	c 638	24	4.9 180629	2	AC090308	Homo sapi
566	24	4.9 157268	2	AC025063	AC025063	Homo sapi	c 639	24	4.9 181210	9	AC011742	Homo sapi
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568	24	4.9 157982	9	AL589844	AL589844	Human DNA	c 641	24	4.9 181804	9	AC107068	Homo sapi
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570	24	4.9 159971	2	AC091951	AC091951	Homo sapi	c 643	24	4.9 182547	9	AP001201	Homo sapi
571	24	4.9 160232	2	AC079313	AC079313	Homo sapi	c 644	24	4.9 183182	2	AC019207	Homo sapi
572	24	4.9 160999	2	AP003369	AP003369	Oryza sat	c 645	24	4.9 183279	9	AC073263	Homo sapi
573	24	4.9 161685	2	AC013629	AC013629	Homo sapi	c 646	24	4.9 183768	9	AC020900	Homo sapi
574	24	4.9 162511	9	AC009470	AC009470	Homo sapi	c 647	24	4.9 183976	9	AL356056	Human DNA
575	24	4.9 162813	2	AC021833	AC021833	Homo sapi	c 648	24	4.9 184026	2	AC026638	Homo sapi
576	24	4.9 162881	9	AC022174	AC022174	Homo sapi	c 649	24	4.9 184289	9	AL359878	Human DNA

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652	24	4.9	186236	2	AC123982	Pan trogl	AC123982	Pan trogl	C 725	23	4.7	5864	6	AR140568	Sequence
653	24	4.9	186722	9	AC076971	Homo sapi	AC076971	Homo sapi	C 726	23	4.7	10120	6	AR14072	Sequence
654	24	4.9	187628	9	AC011311	Homo sapi	AC011311	Homo sapi	C 727	23	4.7	10918	9	HS010395	Homo sapi
655	24	4.9	188095	4	AC091505	Sus scrof	AC091505	Sus scrof	C 728	23	4.7	11174	9	AC104104	Homo sapi
656	24	4.9	188139	2	AC125230	Homo sapi	AC125230	Homo sapi	C 729	23	4.7	11271	6	AX014083	Sequence
657	24	4.9	188164	9	AC019208	Homo sapi	AC019208	Homo sapi	C 730	23	4.7	11337	9	AL450043	Human DNA
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659	24	4.9	189413	9	AF129075	Homo sapi	AF129075	Homo sapi	C 732	23	4.7	16996	9	HSN85E10	Human DNA
660	24	4.9	189987	9	AF004716	Homo sapi	AF004716	Homo sapi	C 733	23	4.7	16996	3	CE272D1	Caenorhabdi
661	24	4.9	190144	9	AL590080	Human DNA	AL590080	Human DNA	C 734	23	4.7	23451	9	HS799F10	Human DNA
662	24	4.9	190815	9	AC007066	Homo sapi	AC007066	Homo sapi	C 735	23	4.7	24888	9	HSE78H10	Human DNA
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664	24	4.9	190891	2	AC058800	Homo sapi	AC058800	Homo sapi	C 737	23	4.7	29718	9	HS310H5	Human DNA
665	24	4.9	190931	2	AC007921	Homo sapi	AC007921	Homo sapi	C 738	23	4.7	31705	9	HS400626	Homo sapi
666	24	4.9	191496	2	AC009130	Homo sapi	AC009130	Homo sapi	C 739	23	4.7	32746	2	AC013224	Drosophila
667	24	4.9	191768	9	AC092357	Homo sapi	AC092357	Homo sapi	C 740	23	4.7	33466	2	AC087046	Homo sapi
668	24	4.9	192046	2	AC113688	Rattus no	AC113688	Rattus no	C 741	23	4.7	35528	9	AC004495	Homo sapi
669	24	4.9	192773	2	AL7311547	Homo sapi	AL7311547	Homo sapi	C 742	23	4.7	36454	9	AL627144	Human DNA
670	24	4.9	194020	9	HUAC004125	Homo sapi	AC004125	Homo sapi	C 743	23	4.7	36589	9	AP001049	Homo sapi
671	24	4.9	196247	2	HSJ651N20	Homo sapi	AL117346	Homo sapi	C 744	23	4.7	36589	9	AP000543	Homo sapi
672	24	4.9	196662	9	AP001107	Homo sapi	AP001107	Homo sapi	C 745	23	4.7	38580	9	HSNOD1G1	Homo sapi
673	24	4.9	196917	2	AC087828	Homo sapi	AC087828	Homo sapi	C 746	23	4.7	39188	9	AC004754	Homo sapi
674	24	4.9	197905	2	AL645536	Homo sapi	AL645536	Homo sapi	C 747	23	4.7	39443	9	AC010505	Homo sapi
675	24	4.9	198105	2	AC028160	Homo sapi	AC028160	Homo sapi	C 748	23	4.7	39915	9	AC010512	Homo sapi
676	24	4.9	198550	9	AC012170	Homo sapi	AC012170	Homo sapi	C 749	23	4.7	40203	9	AC001643	Genomic s
677	24	4.9	199503	9	AC018901	Homo sapi	AC018901	Homo sapi	C 750	23	4.7	41569	9	HS141418	Human DNA
678	24	4.9	200498	2	AP002378	Homo sapi	AP002378	Homo sapi	C 751	23	4.7	42642	9	AC006277	Homo sapi
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683	24	4.9	207682	9	AC012564	Homo sapi	AC012564	Homo sapi	C 756	23	4.7	47722	2	AC113140	Homo sapi
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686	24	4.9	211345	2	AL731733	Homo sapi	AL731733	Homo sapi	C 759	23	4.7	56306	9	HSJ698015	Human DNA
687	24	4.9	212237	9	AC079235	Homo sapi	AC079235	Homo sapi	C 760	23	4.7	56408	2	AF527418	Homo sapi
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839	23	4.7	110000	2	AC011600	AC011600 Homo sapi	c 911	23	4.7	143799	9	AC011059	AC011059 Homo sapi
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848	23	4.7	112303	9	AC093836	AC093836 Homo sapi	c 920	23	4.7	146463	2	AC068306	AC068306 Homo sapi
849	23	4.7	113250	2	AP001540	AC004900 Homo sapi	c 921	23	4.7	146954	9	AL590640	AL590640 Human DNA
850	23	4.7	113980	2	AP001540	AP001540 Homo sapi	c 922	23	4.7	147913	9	HS23613A2	AL121990 Human DNA
851	23	4.7	114191	9	AL451007	AL451007 Human DNA	c 923	23	4.7	148203	2	AC022187	AC022187 Homo sapi
852	23	4.7	114957	9	CNS05TEH	AL359219 Human chr	c 924	23	4.7	148280	9	AC004474	AC004474 Homo sapi
853	23	4.7	115725	30	AC025481	AC025481 Homo sapi	c 925	23	4.7	148308	9	AC113192	AC113192 Homo sapi
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ALIGNMENTS

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LOCUS AF123659 Homo sapiens FEZ1 (FEZ1) mRNA, complete cds. 5492 bp mRNA
DEFINITION AF123659 Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.
ACCESSION AF123659
VERSION AF123659.1 GI:4572475
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5492)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
99199287
MEDLINE
PUBMED
10097140
2 (bases 1 to 5492)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
FEATURES
Location/Qualifiers.
1..5492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8p22"
1..5492
/gene="FEZ1"
112..1902
/gene="FEZ1"
/codon_start=1
/product="FEZ1"
/protein_id="AAD23840.1"
/db_xref="GI:4572476"
/translat="MGVSLSLSHSGHSFKHCKRASQVKKLRKSSHLKLNRYSDGLLRF
GFSDGSHGKSSKMGKDFYIKVQKARSHHDPDYALSSDGLGQAGVDFDPST
PKLMPSPNQLMGSEKGAVRPAFKPVLPRSCAILHSSPESASHOLHAPPDPKPEQ
ELKPLGCSALSDSGRNSSLPHTSTSSYQDLPLVTPVPSRGGSHNITQGLV
LQDSNMSLKALSFSDGSGKSHSNKADPCSRPSIDTDCSIOELEOKLUREGA
VLQKRSFEKLEASLAYEPRRCRDELEPEPKGNKLRQAQSKSQAQVHLHQ
LQLOQKEQLRQLESLKMEQDLLETKLRISYERKTSFGPALEETQWECQSGEIS
LKKQOLKESQTEVNKASAILGLKQDKTRGLGLELRFTQDLEGALRTKGLLEVLC
ENELORKNEALLREKVNLELOELRAQALARMGPPPTPEQVPALORLERLR
AELEERQHDQSSGFQHERLWKEKEKVIQYQKLOQSOYVAMYQVORNORLEKALQ
LARGSAGPFLVDLEGADIPYEDIIATSI"
BASE COUNT 1137 a 1704 c 1565 g 1086 t
ORIGIN
Query Match 100.0%; Score 486; DB 9; Length 5492;
Best Local Similarity 100.0%; Pred. No. 1.4e-261;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGATTGCAGATGTGAGCACCACCGTCGCTGGCCAGATTTTCTTTTATTTCTTTCTTTT 60
Db 3557 AGATTGCAGATGTGAGCACCACCGTCGCTGGCCAGATTTTCTTTTATTTCTTTT 3616
Qy 61 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 120
Db 3617 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3676
Qy 121 ATTTTGTACTGTAGCCACACGCTGTTCTCAGAGACGATCCCTCCCATGCTGCTGCG 180
Db 3677 ATTTTGTACTGTAGCCACACGCTGTTCTCAGAGACGATCCCTCCCATGCTGCTGCG 3736
Qy 181 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 3737 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3796
Qy 241 CCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 3797 CCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3856
Qy 301 CTTTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 3857 CTTTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3916
Qy 361 CAGATGCACCTTTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Db 3917 CAGAGTACCTTTCTGTGGCTGGCTCTACCTTCCCTGCTCCCTGAGGTTAAACGGTGCCA 3976
Qy 421 TCCTGCCATCTCAACACACAGAGAGCTTTCTTGGAAATTTCAACACATTGCTCTTAGTC 480
Db 3977 TCCTGCCATCTCAACACACAGAGAGCTTTCTTGGAAATTTCAACACATTGCTCTTAGTC 4036

Qy 481 CCAAGC 486
Db 4037 CCAAGC 4042

RESULT 2
AF123653 9108 bp DNA linear PRI 07-APR-1999
DEFINITION Homo sapiens FEZ1 (FEZ1) gene, complete cds.
ACCESSION AF123653
VERSION AF123653.1 GI:4572463

KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9108)
AUTHORS Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.
TITLE The FEZ1 gene at chromosome 9p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 9108)
AUTHORS Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA

FEATURES

source
1. 9108
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p22"
<112. >5553
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/gene="FEZ1"
/product="FEZ1"
/join(112. 456,1707. .2510,4912. 5553)
/gene="FEZ1"
/codon_start=1
/product="FEZ1"
/protein_id="AAD23834.1"
/db_xref="GI:4572464"
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PKLPFPNSOLEMSEKGVAPRTAFKVPVPSGAILHSPESASHOLHPAPPNPKPEQ
ELKPLCSGLSDSGRMSGLPHTSTSSSYQLDPLVTPVPTSPRFGSNAHNTQGLV
LQDSNMMLKALSFSDGSKLGHNSKADGFCVSPSTIDECISQLEOKLLREGA
LQKQRFSEKELASSLAYBERPRRCRDELEGGPKGNKKLQKASQRAQVQLHLQ
VLQKQKRLQRLQESLMKEFDLLETKLRSYERKTSFGPALEETQWEVCQSGEIS
LLKQKLESQTEVNAKASEILGLKAQLTRGKLEGLRTQDLEGALRTKGLLELYC
ENELQKNEALLREKVNLLQELQELRAQALARDMGPTTPEDVPALQRELERLR
ALREERQGHQDQSSGFQHERLVWKEKEKVIQYQKQLQSQYVAMYQNRLEKALQO
LARGDSAGEPLEVLEADIPYEDIATETI"
BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others
ORIGIN

Query Match 100.0%; Score 486; DB 9; Length 9108;
Best Local Similarity 100.0%; Pred. No. 1.4e-261;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGATTGCAGATGTGAGCCACCGCTCGGCGAGATTTTCTTTTATTCTTCTTTT 60

Db 7208 AGATTGCAGATGTGAGCCACCGCTCGCTGGCGAGATTTTCTTTTATTCTTCTTTT 7267
Qy 61 CTTTCTTGTCTTCTTGTCTTTTTCAGAGCAAGCAGACCTAGCAGGCTGTTCATGTTCT 120
Db 7268 CTTTCTTGTCTTCTTGTCTTTTTCAGAGCAAGCAGACCTAGCAGGCTGTTCATGTTCT 7327
Qy 121 ATTTTGACTGTATGCCACACAGCTGCTGTCTTCAGAGACAGCATCCCTTCCACATGCCTGCG 180
Db 7328 ATTTTGACTGTATGCCACACAGCTGCTGTCTTCAGAGACAGCATCCCTTCCACATGCCTGCG 7387
Qy 181 CTTGCTGCTGCTGAGATGAGGAGGGAGCGTCTGGAACTTTCGCACTCAAGGCCAGTC 240
Db 7388 CTTGCTGCTGCTGAGATGAGGAGGGAGCGTCTGGAACTTTCGCACTCAAGGCCAGTC 7447
Qy 241 CCATTTCTGCTCGCTCAGCGCTGCGCTTACAGACCCCGAGCTAGGGTGGGGAGATG 300
Db 7448 CCATTTCTGCTCGCTCAGCGCTGCGCTTACAGACCCCGAGCTAGGGTGGGGAGATG 7507
Qy 301 CTTTCTCTTGGCCCCCGCCCTCATGGGTCCTAGAGCCCTTCCCTGAGTGGGGCTGAGGC 360
Db 7508 CTTTCTCTTGGCCCCCGCCCTCATGGGTCCTAGAGCCCTTCCCTGAGTGGGGCTGAGGC 7567
Qy 361 CAGAGTCACCTTTTCTGTGCTGCTACCTTCTGCTGCTGCTGAGGTTAAACGGTGCCCA 420
Db 7568 CAGAGTCACCTTTTCTGTGCTGCTACCTTCTGCTGCTGAGGTTAAACGGTGCCCA 7627
Qy 421 TCTGTGCATCTCTCAACGACAGAGGAGCTTTTCTTGGAAATTTCAACCATTCCTCTTAGTC 480
Db 7628 TCTGTGCATCTCTCAACGACAGAGGAGCTTTTCTTGGAAATTTCAACCATTCCTCTTAGTC 7687
Qy 481 CCAAGC 486
Db 7688 CCAAGC 7693

RESULT 3

AC025853 173264 bp DNA linear HTG 17-JUN-2002
LOCUS AC025853
DEFINITION IN PROGRESS ***, 3 unordered pieces.
ACCESSION AC025853
VERSION AC025853.13 GI:21431202
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173264)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-353K12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173264)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G.,
Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Gage,D.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teshaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,

chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrio>
 RP11-142P1 is from the library RP11-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-142P1 it may be shorter because we sequence overlapping sections only once, except for a short overlap.
 The true left end of clone RP11-142P1 is at 1 in this sequence. The true left end of clone RP11-390B4 is at 95431 in this sequence. The true right end of clone RP11-161K20 is at 28876 in this sequence.

FEATURES

source

1. 97430
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-142P1"
 /clone_lib="RP11-11.1"

BASE COUNT 29078 a 20172 c 20123 g 28057 t

ORIGIN

Query Match 7.8%; Score 38; DB 9; Length 97430;
 Best Local Similarity 100.0%; Pred. NO. 8.8e-10;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 CAGATGTGAGCCACCGTGGCGCAGATTTTCTTTT 44
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 Db 26327 CAGATGTGAGCCACCGTGGCGCAGATTTTCTTTT 26290

RESULT 5

AC010367

LOCUS

AC010367 137845 bp DNA linear HTG 20-APR-2001
 Homo sapiens chromosome 5 clone CTD-2044L23, WORKING DRAFT
 SEQUENCE, 17 unordered pieces.

ACCESSION

AC010367

VERSION

AC010367.4 GI:13699509

KEYWORDS

HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 137845)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished

2 (bases 1 to 137845)

DOE Joint Genome Institute.

Direct Submission

Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Apr 20, 2001 this sequence version replaced gi:7710742.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: <http://www.jgi.doe.gov>

Project Information

Center Project Name: 644732

Center clone name: CITB-H1_2044L23

Summary Statistics

Consensus quality: 122756 bases at least Q40

Consensus quality: 127174 bases at least Q30

Consensus quality: 129642 bases at least Q20

Estimated insert size: 121000; pulse field gel estimation

Estimated insert size: 136245; sum-of-contigs estimation

Quality coverage: 6.63 in Q20 bases; pulse field gel estimation

Quality coverage: 5.99 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1041: contig of 1041 bp in length
 * 1042
 * 1141: gap of unknown length
 * 1142
 * 1143: contig of 1042 bp in length
 * 2184
 * 2183: gap of unknown length
 * 2184
 * 3529: contig of 1246 bp in length
 * 3530
 * 3529: gap of unknown length
 * 4897: contig of 1268 bp in length
 * 4898
 * 4897: gap of unknown length
 * 4998
 * 6540: contig of 1543 bp in length
 * 6541
 * 6540: gap of unknown length
 * 6641
 * 7735: contig of 1095 bp in length
 * 7736
 * 7735: gap of unknown length
 * 7836
 * 8852: contig of 1017 bp in length
 * 8853
 * 8852: gap of unknown length
 * 10065: contig of 1113 bp in length
 * 10066
 * 10065: gap of unknown length
 * 11335: contig of 1170 bp in length
 * 11336
 * 11335: gap of unknown length
 * 11436
 * 12444: contig of 1009 bp in length
 * 12445
 * 12444: gap of unknown length
 * 12545
 * 13853: contig of 1308 bp in length
 * 13853
 * 13852: gap of unknown length
 * 13953
 * 15056: contig of 1104 bp in length
 * 15057
 * 15156: gap of unknown length
 * 23003: contig of 7847 bp in length
 * 23004
 * 23103: gap of unknown length
 * 23104
 * 41386: contig of 18283 bp in length
 * 41387
 * 4186: gap of unknown length
 * 68942: contig of 27456 bp in length
 * 68943
 * 89042: gap of unknown length
 * 98301: contig of 29259 bp in length
 * 98302
 * 98401: gap of unknown length
 * 98402
 * 137845: contig of 39444 bp in length.

FEATURES

source

1. 137845
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTD-2044L23"
 /clone_lib="CalTech human BAC library D"

BASE COUNT 38706 a 29358 c 29046 g 39089 t 1636 others

ORIGIN

Query Match 6.4%; Score 31; DB 2; Length 137845;
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GATTGAGATGTGAGCCACCGTGGCTGGCCA 32

|||||

Db 36892 GATTGAGATGTGAGCCACCGTGGCTGGCCA 36922

RESULT 6

AL135778/c

LOCUS

AL135778

DEFINITION

Human DNA sequence from clone RP1-119C5 on chromosome 6, complete

sequence.

ACCESSION

AL135778

VERSION

AL135778.9 GI:123330708

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152786)

Kimberley, A.

Direct Submission

JOURNAL

Submitted (27-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Jan 22, 2001 this sequence version replaced gi:10715708.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>
RPI-119C5 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: PCYPAC2

This sequence is the entire insert of clone RPI-119C5 The true left end of clone RPI-327D12 is at 77349 in this sequence. The true left end of clone RPI-126E20 is at 128858 in this sequence. The true right end of clone RPI-146G22 is at 135074 in this sequence.

FEATURES

source

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/chromosome="6"
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/clone_lib="RPCI-1"

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831. .1017
/note="AluSg/x repeat: matches 118. .299 of consensus"
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1193. .1503
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repeat_region
1968. .2190
/note="MLT1H repeat: matches 82. .310 of consensus"
repeat_region
2223. .2345
/note="MST-INTERNAL repeat: matches 1518. .1649 of consensus"
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2779. .3260
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repeat_region
3261. .3557
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repeat_region
3558. .3656
/note="L1MC5 repeat: matches 7771. .7871 of consensus"
repeat_region
3696. .3842
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repeat_region
4228. .4538
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4550. .4752
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repeat_region
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repeat_region
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repeat_region
7569. .8002

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8003. .8018
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8679. .9302
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9349. .10135
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10168. .10768
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10769. .11916
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12678. .13054
/note="L1PA16 repeat: matches 5613. .5964 of consensus"
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13358. .13545
/note="L1PA16 repeat: matches 5964. .6157 of consensus"
13555. .14247
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14370. .14443
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14533. .14730
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14745. .14878
/note="FLAM_C repeat: matches 1. .132 of consensus"
15035. .15110
/note="L1M4 repeat: matches 5017. .5094 of consensus"
15128. .15446
/note="MER7A repeat: matches 1. .327 of consensus"
17361. .17606
/note="MLT1B repeat: matches 4. .248 of consensus"
17607. .17993
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18005. .18139
/note="FLAM_C repeat: matches 11. .143 of consensus"
18179. .18368
/note="AluJo repeat: matches 122. .311 of consensus"
18438. .18654
/note="MER20 repeat: matches 1. .218 of consensus"
19158. .19564
/note="MLT1B repeat: matches 5. .409 of consensus"
21068. .21178
/note="L2 repeat: matches 2589. .2692 of consensus"
21476. .21560
/note="MIR repeat: matches 29. .115 of consensus"
22115. .22280
/note="MIR repeat: matches 50. .246 of consensus"
22504. .22781
/note="L2 repeat: matches 2420. .2690 of consensus"
23353. .23650
/note="AluSg repeat: matches 1. .298 of consensus"
24073. .24154
/note="MLT1I repeat: matches 317. .402 of consensus"
24204. .24259
/note="MLT1J repeat: matches 312. .367 of consensus"
24762. .25075
/note="AluX repeat: matches 1. .312 of consensus"
25707. .26058
/note="MLT2FB repeat: matches 1. .354 of consensus"
26070. .26125
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26126. .26189
/note="16 copies 4 mer atct 85% conserved"
26196. .26228
/note="MLT2FB repeat: matches 367. .399 of consensus"

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repeat_region 28125..28193
/note="MIR repeat: matches 77..146 of consensus"
repeat_region 28323..28460
/note="L2 repeat: matches 2571..2703 of consensus"
repeat_region 28992..29605
/note="MER41B repeat: matches 1..635 of consensus"
repeat_region 29842..29883
/note="21 copies 2 mer tt 85% conserved"
repeat_region 31794..32080
/note="Alusq repeat: matches 1..291 of consensus"
repeat_region 32366..32526
/note="FRAM repeat: matches 1..163 of consensus"
repeat_region 33419..33632
/note="AluJo repeat: matches 86..299 of consensus"
repeat_region 34415..34620
/note="MER3 repeat: matches 1..209 of consensus"
repeat_region 35454..35574
/note="FLAM C repeat: matches 1..122 of consensus"
repeat_region 36427..37101
/note="L1ME1 repeat: matches 5444..6151 of consensus"
repeat_region 37230..37336
/note="L1ME3 repeat: matches 6061..6155 of consensus"
repeat_region 37337..37647
/note="AluJb repeat: matches 1..305 of consensus"
repeat_region 37648..37766
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repeat_region 40066..40381
/note="Alusq repeat: matches 1..313 of consensus"
repeat_region 41450..41503
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repeat_region 41452..41508
/note="19 copies 3 mer at 87% conserved"
repeat_region 42164..42270
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repeat_region 42376..42635
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repeat_region 42654..42758
/note="L2 repeat: matches 2597..2706 of consensus"
repeat_region 42904..43196

Query Match 6.4%; Score 31; DB 9; Length 152786;
Best Local Similarity 100.0%; Pred.No. 7.5e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 CAGATGTGAGCCCGCTGCGCCAGATTT 37
Db 31818 CAGATGTGAGCCCGCTGCGCCAGATTT 31788

RESULT 7
AL160395 179959 bp DNA linear PRI 17-MAR-2001
LOCUS Human DNA sequence from clone RP11-474D23 on chromosome 13q33.1-34,
DEFINITION complete sequence.
ACCESSION AL160395
VERSION AL160395.24 GI:13396423
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 179959)
AUTHORS Smith,M.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Mar 20, 2001 this sequence version replaced gi:12655257.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

```

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep

This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr13>

RP11-474D23 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-474D23. The true left end of clone RP11-190K22 is at 105916 in this sequence. The true right end of clone RP11-494P5 is at 37339 in this sequence.

FEATURES

Location/Qualifiers	Source
1..179959	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="13"
	/map="q33.1-34"
	/clone="RP11-474D23"
	/clone_lib="RPCI-11.2"
6..454	
/notes="match: GSS: Em:AQ831485"	
13..304	
/notes="match: GSS: Em:AQ525749"	
25..463	
/notes="match: GSS: Em:AQ634626"	
217..567	
/notes="THE1C repeat: matches 1..371 of consensus"	
1248..1535	
/notes="MLT1C repeat: matches 8..283 of consensus"	
2198..2293	
/notes="L1MB8 repeat: matches 5521..5618 of consensus"	
2294..2640	
/notes="MLT1A1 repeat: matches 13..365 of consensus"	
2654..2921	
/notes="L1MB8 repeat: matches 5615..5894 of consensus"	
3106..3248	
/notes="AluJb repeat: matches 142..284 of consensus"	
3333..3498	
/notes="L2 repeat: matches 2079..2266 of consensus"	
4415..4466	
/notes="26 copies 2 mer gg 71% conserved"	
5113..5418	
/notes="Alusx repeat: matches 5..312 of consensus"	
5502..5910	
/notes="match: STS: Em:HSPH25D3"	
7094..7277	
/notes="2 copies 92 mer 96% conserved"	
8059..8455	
/notes="match: GSS: Em:AQ205997"	
8130..8211	
/notes="2 copies 41 mer 89% conserved"	
9508..9577	
/notes="MIR repeat: matches 23..95 of consensus"	
9649..9720	
/notes="2 copies 36 mer 90% conserved"	
9704..10214	
/notes="Cpg island"	
/evidence="not_experimental"	

```
repeat_region 9850..9953
/note="2 copies 52 mer 90% conserved"
repeat_region 9888..10004
/note="3 copies 39 mer 85% conserved"
repeat_region 10022..10138
/note="3 copies 39 mer 83% conserved"
repeat_region 10119..10222
/note="2 copies 52 mer 91% conserved"
misc_feature complement(12824..13054)
/note="match: GSS: Em:AQ008472"
repeat_region 13051..13542
/note="LTR38 repeat: matches 35..603 of consensus"
misc_feature 13804..14058
/note="Sequence from overlapping clone BA494P5 (AL139086).
Assembly confirmed by restriction digest."
repeat_region 14054..16280
/note="L1MB6 repeat: matches 3900..6148 of consensus"
repeat_region 16270..17065
/note="L1M4 repeat: matches 1299..2069 of consensus"
repeat_region 17066..17420
/note="THS1C repeat: matches 1..371 of consensus"
repeat_region 17421..18640
/note="L1M4 repeat: matches -12..1299 of consensus"
misc_feature 18456..18874
/note="match: GSS: Em:B43739"
misc_feature complement(19474..20004)
/note="match: GSS: Em:AQ25415"
repeat_region 20661..20819
/note="MLT1F repeat: matches 300..501 of consensus"
repeat_region 20799..21111
/note="MLT1F repeat: matches 6..332 of consensus"
repeat_region 21598..22003
/note="MLT1B repeat: matches 6..390 of consensus"
repeat_region 22842..22923
/note="2 copies 41 mer 92% conserved"
repeat_region 22878..23067
/note="5 copies 38 mer 83% conserved"
repeat_region 25852..26039
/note="Aluub repeat: matches 116..302 of consensus"
repeat_region 28738..29038
/note="AluX repeat: matches 1..310 of consensus"
repeat_region 30142..30536
/note="HERVL repeat: matches 4031..4458 of consensus"
repeat_region 30579..31009
/note="MSTB repeat: matches 1..426 of consensus"
repeat_region 31902..32285
/note="MSTA repeat: matches 1..426 of consensus"
repeat_region 32370..32924
/note="L1MB1 repeat: matches 5613..6163 of consensus"
repeat_region 32925..33227
/note="AluSC repeat: matches 1..303 of consensus"
repeat_region 33228..33465
/note="L1MB1 repeat: matches 5378..5613 of consensus"
repeat_region 33466..33768
/note="AluY repeat: matches 1..303 of consensus"
repeat_region 33769..35161
/note="L1MB1 repeat: matches 3934..5378 of consensus"
repeat_region 35189..37037
/note="L1M1 repeat: matches 1648..3555 of consensus"
repeat_region 37038..37332
/note="Aluub repeat: matches 1..294 of consensus"
repeat_region 37333..37630
/note="L1M1 repeat: matches 3555..3841 of consensus"
repeat_region 37633..37762
/note="FLAM C repeat: matches 3..132 of consensus"
repeat_region 37871..38362
/note="L1MB1 repeat: matches 5556..6059 of consensus"
repeat_region 38531..38570
/note="20 copies 2 mer aa 77% conserved"
misc_feature complement(40607..41026)
/note="match: GSS: Em:AQ110612"
misc_feature 40640..41524
/note="Single clone region. Sequence from reads from a
```

```
short insert library derived from a clone PCR. Restriction
digest data confirm the assembly."
repeat_region 41021..41050
/note="5 copies 6 mer cctct 96% conserved"
repeat_region 41053..41136
/note="FLAM repeat: matches 53..131 of consensus"
repeat_region 41161..41303
/note="MER69A repeat: matches 23..177 of consensus"
misc_feature 41285..41455
/note="match: GSS: Em:AQ091575"
repeat_region 41462..41696
/note="5 copies 47 mer 67% conserved"
repeat_region 41478..41705
/note="6 copies 38 mer 66% conserved"
repeat_region 41523..41669
/note="3 copies 49 mer 74% conserved"
repeat_region 41539..41814
/note="3 copies 92 mer 71% conserved"
repeat_region 41572..41787
/note="4 copies 54 mer 68% conserved"
repeat_region 41619..41698
/note="5 copies 16 mer 72% conserved"
misc_feature 41692..41696
/note="Single clone region. Sequence from reads from a
short insert library derived from a clone PCR. Restriction
digest data confirm the assembly."
repeat_region 42031..42369
/note="L1PA3 repeat: matches 5809..6146 of consensus"
repeat_region 42779..43376
/note="MBR77 repeat: matches 54..620 of consensus"
repeat_region 45002..45401
/note="MLT1D repeat: matches 88..501 of consensus"
repeat_region 45602..45983
/note="L2 repeat: matches 251..704 of consensus"

Query Match 6.4%; Score 31; DB 9; Length 179959;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GATTGAGATGTGAGCCACCGTCGCTGGCCA 32
|||||
Db 165585 GATTGAGATGTGAGCCACCGTCGCTGGCCA 165615

RESULT 8
AC008675/c 186415 bp DNA linear PRI 20-DEC-2000
LOCUS Homo sapiens chromosome 5 clone CTB-4518, complete sequence.
DEFINITION AC008675
ACCESSION AC008675
VERSION AC008675.5 GI:11908270
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 186415)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186415)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 186415)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 20, 2000 this sequence version replaced gi:7709256.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
```

www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.4% of Sequence;
 Estimated Total Number of Errors is 1.3.

FEATURES

source
 1. .186415
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTB-45J8"
 BASE COUNT 53455 a 41083 c 40655 g 51222 t
 ORIGIN

Query Match 6.4%; Score 31; DB 9; Length 186415;
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GATTGCAGATGTGAGCCACCGTGCCTGGCCA 32
 |||||
 DB 112668 GATTGCAGATGTGAGCCACCGTGCCTGGCCA 112638

RESULT 9

AC018757 186418 bp DNA linear PRI 03-OCT-2001
 LOCUS
 DEFINITION Homo sapiens chromosome 5 clone CTB-45J8, complete sequence.
 AC018757
 VERSION
 KEYWORDS HTG.

SOURCE AC018757.6 GI:15887297

ORGANISM

Homo sapiens.
 Homo sapiens
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 186418)
 DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE

AUTHORS
 TITLE Direct Submission

JOURNAL

UNPUBLISHED

REFERENCE

2 (bases 1 to 186418)
 DOE Joint Genome Institute.
 Direct Submission
 Submitted (19-DEC-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 186418)

REFERENCE

AUTHORS
 TITLE Direct Submission
 JOURNAL
 Submitted (01-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 4 (bases 1 to 186418)

REFERENCE

AUTHORS
 TITLE Direct Submission

JOURNAL

Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Oct 3, 2001 this sequence version replaced gi:9625331.
 Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.4% of Sequence;

Estimated Total Number of Errors is 1.1.

FEATURES

source
 1. .186418
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTB-45J8"
 BASE COUNT 51223 a 40655 c 41083 g 53456 t
 ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 7.5e-06;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 GATTGCAGATGTGAGCCACCGTGCCTGGCCA 32

|||||

Db 73750 GATTGCAGATGTGAGCCACCGTGCCTGGCCA 73780

RESULT 10

AC005054 197456 bp DNA linear HTG 17-AUG-2000
 LOCUS
 DEFINITION Homo sapiens chromosome UNK clone CTB-45H5, *** SEQUENCING IN
 PROGRESS ***, 18 unordered pieces.

AC005054

ACCESSION

AC005054.2 GI:9838352

VERSION

HTG; HTGS PHASE1.

KEYWORDS

Homo sapiens.

SOURCE

Homo sapiens

ORGANISM

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 197456)
 Waterston, R. H.
 The sequence of Homo sapiens clone

REFERENCE

AUTHORS

TITLE

Unpublished

JOURNAL

2 (bases 1 to 197456)

REFERENCE

Waterston, R. H.

AUTHORS

Direct Submission

TITLE

Submitted (12-JUN-1998) Genome Sequencing Center, Washington

JOURNAL

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Aug 17, 2000 this sequence version replaced gi:3212937.

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

----- Project Information -----

Center project name: H RG045H05

----- Summary_Statistics -----

Sequencing vector: M13; 100%

Sequencing vector: plasmid; 0%

Chemistry: Dye-primer ET; 71% of reads

Chemistry: Dye-terminator Big Dye; 29% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: bases at least Q40

Consensus quality: bases at least Q30

Consensus quality: bases at least Q20

Insert size: 181000; agarose-fp

Insert size: 195258; sum-of-contigs

Quality coverage: in Q20 bases; agarose-fp

Quality coverage: in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 18 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1. 5084: contig of 5084 bp in length

* 5085 5184: gap of unknown length

* 5185 14399: contig of 9215 bp in length

* 14400 14499: gap of unknown length

* 14500 22836: contig of 8337 bp in length

* 22837 22937: gap of unknown length

* 22937 33373: contig of 10437 bp in length

* 33374 33474: gap of unknown length

* 33474 47419: contig of 13946 bp in length

* 47420 47519: gap of unknown length

* 47520 66575: contig of 19056 bp in length

* 66576 66676: gap of unknown length

* 66676 81991: contig of 15315 bp in length

* 81991 82091: gap of unknown length

* 82091 105847: contig of 23757 bp in length

* 105848 105948: gap of unknown length

* 105948 129371: contig of 23324 bp in length

* 129371 129372: gap of unknown length

```

* 129372 164242: contig of 34871 bp in length
* 164243 164342: gap of unknown length
* 164343 164840: contig of 498 bp in length
* 164841 164940: gap of unknown length
* 164941 167875: contig of 2935 bp in length
* 167876 167975: gap of unknown length
* 167976 172505: contig of 4530 bp in length
* 172506 172605: gap of unknown length
* 172606 176804: contig of 4199 bp in length
* 176805 176904: gap of unknown length
* 176905 180960: contig of 4056 bp in length
* 180961 181060: gap of unknown length
* 181061 185808: contig of 4748 bp in length
* 185809 185908: gap of unknown length
* 185909 190832: contig of 4924 bp in length
* 190833 190932: gap of unknown length
* 190933 197456: contig of 6524 bp in length.
FEATURES
    source
        1. 197456
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="UNK"
            /clones="CTB-45H5"
        1. 5084
            /note="assembly_name:Contig100"
        5185..14399
            /note="assembly_name:Contig101"
        14500..22836
            /note="assembly_name:Contig103"
        22937..33373
            /note="assembly_name:Contig104"
        33474..47419
            /note="assembly_name:Contig105"
        47520..66575
            /note="assembly_name:Contig106"
        66676..81990
            /note="assembly_name:Contig107"
        82091..105847
            /note="assembly_name:Contig108"
        105948..129271
            /note="assembly_name:Contig109"
        129372..164242
            /note="assembly_name:Contig110"
        164343..164840
            /note="assembly_name:Contig18"
        164941..167875
            /note="assembly_name:Contig91"
        167976..172505
            /note="assembly_name:Contig94"
        172606..176804
            /note="assembly_name:Contig95"
        176905..180960
            /note="assembly_name:Contig96"
        181061..185808
            /note="assembly_name:Contig97"
        185909..190832
            /note="assembly_name:Contig98"
        190933..197456
            /note="assembly_name:Contig99"
BASE COUNT 51971 a 47509 c 46808 g 49428 t 1740 others
ORIGIN
    Query Match 6.4%; Score 31; DB 2; Length 197456;
    Best Local Similarity 100.0%; Pred. No. 7.5e-06;
    Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GATTGCAGATGTGAGCCACCGCTGGCCCA 32
Db 151689 GATTGCAGATGTGAGCCACCGCTGGCCCA 151719
RESULT 11
AC018709

```

```

LOCUS AC018709 161013 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-215A19 from 4, complete sequence.
AC018709
VERSION AC018709.9 GI:15431210
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 161013)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
MEDLINE
PUBMED 9847074
2 (bases 1 to 161013)
Harkins,C. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-215A19
Unpublished (2001)
3 (bases 1 to 161013)
Waterston,R.H.
Direct Submission
Submitted (16-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 161013)
Waterston,R.H.
Direct Submission
Submitted (05-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 161013)
Waterston,R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 5, 2001 this sequence version replaced gi:15383864.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0215A19
-----
NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute

```


(http://bacpac.med.buffalo.edu)
 VECTOR: pBACE3.6
 NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the right is AC015601. Actual start of this
 clone is at base position 1 of RP11-215A19; actual end is at base
 position 161013 of RP11-215A19.

Unresolved tandem repeats from base position 92006 to 96846 and
 from 136330 to 138682.

FEATURES

source

Location/Qualifiers

1. 161013
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="4"
 /map="4"
 /clone="RP11-215A19"
 /clone.lib="RCI-11"
 972. 7069
 /rpt_family="MER121"
 1089. 1119
 /rpt_family="AT_rich"
 1646. 1986
 /rpt_family="MaLR"
 2635. 2935
 /rpt_family="Alu"
 3270. 3308
 /rpt_family="L1"
 3346. 3383
 /rpt_family="T-rich"
 3358. 3664
 /rpt_family="Alu"
 4164. 4192
 /rpt_family=" "(TTTTTGT)n"
 4659. 4686
 /rpt_family="AT_rich"
 6039. 6349
 /rpt_family="Alu"
 6428. 6525
 /rpt_family="MaLR"
 7200. 7281
 /rpt_family="L2"
 7760. 7941
 /rpt_family="MIR"
 8830. 9056
 /rpt_family="Alu"
 9801. 10106
 /rpt_family="Alu"
 10081. 10106
 /rpt_family=" (CAAAA)n"
 10132. 10354
 /rpt_family="MER1_type"
 10696. 10727
 /rpt_family="Alu"
 10728. 10928
 /rpt_family="Alu"
 11144. 11369
 /rpt_family="Alu"
 12940. 12960
 /rpt_family="AT_rich"
 13120. 13240
 /rpt_family="AchHobo"
 13388. 13686
 /rpt_family="Alu"
 15179. 15594
 /rpt_family="MaLR"
 15667. 16695
 /rpt_family="L1"
 16718. 16848
 /rpt_family="Alu"
 16848. 16874
 /rpt_family=" (TA)n"
 17005. 17196
 /rpt_family="L1"

repeat_region 17298. 17427
 /rpt_family="L1"
 repeat_region 17429. 17848
 /rpt_family="MaLR"
 repeat_region 17875. 18060
 /rpt_family="L1"
 repeat_region 18068. 18689
 /rpt_family="L1"
 repeat_region 18694. 18839
 /rpt_family="Alu"
 repeat_region 18840. 19457
 /rpt_family="ERV1"
 repeat_region 19458. 19773
 /rpt_family="ERV1"
 repeat_region 20819. 21214
 /rpt_family="MaLR"
 repeat_region 22075. 22454
 /rpt_family="MaLR"
 repeat_region 22730. 23725
 /rpt_family="ERVK"
 repeat_region 23921. 24249
 /rpt_family="ERVK"
 repeat_region 24265. 25207
 /rpt_family="L2"
 repeat_region 25227. 25258
 /rpt_family="AT_rich"
 repeat_region 26245. 26641
 /rpt_family="ERV1"
 repeat_region 27656. 27877
 /rpt_family="MIR"
 repeat_region 28374. 28465
 /rpt_family="L1"
 repeat_region 28481. 28523
 /rpt_family="AT_rich"
 repeat_region 29331. 29614
 /rpt_family="Alu"
 repeat_region 29613. 29669
 /rpt_family=" (TAA)n"
 repeat_region 29820. 30548
 /rpt_family="L1"
 repeat_region 30534. 30562
 /rpt_family="AT_rich"
 repeat_region 30645. 31005
 /rpt_family="L1"
 repeat_region 31007. 31112
 /rpt_family="MaLR"
 misc_feature 31097. 32264
 /note="CpG island (GCG=56.9, o/e=0.90, #CpGs=83)"
 repeat_region 32251. 32430
 /rpt_family="MaLR"
 repeat_region 32433. 32560
 /rpt_family="L2"
 repeat_region 33839. 34129
 /rpt_family="Alu"

Query Match 6.2%; Score 30; DB 9; Length 161013;
 Best Local Similarity 100.0%; Pred.No. 2.7e-05;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATTGAGATGTGAGCCACCGTGGCTGGCC 31
 |||||
 Db 10900 GATTGAGATGTGAGCCACCGTGGCTGGCC 10929

RESULT 12

AC012525/c

LOCUS

DEFINITION AC012525 240000 bp DNA linear HTG 14-DEC-1999
 Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 12
 unordered pieces.

ACCESSION AC012525

VERSION AC012525.6 GI:6573826

KEYWORDS HTG; HTGS PHASE1.

SOURCE Homo sapiens.

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 240000)
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 240000)
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1999) Department of Genetics, Stanford Human
Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT On Dec 14, 1999 this sequence version replaced gi:6503313.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1219: contig of 1219 bp in length
* 1220 4866: gap of unknown length
* 4867 13049: contig of 4536 bp in length
* 9403 13049: gap of unknown length
* 13050 18200: contig of 5151 bp in length
* 18201 21846: gap of unknown length
* 21847 28549: contig of 6703 bp in length
* 28550 32196: gap of unknown length
* 32196 54074: contig of 18233 bp in length
* 54074 54075: gap of unknown length
* 54075 68978: contig of 14904 bp in length
* 68978 72624: gap of unknown length
* 72624 93784: contig of 21160 bp in length
* 93785 97430: gap of unknown length
* 97431 116930: contig of 19500 bp in length
* 116931 120576: gap of unknown length
* 120577 134768: contig of 14192 bp in length
* 134769 138414: gap of unknown length
* 138415 164480: contig of 28066 bp in length
* 164481 168127: gap of unknown length
* 168127 192568: contig of 24442 bp in length
* 192569 196214: gap of unknown length
* 196215 240000: contig of 43786 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
BASE COUNT 59361 a 41510 c 41283 g 57734 t 40112 others
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Query Match          6.2%; Score 30; DB 2; Length 240000;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATTGCAGATGTCGACCCACCGTCGCTGCC 31
|||||
Db 178588 GATTGCAGATGTCGACCCACCGTCGCTGCC 178559

RESULT 13
HSJ395C13/c LOCUS HSJ395C13 150336 bp DNA linear PRI 02-MAR-2000
DEFINITION Human DNA sequence from clone RP3-395C13 on chromosome 6q25.2-26.
Contains STSs, GSSs and a putative CpG island, complete sequence.
ACCESSION AL117344
VERSION AL117344.12 GI:6634463
KEYWORDS HTG; CpG island.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 150336)
AUTHORS Laird,G.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
COMMENT On Dec 23, 1999 this sequence version replaced gi:6523733.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; SW., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-395C13 is
from the library RPCI-3 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RP3-395C13. This
sequence was generated from part of bacterial clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6.
FEATURES             Location/Qualifiers
     source           1..150336
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="q25.2-26"
                     /clone="RP3-395C13"
                     /clone_lib="RPCI-3"
     repeat_region    1..237
                     /note="AluX repeat: matches 1..237 of consensus"
     repeat_region    250..504
                     /note="L1M4 repeat: matches 3829..4093 of consensus"
                     /note="L1M4 repeat: matches 3829..4093 of consensus"
     repeat_region    506..1074
                     /note="MER73 repeat: matches 54..634 of consensus"
                     /note="MER73 repeat: matches 54..634 of consensus"
     repeat_region    1071..1142
                     /note="MER66B repeat: matches 9..80 of consensus"
     repeat_region    1143..1438
                     /note="AluX repeat: matches 1..295 of consensus"
     repeat_region    1439..1843
                     /note="MER66B repeat: matches 79..486 of consensus"
     misc_feature     1774..2182
                     /note="match: GSS: Em:AQ712830"
     misc_feature     1786..2449
                     /note="match: GSS: Em:AQ743356"
     repeat_region    1844..1901
                     /note="MER73 repeat: matches 1..62 of consensus"
     repeat_region    2270..2416
                     /note="L1M4 repeat: matches 6717..6864 of consensus"
     repeat_region    2417..2728
                     /note="AluX repeat: matches 1..312 of consensus"
     repeat_region    2729..3089
                     /note="L1M4 repeat: matches 6864..7217 of consensus"
     repeat_region    3090..3381
                     /note="AluJb repeat: matches 1..286 of consensus"
     repeat_region    3382..3577
                     /note="L1M4 repeat: matches 7217..7414 of consensus"
     repeat_region    4253..4501
                     /note="AluJo repeat: matches 42..287 of consensus"
     repeat_region    5315..5559
                     /note="L1M4 repeat: matches 7410..7674 of consensus"

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repeat_region 5857. .6153
/note="AluY repeat: matches 12. .308 of consensus"
repeat_region 6289. .6602
/note="AluYb8 repeat: matches 1. .313 of consensus"
repeat_region 6610. .6837
/note="AluSp repeat: matches 1. .300 of consensus"
repeat_region 7519. .7637
/note="L1R16C repeat: matches 86. .208 of consensus"
repeat_region 7638. .8168
/note="MER1A repeat: matches 1. .527 of consensus"
repeat_region 8169. .8325
/note="L1R16C repeat: matches 208. .351 of consensus"
repeat_region 8576. .8773
/note="MIR repeat: matches 33. .230 of consensus"
repeat_region 8955. .9352
/note="MER57B repeat: matches 1. .403 of consensus"
repeat_region 9671. .9767
/note="L2 repeat: matches 2294. .2389 of consensus"
repeat_region 9818. .10015
/note="L2 repeat: matches 2543. .2750 of consensus"
repeat_region 10049. .10292
/note="MER8 repeat: matches 2. .239 of consensus"
repeat_region 10668. .11164
/note="MLR1B repeat: matches 54. .564 of consensus"
misc_feature complement(11061. .11548)
/note="match: GSS: Em:AQ0567270"
repeat_region 11272. .11383
/note="L1MC5 repeat: matches 7676. .7783 of consensus"
repeat_region 11912. .12069
/note="MIR repeat: matches 48. .240 of consensus"
misc_feature 12124. .14438
/note="CpG island"
evidences=not_experimental
repeat_region 13176. .13202
/note="9 copies 3 mer gag 96% conserved"
repeat_region 17042. .17173
/note="AluJo repeat: matches 2. .134 of consensus"
repeat_region 17191. .17475
/note="AluJo repeat: matches 1. .291 of consensus"
repeat_region 17758. .17867
/note="MIR repeat: matches 20. .153 of consensus"
repeat_region 17896. .18173
/note="MIR repeat: matches 3. .262 of consensus"
repeat_region 18128. .18182
/note="L2 repeat: matches 2699. .2746 of consensus"
repeat_region 18318. .18459
/note="FLAM C repeat: matches 1. .133 of consensus"
repeat_region 19810. .19928
/note="L2 repeat: matches 2633. .2750 of consensus"
misc_feature 20131. .20372
/note="match: STS: Em:H66317"
repeat_region 21259. .21591
/note="L1MC4 repeat: matches 7634. .7976 of consensus"
repeat_region 21585. .23046
/note="L1MEC repeat: matches 1027. .2134 of consensus"
misc_feature complement(22773. .23157)
/note="match: GSS: Em:AQ054658"
repeat_region 23974. .24075
/note="L1ME repeat: matches 5751. .5864 of consensus"
repeat_region 24739. .24766
/note="L4 copies 2 mer tg 100% conserved"
repeat_region 24947. .25271
/note="AluSp repeat: matches 1. .313 of consensus"
repeat_region 26360. .26599
/note="MLR1G repeat: matches 23. .250 of consensus"
repeat_region 26777. .26880
/note="MLR1H repeat: matches 430. .542 of consensus"
repeat_region 2749. .27558
/note="AluJo repeat: matches 1. .305 of consensus"
repeat_region 27608. .27902
/note="AluSC repeat: matches 2. .296 of consensus"
repeat_region 29348. .29826
/note="MLR1D repeat: matches 1. .501 of consensus"

repeat_region 30094. .30193
/note="50 copies 2 mer cc 65% conserved"
repeat_region 32671. .33086
/note="L2 repeat: matches 2267. .2695 of consensus"
repeat_region 33513. .33558
/note="MIR repeat: matches 99. .145 of consensus"
repeat_region 34826. .35127
/note="AluX repeat: matches 1. .293 of consensus"
repeat_region 36069. .36166
/note="MIR repeat: matches 119. .227 of consensus"
repeat_region 36227. .36527
/note="AluY repeat: matches 1. .304 of consensus"
repeat_region 37336. .37624
/note="AluSq repeat: matches 1. .291 of consensus"
repeat_region 38649. .38748
/note="MER91B repeat: matches 79. .179 of consensus"
repeat_region 38763. .38893
/note="MER91B repeat: matches 1. .123 of consensus"
repeat_region 39165. .39317
/note="MIR repeat: matches 31. .214 of consensus"
repeat_region 40216. .40397
/note="MLT1J repeat: matches 342. .515 of consensus"
repeat_region 40398. .41010
/note="L1PA10 repeat: matches 5543. .6158 of consensus"
repeat_region 41011. .41318
/note="MLT1J repeat: matches 5. .342 of consensus"
repeat_region 41622. .41734
/note="L2 repeat: matches 2620. .2744 of consensus"
repeat_region 41904. .42172
/note="AluX repeat: matches 52. .311 of consensus"
misc_feature 42753. .43222
/note="match: GSS: Em:AQ807609"
repeat_region 42787. .43087
/note="AluSC repeat: matches 1. .301 of consensus"
repeat_region 43143. .43243
/note="MER5B repeat: matches 1. .104 of consensus"
repeat_region 43308. .43493
/note="L1MD2 repeat: matches 5873. .6071 of consensus"
repeat_region 43740. .43810
/note="L1MD3 repeat: matches 7666. .7740 of consensus"
repeat_region 43865. .43912
/note="MER5B repeat: matches 129. .176 of consensus"
repeat_region 43981. .44030
/note="25 copies 2 mer ta 72% conserved"

Query Match 6.0%; Score 29; DB 9: Length 150336;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGTGAGCCACCGTGCCTGGCCAGATTTTT 39
|||||
Db 73670 TGTGAGCCACCGTGCCTGGCCAGATTTTT 73642

RESULT 14
AC026947/c AC026947 153234 bp DNA linear HTG 24-AUG-2002
LOCUS Homo sapiens chromosome 11 clone RP11-305L22 map 11, WORKING DRAFT
DEFINITION SEQUENCE, 13 unordered pieces.
ACCESSION AC026947
VERSION AC026947.2 GI:7622423
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 153234)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 11, clone RP11-305L22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 153234)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McSwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivier, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severly, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tsefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 153234)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F., Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McSwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivier, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severly, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tsefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 20, 2000 this sequence version replaced gi:7328812.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7852
Center clone name: 305_L_22

----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145261 bases at least Q40
Consensus quality: 149899 bases at least Q30
Consensus quality: 151298 bases at least Q20
Insert size: 139000; agarose-fp
Insert size: 152034; sum-of-ctnigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 1285: contig of 1285 bp in length
* 1286 1385: gap of 100 bp
* 1386 4149: contig of 2764 bp in length
* 4150 4249: gap of 100 bp
* 4250 9346: contig of 5097 bp in length
* 9347 9446: gap of 100 bp
* 9447 15111: contig of 5665 bp in length
* 15112 15211: gap of 100 bp
* 15212 22415: contig of 7204 bp in length
* 22416 22515: gap of 100 bp
* 22516 33763: contig of 11248 bp in length
* 33764 33863: gap of 100 bp
* 33864 44898: contig of 11035 bp in length
* 44899 44998: gap of 100 bp
* 44999 55715: contig of 10717 bp in length
* 55716 55815: gap of 100 bp
* 55816 68530: contig of 12715 bp in length
* 68531 68630: gap of 100 bp
* 68631 83353: contig of 14723 bp in length
* 83354 83453: gap of 100 bp
* 83454 98362: contig of 14909 bp in length
* 98363 98462: gap of 100 bp
* 98463 123453: contig of 24991 bp in length
* 123454 123553: gap of 100 bp
* 123554 153234: contig of 29681 bp in length.

FEATURES

Source
1. 153234
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/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-305L22"
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misc_feature
1. 1285
/notes="assembly_fragment"
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1386. 4149
/notes="assembly_fragment"
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4250. 9346
/notes="assembly_fragment"
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9447. 15111
/notes="assembly_fragment"
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vector_side:right
33864. 44898
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44999. 55715
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misc_feature
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vector_side:right
55816. 68530
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68631. 83353
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83454. 98362
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98463. 123453
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123554. 153234
/notes="assembly_fragment"
BASE COUNT 43264 a 32774 c 32544 g 43451 t 1201 others
ORIGIN

Query Match

6.0%; Score 29; DB 2; Length 153234;

Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGTGAGCACCGTGCCTGGCCAGATTTTTT 39

Db 134823 TGTGAGCACCGTGCCTGGCCAGATTTTTT 134795

RESULT 15

AC113193 AC113193 182208 bp DNA linear PRI 17-AUG-2002
Homo sapiens chromosome 11, clone RP11-1026G19, complete sequence.

AC113193 AC113193 6 Gi:22296723

VERSION AC113193.6

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 182208) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 11, clone RP11-1026G19

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 182208)

Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,V., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Gardyna,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Lander,E., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
Miengwa,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,J., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (26-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 182208)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (26-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 182208)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 182208)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

TITLE

JOURNAL

COMMENT

Submitted (17-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 17, 2002 this sequence version replaced gi:22123384.
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L21157

Center clone name: 1026_G_19

Only the first 182.2 kilobases of this clone are being submitted.
The remainder overlaps accession number AC023950 [WICGR project
L6298].

FEATURES

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 85.7978 Seconds
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12756.396 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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14	26	5.3	169739	24	ABO88186	Human osteoblast d
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C 116	23	4.7	161425	22	AAH02340	Human AKAP10 gene	C 189	22	4.5	7042	22	AAH91128	Wild type Apar-1 c
C 117	23	4.7	162025	22	AAH02339	Human AKAP10 gene	C 190	22	4.5	7042	24	AAK93574	Human apoptotic pr
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C 126	22	4.5	145	22	AAK27765	Human secreted pro	C 199	22	4.5	11076	22	AAK06733	Human reproductive
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C 132	22	4.5	342	22	AAI80299	Human polynucleoti	C 205	22	4.5	12758	22	ABA15345	Human nervous syst
C 133	22	4.5	361	22	AAK58167	Human immune/haema	C 206	22	4.5	12842	22	ABA20815	Human nervous syst
C 134	22	4.5	380	22	AAK57621	Human immune/haema	C 207	22	4.5	12970	22	AAK05001	Human reproductive
C 135	22	4.5	385	22	AAI88472	Human polynucleoti	C 208	22	4.5	12970	23	ABL97894	Human testicular a
C 136	22	4.5	389	22	AAK38637	Novel human diagno	C 209	22	4.5	13204	20	AAK32189	Human platelet gly
C 137	22	4.5	390	22	AAI80520	Human polynucleoti	C 210	22	4.5	13401	22	AAK89558	Human digestive sy
C 138	22	4.5	390	22	AAI90572	Human polynucleoti	C 211	22	4.5	13403	22	AAK89557	Human digestive sy
C 139	22	4.5	400	14	AAQ59771	Human brain expres	C 212	22	4.5	13493	22	AAK74889	Human immune/haema
C 140	22	4.5	403	21	AAH30089	Human colon cancer	C 213	22	4.5	13493	22	AAK82826	Human immune/haema
C 141	22	4.5	403	22	AAH30046	Human polynucleoti	C 214	22	4.5	14040	22	ABA08209	Human ovarian and
C 142	22	4.5	419	22	AAK70168	Human immune/haema	C 215	22	4.5	14040	22	AAK02790	Human reproductive
C 143	22	4.5	419	22	AAK70170	Human immune/haema	C 216	22	4.5	14040	22	AAK07517	Human reproductive
C 144	22	4.5	433	22	AAI84165	Human polynucleoti	C 217	22	4.5	18389	22	AAK74864	Human immune/haema
C 145	22	4.5	448	22	AAK35438	Human cardiovascular	C 218	22	4.5	18389	22	AAK82632	Human immune/haema
C 146	22	4.5	452	22	AAI32076	Human polynucleoti	C 219	22	4.5	20365	22	AAK70165	Human immune/haema
C 147	22	4.5	471	22	AAI25057	Human breast cance	C 220	22	4.5	20365	22	AAK70165	Human immune/haema
C 148	22	4.5	486	23	ABV09226	Human prostate exp	C 221	22	4.5	20365	22	AAK82631	Human immune/haema
C 149	22	4.5	531	22	ABAI1133	Human nervous syst	C 222	22	4.5	20365	22	AAK82631	Human immune/haema
C 150	22	4.5	569	23	ABV39377	Human prostate exp	C 223	22	4.5	20444	22	AAK34643	Human DNA for a no
C 151	22	4.5	569	23	ABV43977	Human prostate exp	C 224	22	4.5	20444	22	AAK06734	Human reproductive
C 152	22	4.5	609	22	AAK72134	Human immune/haema	C 225	22	4.5	20444	22	AAK66859	Human immune/haema
C 153	22	4.5	609	22	AAK72135	Human immune/haema	C 226	22	4.5	20444	22	AAK62840	Human breast or ov
C 154	22	4.5	646	22	AAK36382	Human cardiovascular	C 227	22	4.5	21446	22	AAK70163	Human immune/haema
C 155	22	4.5	653	22	AAH64864	Human secreted pro	C 228	22	4.5	21446	22	AAK70163	Human immune/haema

229	4.5	21446	22	AAK82629	Human immune/haema	c 302	21	4.3	358	22	AAI89752	Human polynucleoti
230	4.5	21446	22	AAK82629	Human immune/haema	c 303	21	4.3	359	22	AAI85150	Human polynucleoti
231	4.5	21621	22	AAK74867	Human immune/haema	c 304	21	4.3	365	24	ABL84956	Human ovarian canc
232	4.5	21724	22	AAK86125	Human immune/haema	c 305	21	4.3	366	24	ABO56337	Human colon cancer
233	4.5	21724	22	AAK86125	Human immune/haema	c 306	21	4.3	370	22	AAI83153	Human polynucleoti
234	4.5	21727	22	AAK86126	Human immune/haema	c 307	21	4.3	378	22	AAI88343	Human polynucleoti
235	4.5	21727	22	AAK86126	Human immune/haema	c 308	21	4.3	380	22	AAI91393	Human polynucleoti
236	4.5	22299	22	AAK40317	DNA encoding novel	c 309	21	4.3	392	22	AAI92469	Human polynucleoti
237	4.5	22299	22	AAK40317	DNA encoding novel	c 310	21	4.3	393	22	AAI92804	Human polynucleoti
238	4.5	23378	22	AAK89555	Human digestive sy	c 311	21	4.3	393	22	AAI92804	Human polynucleoti
239	4.5	23378	22	AAK89555	Human digestive sy	c 312	21	4.3	393	22	AAI92804	Human polynucleoti
240	4.5	23378	22	AAK89555	Human digestive sy	c 313	21	4.3	393	22	AAI92804	Human polynucleoti
241	4.5	23457	22	AAK74866	Human immune/haema	c 314	21	4.3	394	22	AAI92804	Human polynucleoti
242	4.5	26427	22	ABA20762	Human nervous syst	c 315	21	4.3	397	24	ABK46028	CDNA encoding colo
243	4.5	31405	22	AAK70763	Human nervous syst	c 316	21	4.3	400	23	AAK75460	DNA encoding novel
244	4.5	31405	22	AAK70763	Human nervous syst	c 317	21	4.3	401	22	AAK96184	Human neurogulin g
245	4.5	31405	22	AAK83153	Human immune/haema	c 318	21	4.3	401	22	AAK96185	Human neurogulin g
246	4.5	32134	22	ABA15354	Human immune/haema	c 319	21	4.3	401	22	AAK96186	Human neurogulin g
247	4.5	32134	22	ABA15354	Human immune/haema	c 320	21	4.3	401	22	AAK96666	Human neurogulin g
248	4.5	32134	22	ABA15354	Human immune/haema	c 321	21	4.3	401	22	AAK97677	Human neurogulin g
249	4.5	32170	22	AAK70763	Human reproductive	c 322	21	4.3	401	22	AAK97677	Human neurogulin g
250	4.5	32196	22	AAK89555	Human nervous syst	c 323	21	4.3	401	22	AAK98159	Human neurogulin g
251	4.5	33147	22	AAK67282	Human immune/haema	c 324	21	4.3	402	22	AAK98679	Human ovarian canc
252	4.5	33501	22	AAK64829	Human immune/haema	c 325	21	4.3	404	23	ABV43752	Human prostate exp
253	4.5	39328	24	ABL51800	Human lipase endot	c 326	21	4.3	405	22	AAI84455	Human polynucleoti
254	4.5	47090	22	AAK68725	Human immune/haema	c 327	21	4.3	405	22	AAI91879	Human polynucleoti
255	4.5	47090	22	AAK68725	Human immune/haema	c 328	21	4.3	405	23	ABV34903	Human prostate exp
256	4.5	48203	22	AAK70161	Human immune/haema	c 329	21	4.3	408	20	AAK56607	Human W32430. RC DN
257	4.5	48203	22	AAK81663	Human immune/haema	c 330	21	4.3	408	22	AAI85328	Human polynucleoti
258	4.5	48203	22	AAK82628	Human immune/haema	c 331	21	4.3	409	22	AAI82369	Human polynucleoti
259	4.5	48204	22	AAK70164	Human immune/haema	c 332	21	4.3	414	21	AAH30988	Human colon cancer
260	4.5	48204	22	AAK81666	Human immune/haema	c 333	21	4.3	414	23	ABV43358	Human prostate exp
261	4.5	48204	22	AAK82630	Human immune/haema	c 334	21	4.3	422	20	ABV19990	Human prostate exp
262	4.5	49312	21	AAH51594	Human genomic sequ	c 335	21	4.3	424	20	AAK56588	Human prostate exp
263	4.5	50575	23	ABL29244	Drosophila melanog	c 336	21	4.3	431	22	AAK65038	Human R87078. DNA f
264	4.5	58708	22	AAK64739	Human immune/haema	c 337	21	4.3	442	20	AAK56600	Human immune/haema
265	4.5	59065	24	ABL42416	Human immune/haema	c 338	21	4.3	451	24	ABQ89572	Human prostate exp
266	4.5	122186	22	AAK89560	Human histone deac	c 339	21	4.3	458	23	ABV49750	Human prostate exp
267	4.5	128978	24	AAK83459	Human cDNA differe	c 340	21	4.3	463	22	AAK79697	Human immune/haema
268	4.5	145831	24	ABL62309	Colon adenocarcino	c 341	21	4.3	463	22	AAK89409	Human digestive sy
269	4.5	145831	24	ABL62309	Colon adenocarcino	c 342	21	4.3	475	22	AAK79696	Human immune/haema
270	4.5	145831	24	ABL62309	Colon adenocarcino	c 343	21	4.3	475	23	ABV52832	Human prostate exp
271	4.5	145831	24	ABL62309	Colon adenocarcino	c 344	21	4.3	477	23	AAI88018	Human polynucleoti
272	4.5	145831	24	ABL62309	Colon adenocarcino	c 345	21	4.3	477	23	ABV40621	Human prostate exp
273	4.5	149480	24	ABL61947	Kidney cancer rela	c 346	21	4.3	481	20	AAK83080	Human immune/haema
274	4.5	149480	24	ABL61947	Kidney cancer rela	c 347	21	4.3	482	20	AAK56596	Human N54909. RC DN
275	4.5	175737	24	ABK83571	Human cDNA differe	c 348	21	4.3	482	24	ABL67344	Thyroid cancer rel
276	4.3	111	24	ABN86810	Human gas vacuole	c 349	21	4.3	511	23	ABV57220	Human prostate exp
277	4.3	111	22	AAK68344	Human immune/haema	c 350	21	4.3	529	23	ABV18570	Human prostate exp
278	4.3	111	22	AAK85110	Human immune/haema	c 351	21	4.3	552	22	ABA17597	Human nervous syst
279	4.3	194	21	AAK404989	Human secreted pro	c 352	21	4.3	555	22	AAK82704	Human immune/haema
280	4.3	208	21	AAK21550	Human secreted pro	c 353	21	4.3	565	22	AAK82705	Human immune/haema
281	4.3	243	22	AAK83640	Human immune/haema	c 354	21	4.3	570	23	ABV51378	Human prostate exp
282	4.3	252	20	AAK56612	Human 689191 DNA f	c 355	21	4.3	622	23	ABV48353	Human prostate exp
283	4.3	263	15	AAQ77248	Human genome fragm	c 356	21	4.3	626	24	ABN63700	Human cancer relat
284	4.3	263	20	AAK56611	Human 840069 DNA f	c 357	21	4.3	631	21	AAA16349	Human colon cancer
285	4.3	286	22	AAK60210	Human immune/haema	c 358	21	4.3	639	23	ABV51454	Human prostate exp
286	4.3	292	22	AAI81021	Human polynucleoti	c 359	21	4.3	662	24	ABN61073	Human cancer relat
287	4.3	296	22	ABA18375	Human nervous syst	c 360	21	4.3	700	22	AAH92917	Human inflammatory
288	4.3	300	21	AAA00667	Human colon cancer	c 361	21	4.3	724	21	AAA01956	Human colon cancer
289	4.3	309	22	AAI88715	Human polynucleoti	c 362	21	4.3	725	22	AAK22964	Human prostate can
290	4.3	309	22	AAK59144	Human immune/haema	c 363	21	4.3	745	21	AAA47443	Human TANGO 222 co
291	4.3	319	22	AAI37510	Human musculoskele	c 364	21	4.3	760	24	ABQ88854	Human prostate exp
292	4.3	329	21	AAK13305	Human secreted pro	c 365	21	4.3	795	22	AAH05002	Human cDNA clone (
293	4.3	334	22	AAK55819	Human immune/haema	c 366	21	4.3	797	23	ABV13790	Human prostate exp
294	4.3	337	22	AAK38182	Novel human diagn	c 367	21	4.3	801	22	AAH03746	Human cDNA clone (
295	4.3	343	22	AAK74601	Human immune/haema	c 368	21	4.3	801	24	ABQ89387	Human prostate exp
296	4.3	343	22	AAK74602	Human immune/haema	c 369	21	4.3	847	22	AAH07714	Human cDNA clone (
297	4.3	351	22	AAK62549	Human immune/haema	c 370	21	4.3	856	22	AAH03627	Human cDNA clone (
298	4.3	351	22	AAK64729	Novel human polynu	c 371	21	4.3	941	22	AAK78948	Human immune/haema
299	4.3	354	23	ABV56004	Human prostate exp	c 372	21	4.3	963	23	AAK68880	DNA encoding novel
300	4.3	356	22	AAK61263	Human immune/haema	c 373	21	4.3	978	24	ABK13711	DNA encoding s-acy
301	4.3	357	20	AAK56610	Human HUMGS02649 D	c 374	21	4.3	1001	21	AAH51395	Human PGDH related

375	21	4.3	1001	21	AAH51396	Human PGDH related	C 448	21	4.3	7373	22	AA541749	Genomic sequence #
376	21	4.3	1002	22	AAH06938	Human reproductive	C 449	21	4.3	7417	22	AAK70374	Human immune/haema
377	21	4.3	1092	24	AAV31336	Mortierella alpina	C 450	21	4.3	7855	22	AAK70210	Human immune/haema
378	21	4.3	1095	19	ABL99927	Human secretory po	C 451	21	4.3	8140	22	ABA20556	Human nervous syst
379	21	4.3	1167	20	AAH97867	Human secreted pro	C 452	21	4.3	8167	22	AAH05420	Human reproductive
380	21	4.3	1231	24	ABN86805	Human gas vacuole	C 453	21	4.3	8223	22	AAK65546	Human immune/haema
381	21	4.3	1352	22	AAH08423	Human secreted pro	C 454	21	4.3	8253	22	AA540470	DNA encoding human
382	21	4.3	1370	20	AAH97820	Human secreted pro	C 455	21	4.3	8253	22	AAH04087	Human reproductive
383	21	4.3	1450	24	ABL41337	Human PF11D subuni	C 456	21	4.3	8326	22	AA539819	Genomic sequence #
384	21	4.3	1496	22	AAH03200	Human reproductive	C 457	21	4.3	8326	22	AAK90175	Human digestive sy
385	21	4.3	1496	22	AAH06934	Human reproductive	C 458	21	4.3	8349	23	AA580324	DNA encoding novel
386	21	4.3	1496	22	AAH06941	Human reproductive	C 459	21	4.3	8418	22	AA541906	Genomic sequence #
387	21	4.3	1511	22	AAH15324	Human cDNA sequenc	C 460	21	4.3	8448	22	AA540680	DNA encoding human
388	21	4.3	1572	22	AAH08366	Human secreted pro	C 461	21	4.3	8448	22	AAH06568	Human reproductive
389	21	4.3	1598	22	ABA13401	Human nervous syst	C 462	21	4.3	8487	22	AAH37089	Human musculoskele
390	21	4.3	1614	22	AAH17079	Human cDNA sequenc	C 463	21	4.3	8535	22	AAK77167	Human immune/haema
391	21	4.3	1671	22	AA541905	Genomic sequence #	C 464	21	4.3	8807	22	AA535915	Human cardiovascular
392	21	4.3	1672	23	ABK42296	Genomic sequence #	C 465	21	4.3	9192	22	AAH35853	Human musculoskele
393	21	4.3	1765	22	AAH14927	Human cDNA sequenc	C 466	21	4.3	9192	23	ABK42359	Genomic sequence #
394	21	4.3	1793	22	AAK66938	Human immune/haema	C 467	21	4.3	9397	22	AAK78065	Human immune/haema
395	21	4.3	1965	22	AAI60430	Human polynucleoti	C 468	21	4.3	9439	22	AAI99373	Human excretory re
396	21	4.3	2022	22	AAH73397	Human G protein co	C 469	21	4.3	9439	22	AAH35859	Human musculoskele
397	21	4.3	2061	19	AAV63173	cDNA from clone da	C 470	21	4.3	9439	22	AAI63723	Human kidney relat
398	21	4.3	2066	20	AAH37716	Human cDNA clone D	C 471	21	4.3	9474	24	ABK50462	Human histamine re
399	21	4.3	2092	22	AA536430	Human cardiovascular	C 472	21	4.3	9566	22	AA540682	DNA encoding human
400	21	4.3	2320	21	AAK77434	Human ORFX ORF2989	C 473	21	4.3	9566	22	AAH06570	Human reproductive
401	21	4.3	2469	22	AAK87105	Human immune/haema	C 474	21	4.3	9629	22	AAH97855	Human neuroblastom
402	21	4.3	2473	22	AAK87106	Human immune/haema	C 475	21	4.3	9799	22	AAH97860	Human neuroblastom
403	21	4.3	2516	21	AA559323	DNA encoding a hum	C 476	21	4.3	10053	22	AAK73765	Human immune/haema
404	21	4.3	2566	22	AAH17845	Human cDNA sequenc	C 477	21	4.3	10053	24	ABN79990	Human chemically m
405	21	4.3	2702	22	AAK72621	Human immune/haema	C 478	21	4.3	10091	22	AAK69350	Human immune/haema
406	21	4.3	2713	22	AAK72622	Human immune/haema	C 479	21	4.3	10351	24	ABK88932	Human CDLE cDNA
407	21	4.3	2713	22	AAK72625	Human immune/haema	C 480	21	4.3	10388	22	AAI98966	Human excretory re
408	21	4.3	2713	22	AAK85252	Human immune/haema	C 481	21	4.3	10388	22	AAI63316	Human kidney relat
409	21	4.3	2749	22	AAH18717	Human cDNA sequenc	C 482	21	4.3	10884	21	AAK66549	Human kinesin-like
410	21	4.3	2813	22	AAK77165	Human immune/haema	C 483	21	4.3	10989	22	AAK69531	Human immune/haema
411	21	4.3	2813	22	AAK77166	Human immune/haema	C 484	21	4.3	11283	22	AAK82965	Human immune/haema
412	21	4.3	2904	22	AAH17918	Human cDNA sequenc	C 485	21	4.3	11294	22	AAK82968	Human immune/haema
413	21	4.3	3009	22	AAI98965	Human excretory re	C 486	21	4.3	11453	22	AA542059	Genomic sequence #
414	21	4.3	3011	22	AA541928	Human kidney relat	C 487	21	4.3	11453	22	AA542060	Genomic sequence #
415	21	4.3	3011	22	AA535102	Genomic sequence #	C 488	21	4.3	11453	22	AAK70914	Human immune/haema
416	21	4.3	3011	22	AA535102	DNA #52 encoding h	C 489	21	4.3	11453	22	AAK70915	Human immune/haema
417	21	4.3	3284	19	AAV31337	Mortierella alpina	C 490	21	4.3	11742	22	ABA20557	Human nervous syst
418	21	4.3	3598	22	AAI64774	Human Glucose tran	C 491	21	4.3	11742	22	AAK70609	Human immune/haema
419	21	4.3	3806	22	AAK75099	Human immune/haema	C 492	21	4.3	12774	22	ABA15302	Human nervous syst
420	21	4.3	3851	21	AAK77558	Human ORFX ORF3113	C 493	21	4.3	12774	22	AAK72738	Human immune/haema
421	21	4.3	4066	19	AAV59181	Human bak gene pro	C 494	21	4.3	13216	22	AAK73092	Human immune/haema
422	21	4.3	4106	22	AAH05051	Human reproductive	C 495	21	4.3	13216	22	AAK87561	Human immune/haema
423	21	4.3	4106	23	ABL97944	Human testicular a	C 496	21	4.3	13309	22	AAK83980	Human immune/haema
424	21	4.3	4192	20	AAH00725	Human aggrecan deg	C 497	21	4.3	13392	22	AA540469	DNA encoding human
425	21	4.3	4224	22	AAI99372	Human excretory re	C 498	21	4.3	13392	22	AAH04086	Human reproductive
426	21	4.3	4224	22	AAI63722	Human kidney relat	C 499	21	4.3	14221	22	AA540881	DNA encoding human
427	21	4.3	4300	22	AAK82193	Human immune/haema	C 500	21	4.3	14221	22	AAH06569	Human reproductive
428	21	4.3	4301	22	AAI68146	Human aggrcanase-	C 501	21	4.3	14221	22	AA527844	DNA encoding novel
429	21	4.3	4303	21	AA595826	Human metalloprote	C 502	21	4.3	14846	22	AAK83135	Human immune/haema
430	21	4.3	4303	22	AA546100	Human DNA encoding	C 503	21	4.3	15254	22	AAK83137	Human immune/haema
431	21	4.3	4407	21	AA537111	Human PRO1563 (UNQ	C 504	21	4.3	15255	22	AAK83136	Human immune/haema
432	21	4.3	4407	22	AAH54426	Probe #46 used in	C 505	21	4.3	15256	22	AAK83134	Human immune/haema
433	21	4.3	4430	22	AAH18210	Human cDNA sequenc	C 506	21	4.3	15275	22	AA535975	Human cardiovascular
434	21	4.3	4688	22	ABA18600	Human nervous syst	C 507	21	4.3	15812	22	ABA18253	Human nervous syst
435	21	4.3	4688	22	AAI99654	Human expressed po	C 508	21	4.3	15843	22	AA536896	Human cardiovascular
436	21	4.3	4688	22	AAK83279	Human immune/haema	C 509	21	4.3	15843	22	AAK67635	Human immune/haema
437	21	4.3	4758	22	AAK83830	Human immune/haema	C 510	21	4.3	16106	22	AAK83468	Human immune/haema
438	21	4.3	5000	24	ABK86965	Human STG genomic	C 511	21	4.3	16161	22	AAK83469	Human immune/haema
439	21	4.3	5159	22	AAH37342	Human musculoskele	C 512	21	4.3	16488	24	AA525856	Human diptheria t
440	21	4.3	5281	22	AAH05101	Human reproductive	C 513	21	4.3	16488	24	AA525895	Human diptheria t
441	21	4.3	5281	23	ABL97994	Human testicular a	C 514	21	4.3	16596	22	AAK90993	Human digestive sy
442	21	4.3	5284	22	AAH05100	Human reproductive	C 515	21	4.3	16596	22	AA532028	Human liver associ
443	21	4.3	5284	23	ABL97993	Human testicular a	C 516	21	4.3	16596	22	ABN90383	Human liver antige
444	21	4.3	5460	24	ABK51683	Human ABCG5 upstre	C 517	21	4.3	16772	22	ABA20862	Human nervous syst
445	21	4.3	5805	22	AAH05695	Human reproductive	C 518	21	4.3	16774	22	AA536895	Human cardiovascular
446	21	4.3	6534	22	AAH02766	Human reproductive	C 519	21	4.3	16774	22	AA536898	Human cardiovascular
447	21	4.3	7373	22	ABA06810	Human genomic DNA	C 520	21	4.3	16774	22	AAK67634	Human immune/haema

521	21	4.3	16774	22	AAK67637	Human immune/haema
522	21	4.3	16817	22	AAK87099	Human immune/haema
C 523	21	4.3	16852	22	AAK72507	Human immune/haema
C 524	21	4.3	16852	22	AAK84641	Human immune/haema
C 525	21	4.3	16876	22	AAK65624	Human immune/haema
C 526	21	4.3	16876	22	AAK65685	Human immune/haema
C 527	21	4.3	17165	22	AAK72506	Human immune/haema
C 528	21	4.3	17165	22	AAK84640	Human immune/haema
C 529	21	4.3	17761	22	AAK79415	Human immune/haema
530	21	4.3	17761	23	ABK42709	Genomic sequence #
C 531	21	4.3	18878	22	AAK37441	Human musculoskele
C 532	21	4.3	18925	22	ABA81553	Human phospholipid
C 533	21	4.3	18925	24	AAS94565	Human phospholipid
C 534	21	4.3	18925	24	AAS94692	Human phospholipid
C 535	21	4.3	19387	22	AAS34561	Human DNA for a no
536	21	4.3	19497	22	AAK85311	Human immune/haema
537	21	4.3	19965	22	AAK73166	Human immune/haema
538	21	4.3	19965	24	ABK69932	Human secreted pro
539	21	4.3	20261	22	ABA07368	Human pancreatic c
540	21	4.3	20261	22	AAS30061	Human lung antigen
C 541	21	4.3	20261	22	AAK65412	Human immune/haema
542	21	4.3	20261	22	AAK91099	Human digestive sy
543	21	4.3	20420	22	AAK73165	Human immune/haema
544	21	4.3	20420	24	ABK69933	Human secreted pro
C 545	21	4.3	20433	22	AAK65626	Human immune/haema
C 546	21	4.3	20991	22	AAK87545	Human immune/haema
C 547	21	4.3	21732	22	AAS39820	Genomic sequence #
C 548	21	4.3	21732	22	AAK90176	Human digestive sy
C 549	21	4.3	21982	22	AAK67644	Human immune/haema
550	21	4.3	22161	23	ABK42133	Genomic sequence #
C 551	21	4.3	22467	22	AAS33423	DNA encoding human
552	21	4.3	22467	22	AAS33425	DNA encoding human
C 553	21	4.3	23109	22	AAK82298	Human immune/haema
554	21	4.3	23164	22	AAK79678	Human immune/haema
555	21	4.3	23855	22	AAI99411	Human excretory re
556	21	4.3	23855	22	AAI63761	Human kidney relat
C 557	21	4.3	23934	22	AAI36090	Human musculoskele
558	21	4.3	24279	22	AAK74999	Human immune/haema
559	21	4.3	24329	22	AAK75000	Human immune/haema
560	21	4.3	24329	21	AAK75856	Human immune/haema
C 561	21	4.3	24740	21	AAK87743	Human LMP-1 (HIMP-
C 562	21	4.3	24993	22	AAK65726	Human immune/haema
C 563	21	4.3	25131	22	AAK84544	Human immune/haema
C 564	21	4.3	25837	22	AAK85952	Human immune/haema
565	21	4.3	25895	22	AAK77832	Human immune/haema
C 566	21	4.3	26110	22	AAK65036	Human immune/haema
C 567	21	4.3	26110	22	AAK78526	Human immune/haema
C 568	21	4.3	26657	24	AAI72317	Human transporter
C 569	21	4.3	26664	21	AAK60207	Human transporter
570	21	4.3	26664	21	AAK60207	Human prostate can
571	21	4.3	26664	24	AAK98942	Human prostate can
572	21	4.3	26928	20	AAK232184	Human prothrombin
573	21	4.3	26928	22	ABA82620	Human HBM gene reg
574	21	4.3	26928	24	ABN95780	Gene #2278 used to
C 575	21	4.3	27571	22	ABK22779	Human high bone ma
C 576	21	4.3	27571	22	ABA19222	Human nervous syst
C 577	21	4.3	27572	22	ABA19221	Human nervous syst
578	21	4.3	27869	22	ABA19635	Human nervous syst
C 579	21	4.3	27869	22	AAK66517	Human immune/haema
580	21	4.3	29222	24	ABL39412	Human electron-tra
581	21	4.3	30620	22	AAK66931	Human immune/haema
C 582	21	4.3	30709	24	ABK87217	Human lipase, horm
583	21	4.3	31584	22	AAK81054	Human immune/haema
C 584	21	4.3	31741	22	ABA21231	Human nervous syst
585	21	4.3	31766	24	AAK22781	Human sulphate tra
C 586	21	4.3	32134	22	ABA07813	Human ovarian and
C 587	21	4.3	32134	22	AAK03615	Human reproductive
C 588	21	4.3	32152	22	AAS39621	Genomic sequence #
C 589	21	4.3	32152	22	AAK89020	Human digestive sy
C 590	21	4.3	32152	22	AAK91534	Human digestive sy
591	21	4.3	32152	22	AAI57791	Human colorectal c
C 592	21	4.3	32169	23	ABK43076	Genomic sequence #
593	21	4.3	32189	22	AAK04670	Human reproductive
594	21	4.3	32189	23	ABL97577	Human testicular a
C 595	21	4.3	32191	22	ABA07814	Human ovarian and
C 596	21	4.3	32191	22	AAK03616	Human reproductive
C 597	21	4.3	32194	22	AAK04340	Human amyloid beta
C 598	21	4.3	35972	24	ABK13076	Human immune/haema
C 599	21	4.3	36485	22	AAK68958	Human immune/haema
C 600	21	4.3	36485	22	AAK74751	Human immune/haema
C 601	21	4.3	36933	22	AAK66362	Human immune/haema
C 602	21	4.3	37959	22	AAK81763	Human immune/haema
603	21	4.3	38358	22	AAK73535	Human immune/haema
C 604	21	4.3	39746	23	ABL13398	Drosophila melanog
C 605	21	4.3	41159	22	AAK65631	Human immune/haema
C 606	21	4.3	43089	21	AAK36335	Genomic sequence o
C 607	21	4.3	43950	24	AAK36022	Human kinase genom
C 608	21	4.3	44211	22	AAK85974	Human immune/haema
609	21	4.3	44354	22	AAK77833	Human immune/haema
610	21	4.3	44354	22	AAK77836	Human immune/haema
611	21	4.3	44354	22	AAK77837	Human immune/haema
C 612	21	4.3	47090	22	AAK68725	Human immune/haema
C 613	21	4.3	47090	22	AAK78219	Human immune/haema
C 614	21	4.3	50000	21	AAK96364	Polymorphic repeat
615	21	4.3	50442	22	AAK73083	Human immune/haema
616	21	4.3	50442	22	AAK87551	Human immune/haema
617	21	4.3	51474	22	AAK97846	Human neuroblastom
C 618	21	4.3	52216	22	AAH28355	Nucleotide sequenc
C 619	21	4.3	52216	24	ABL50307	Human musashi prom
C 620	21	4.3	54863	22	AAK86025	Human immune/haema
621	21	4.3	54877	22	AAK86026	Human immune/haema
622	21	4.3	74962	22	AAK87551	Human immune/haema
C 623	21	4.3	81800	24	ABK84756	Human phosphatase
C 624	21	4.3	84495	24	AAS20588	Human methionine a
625	21	4.3	86080	24	ABQ88164	Human osteoblast d
626	21	4.3	86080	24	ABK83561	Human osteoblast d
C 627	21	4.3	112460	24	ABK83567	Human osteoblast d
C 628	21	4.3	119950	20	AAK90201	Human CDNA differe
629	21	4.3	121162	21	AAK66548	Human kinesin-like
C 630	21	4.3	121162	21	AAK66548	Human kinesin-like
C 631	21	4.3	121724	24	ABQ88143	Human osteoblast d
632	21	4.3	123219	23	AAH88703	Human DNA sequence
C 633	21	4.3	129722	24	ABQ88117	Human osteoblast d
C 634	21	4.3	139389	24	ABK84795	Human osteoblast d
635	21	4.3	145831	24	ABL62309	Colon adenocarcino
636	21	4.3	145831	24	ABL66806	Lung cancer relate
637	21	4.3	145831	24	ABL68588	Lung cancer relate
638	21	4.3	145831	24	ABL69213	Prostate cancer re
C 639	21	4.3	147708	24	ABQ88154	Human osteoblast d
C 640	21	4.3	154465	24	AAK28763	Human AKAP allelic
C 641	21	4.3	158245	24	AAK28762	Human AKAP allelic
C 642	21	4.3	160771	24	ABQ88179	Human osteoblast d
C 643	21	4.3	161425	22	AAH02340	Human AKAP10 gene
C 644	21	4.3	162025	22	AAH02339	Human AKAP10 gene
C 645	21	4.3	162025	24	AAK28758	Human AKAP allelic
C 646	21	4.3	162025	24	AAK28759	Human AKAP allelic
647	21	4.3	172570	24	ABQ88207	Human osteoblast d
648	21	4.3	174424	24	ABQ88122	Ovary cancer relat
649	21	4.3	178896	24	ABQ88146	Human osteoblast d
C 650	21	4.3	22930	24	ABK84349	Human CDNA differe
C 651	21	4.3	227968	24	ABK83497	Human CDNA differe
652	21	4.3	302250	24	ABL67703	Oesophagus cancer
C 653	21	4.3	302250	24	ABL67703	Oesophagus cancer
C 654	21	4.3	1503900	22	AAK95240	Human neuroregulin-1
655	21	4.3	1503900	22	AAK96733	Human neuroregulin-1
C 656	20	4.1	41	24	ABN86811	Human gas vacuole
657	20	4.1	41	24	ABL49895	Human Ras GTP enzy
658	20	4.1	45	22	AAI74714	Human silent SNP c
C 659	20	4.1	131	22	ABA18532	Human nervous syst
C 660	20	4.1	133	22	AAK86953	Human immune/haema
C 661	20	4.1	248	22	ABA11201	Human nervous syst
C 662	20	4.1	257	21	AAC23220	Human secreted pro
663	20	4.1	267	21	AAC00382	Human secreted pro
664	20	4.1	275	21	AAK16310	Human secreted pro
C 665	20	4.1	276	23	ABV50354	Human prostate exp
666	20	4.1	281	21	AAA45323	Human secreted exp

c 667	20	4.1	289	23	ABV56681	Human prostate exp
c 668	20	4.1	300	20	AA212665	Human gene express
c 669	20	4.1	300	20	AA398294	Human cancer cell
c 670	20	4.1	301	22	AAK65518	Human immune/haema
c 671	20	4.1	301	22	AAK62056	Human immune/haema
c 672	20	4.1	301	22	AAI62855	Human genomic DNA
c 673	20	4.1	303	20	AAV90033	EST clone DA390
c 674	20	4.1	304	21	AAAC21259	Human secreted pro
c 675	20	4.1	309	22	AAK95258	Human immune/haema
c 676	20	4.1	321	22	AAK57285	Novel human diagno
c 677	20	4.1	334	23	ABV07716	Human prostate exp
c 678	20	4.1	335	22	AAI89622	Human polynucleoti
c 679	20	4.1	337	22	AAI88453	Human polynucleoti
c 680	20	4.1	340	24	ABNG3483	Human cancer relat
c 681	20	4.1	342	22	AAI36458	Human musculoskele
c 682	20	4.1	351	23	ABV01239	Human prostate exp
c 683	20	4.1	352	23	ABV10408	Human prostate exp
c 684	20	4.1	354	22	AAI20745	Human breast cancer
c 685	20	4.1	359	22	AAK64316	Novel human polynu
c 686	20	4.1	360	22	AAI28945	Colon tumour relat
c 687	20	4.1	360	22	AAK65560	Novel human polynu
c 688	20	4.1	361	22	AAI90764	Human polynucleoti
c 689	20	4.1	361	22	AAK64709	Novel human polynu
c 690	20	4.1	365	22	AAI87820	Human polynucleoti
c 691	20	4.1	365	22	AAK60894	Human immune/haema
c 692	20	4.1	372	22	AAI86592	Human polynucleoti
c 693	20	4.1	380	22	AAI08195	Human breast cancer
c 694	20	4.1	381	24	ABL84961	Human ovarian can
c 695	20	4.1	382	24	ABN96516	Gene #3014 used to
c 696	20	4.1	384	22	AAI89017	Human polynucleoti
c 697	20	4.1	384	22	AAK62104	Human immune/haema
c 698	20	4.1	385	22	AAI81318	Human polynucleoti
c 699	20	4.1	391	24	ABL86195	Human ovarian can
c 700	20	4.1	392	23	AAK64572	DNA encoding novel
c 701	20	4.1	397	24	ABL86202	Human ovarian can
c 702	20	4.1	398	23	ABV31579	Human prostate exp
c 703	20	4.1	398	23	ABV40547	Human prostate exp
c 704	20	4.1	399	22	AAI84258	Human polynucleoti
c 705	20	4.1	399	24	ABL77510	Human ovarian can
c 706	20	4.1	401	24	ABL84120	Human ovarian can
c 707	20	4.1	403	22	AAI83109	Human polynucleoti
c 708	20	4.1	403	24	ABNG3060	Human cancer relat
c 709	20	4.1	404	24	ABL84531	Human ovarian can
c 710	20	4.1	405	23	ABV17327	Human prostate exp
c 711	20	4.1	406	22	AAI93723	Human polynucleoti
c 712	20	4.1	408	22	AAI83505	Human polynucleoti
c 713	20	4.1	408	23	ABV37645	Human prostate exp
c 714	20	4.1	410	22	AAI89973	Human polynucleoti
c 715	20	4.1	413	24	ABL87596	Human ovarian can
c 716	20	4.1	414	23	ABV10882	Human prostate exp
c 717	20	4.1	416	22	AAI81524	Human polynucleoti
c 718	20	4.1	416	22	AAI92116	Human polynucleoti
c 719	20	4.1	419	22	ABAI3362	Human nervous syst
c 720	20	4.1	420	22	AAI85418	Human polynucleoti
c 721	20	4.1	421	22	AAI81436	Human polynucleoti
c 722	20	4.1	425	22	AAI93694	Human polynucleoti
c 723	20	4.1	430	22	AAI25940	Human breast cancer
c 724	20	4.1	432	24	AAK65338	Human cancer relat
c 725	20	4.1	436	22	AAK58087	Human immune/haema
c 726	20	4.1	437	22	AAK67734	Human immune/haema
c 727	20	4.1	437	24	ABNG65227	Human cancer relat
c 728	20	4.1	438	23	ABV01713	Human prostate exp
c 729	20	4.1	441	23	ABV32037	Human prostate exp
c 730	20	4.1	441	23	ABV40976	Human prostate exp
c 731	20	4.1	445	22	AAH04811	Human CDNA clone (
c 732	20	4.1	448	22	AAK81752	Human immune/haema
c 733	20	4.1	448	22	AAK81753	Human immune/haema
c 734	20	4.1	449	23	ABV57279	Human prostate exp
c 735	20	4.1	449	24	ABL77420	Human ovarian can
c 736	20	4.1	450	22	AAK86068	Human immune/haema
c 737	20	4.1	450	22	AAK86070	Human immune/haema
c 738	20	4.1	451	24	ABL87595	Human ovarian can
c 739	20	4.1	452	22	AAI92040	Human polynucleoti
c 740	20	4.1	454	23	ABV00376	Human prostate exp
c 741	20	4.1	456	22	AAI84703	Human polynucleoti
c 742	20	4.1	457	23	ABV30721	Human prostate exp
c 743	20	4.1	457	23	ABV39689	Human prostate exp
c 744	20	4.1	462	23	ABV47122	Human polynucleoti
c 745	20	4.1	464	22	AAI91243	Human polynucleoti
c 746	20	4.1	465	23	ABV48386	Human prostate exp
c 747	20	4.1	469	23	ABV09545	Human prostate exp
c 748	20	4.1	473	21	AAK43406	Rat secreted expre
c 749	20	4.1	476	24	ABL80655	Human ovarian can
c 750	20	4.1	478	23	ABV51118	Human prostate exp
c 751	20	4.1	479	22	AAK71910	Human immune/haema
c 752	20	4.1	483	22	ABA14579	Human nervous syst
c 753	20	4.1	483	22	ABA07465	Human ovarian and
c 754	20	4.1	483	22	AAI19105	Human breast cancer
c 755	20	4.1	483	22	AAI00081	Human reproductive
c 756	20	4.1	483	22	AAK69290	Human immune/haema
c 757	20	4.1	483	22	AAK69291	Human immune/haema
c 758	20	4.1	496	24	ABN64038	Human cancer relat
c 759	20	4.1	497	22	AAI91133	Human polynucleoti
c 760	20	4.1	499	22	ABA07691	Human ovarian and
c 761	20	4.1	499	22	ABL02849	Human reproductive
c 762	20	4.1	503	24	ABN60560	Human cancer relat
c 763	20	4.1	507	22	AAH08989	Human CDNA clone (
c 764	20	4.1	507	23	ABV58334	Human prostate exp
c 765	20	4.1	510	23	ABV47571	Human prostate exp
c 766	20	4.1	511	24	ABN65132	Human cancer relat
c 767	20	4.1	513	23	ABV17834	Human prostate exp
c 768	20	4.1	518	22	ABN634632	Human DNA for a no
c 769	20	4.1	521	24	ABN63327	Human cancer relat
c 770	20	4.1	522	24	ABN64650	Human cancer relat
c 771	20	4.1	531	24	ABN61496	Human cancer relat
c 772	20	4.1	537	24	ABL83489	Human ovarian can
c 773	20	4.1	538	22	AAK86407	Human immune/haema
c 774	20	4.1	556	22	AAH10063	Human CDNA clone (
c 775	20	4.1	558	22	AAH13225	Human CDNA clone (
c 776	20	4.1	563	24	ABN64556	Human cancer relat
c 777	20	4.1	564	24	ABL92350	Human breast cancer
c 778	20	4.1	576	22	AAI12299	Human secreted pro
c 779	20	4.1	584	22	AAI05762	Human reproductive
c 780	20	4.1	584	22	AAH12123	Human CDNA clone (
c 781	20	4.1	584	24	ABN61136	Human cancer relat
c 782	20	4.1	587	22	AAI21175	Human breast cancer
c 783	20	4.1	587	23	ABV55967	Human prostate exp
c 784	20	4.1	591	24	ABN15908	Human OREF polynuc
c 785	20	4.1	593	24	ABN65447	Human cancer relat
c 786	20	4.1	600	23	ABV53819	Human prostate exp
c 787	20	4.1	601	23	ABV47625	Human prostate exp
c 788	20	4.1	605	23	ABV58501	Human prostate exp
c 789	20	4.1	605	24	ABN62272	Human cancer relat
c 790	20	4.1	628	22	AAH98619	Human cancer relat
c 791	20	4.1	655	22	AAK69148	Human immune/haema
c 792	20	4.1	655	22	AAK71307	Human immune/haema
c 793	20	4.1	668	22	ABAI4738	Human nervous syst
c 794	20	4.1	681	24	AAI92374	Human secreted pro
c 795	20	4.1	695	22	AAH04791	Human CDNA clone (
c 796	20	4.1	708	22	AAH98981	Human EST-derived
c 797	20	4.1	708	22	ABQ89406	Human prostate exp
c 798	20	4.1	740	22	ABQ89406	Human EST-derived
c 799	20	4.1	745	22	AAH99140	Human gene express
c 800	20	4.1	754	20	AAI15588	Human gene express
c 801	20	4.1	755	20	AAI15590	Human gene express
c 802	20	4.1	755	20	AAI15589	Human gene express
c 803	20	4.1	757	19	AAV16883	Human prostate can
c 804	20	4.1	757	20	AAI26018	Prostate disease m
c 805	20	4.1	757	21	AAI287503	Prostate, breast a
c 806	20	4.1	757	22	AAI03722	Biomarker UC band
c 807	20	4.1	768	22	AAI93777	Human neuroblastom
c 808	20	4.1	769	22	AAI95545	Human neuroblastom
c 809	20	4.1	771	24	ABQ88986	Human prostate exp
c 810	20	4.1	787	20	AAI17095	Human gene express
c 811	20	4.1	787	20	AAI17096	Human gene express
c 812	20	4.1	787	24	ABQ89025	Human prostate exp

813	20	4.1	790	22	AAI96154	Human neuroblastom	c 886	20	4.1	2636	22	AAH16363	Human cDNA sequenc
814	20	4.1	791	20	AAZ17080	Human gene express	c 887	20	4.1	2685	23	ABV22723	Human prostate exp
815	20	4.1	791	20	AAZ17093	Human gene express	c 888	20	4.1	2685	23	ABV22723	Human prostate exp
816	20	4.1	805	22	AAH078337	Human immune/haema	c 889	20	4.1	2793	22	AAH86667	Human immune/haema
817	20	4.1	810	22	AAH04407	Human immune/haema	c 890	20	4.1	2897	22	AAH16645	Human immune/haema
818	20	4.1	820	22	AAH08288	Human cDNA clone (c 891	20	4.1	2955	22	AAH18267	Human cDNA sequenc
819	20	4.1	842	22	AAH03851	Human cDNA clone (c 892	20	4.1	3001	21	AAH51810	Chromosome 13q31-q
820	20	4.1	843	22	AAH21041	Human breast cance	c 893	20	4.1	3022	22	AAH47883	Human Polyisopreny
821	20	4.1	845	24	ABQ89199	Human prostate exp	c 894	20	4.1	3067	22	AAH19210	Human secreted pro
822	20	4.1	846	22	ABAI19661	Human nervous syst	c 895	20	4.1	3105	22	AAH19178	Human secreted pro
823	20	4.1	846	22	ABAI19662	Human nervous syst	c 896	20	4.1	3156	22	AAH15535	Human cDNA sequenc
824	20	4.1	846	22	ABAI19663	Human nervous syst	c 897	20	4.1	3232	22	AAH72305	Human immune/haema
825	20	4.1	871	22	ABA08662	Human secreted pro	c 898	20	4.1	3369	22	ABA15532	Human nervous syst
826	20	4.1	872	22	AAK69147	Human immune/haema	c 899	20	4.1	3369	22	ABA15533	Human nervous syst
827	20	4.1	872	22	AAK71306	Human immune/haema	c 900	20	4.1	3426	22	AAK72154	Human immune/haema
828	20	4.1	904	24	ABL89452	Human polynucleoti	c 901	20	4.1	3529	23	ABL09882	Drosophila melanog
829	20	4.1	1006	20	AAI13533	Enterococcus faeca	c 902	20	4.1	3572	23	ABL09890	Drosophila melanog
830	20	4.1	1017	22	AAK84266	Human immune/haema	c 903	20	4.1	3671	22	AAK80121	Human immune/haema
831	20	4.1	1017	22	AAK84266	Human immune/haema	c 904	20	4.1	3811	22	AAK83558	Human immune/haema
832	20	4.1	1083	22	AAH98517	Human EST-derived	c 905	20	4.1	4180	22	AAK68750	Human immune/haema
833	20	4.1	1177	22	AAAS46115	Human DNA encoding	c 906	20	4.1	4206	22	AAK74675	Human immune/haema
834	20	4.1	1177	22	AAAS46115	Human DNA encoding	c 907	20	4.1	4206	22	AAK74675	Human immune/haema
835	20	4.1	1177	22	AAAS46115	Human DNA encoding	c 908	20	4.1	4364	22	ABAI17796	Human cardiovascular
836	20	4.1	1177	24	ABL95696	Human angiogenesis	c 909	20	4.1	4485	22	AAH34896	Human colon cancer
837	20	4.1	1177	24	ABL95696	Human angiogenesis	c 910	20	4.1	4512	22	ABA07296	Human pancreatic c
838	20	4.1	1177	24	ABK33641	Human PRO1928 cDNA	c 911	20	4.1	4512	22	AAK89941	Human digestive sy
839	20	4.1	1187	22	AAH44196	Human neuronal thr	c 912	20	4.1	4608	22	AAK74675	Human immune/haema
840	20	4.1	1310	22	AAK66149	Human immune/haema	c 913	20	4.1	4610	22	AAK74675	Human immune/haema
841	20	4.1	1318	22	AAH13850	Human cDNA sequenc	c 914	20	4.1	4766	22	AAAS27783	DNA encoding novel
842	20	4.1	1330	22	AAH44316	Human ribosomal pr	c 915	20	4.1	4995	24	ABJ65206	Lung cancer relate
843	20	4.1	1343	22	AAH04320	Human reproductive	c 916	20	4.1	5005	22	AAJ36210	Human musculoskele
844	20	4.1	1363	24	ABK62034	Human P450TEC N-te	c 917	20	4.1	5005	22	AAJ36211	Human musculoskele
845	20	4.1	1385	22	AAAS46131	Human DNA for a no	c 918	20	4.1	5253	22	AAK89859	Human digestive sy
846	20	4.1	1417	22	AAAS36650	Human cardiovascular	c 919	20	4.1	5257	22	AAK89860	Human digestive sy
847	20	4.1	1434	24	ABA97051	Human 2-hydroxy ac	c 920	20	4.1	5363	22	AAK65623	Human immune/haema
848	20	4.1	1467	24	ABK35621	Human cDNA sequenc #12	c 921	20	4.1	5769	22	AAK83560	Human immune/haema
849	20	4.1	1556	24	ABK34673	Human cDNA for nov	c 922	20	4.1	5781	22	AAAS27714	DNA encoding novel
850	20	4.1	1600	22	AAAS31064	Zs191 cDNA fragme	c 923	20	4.1	5782	22	AAAS27715	DNA encoding novel
851	20	4.1	1671	22	AAAS46177	Human DNA encoding	c 924	20	4.1	5935	22	ABD10306	Human Par-4 promot
852	20	4.1	1713	22	AAH15530	Human cDNA sequenc	c 925	20	4.1	5938	24	ABK84688	Human cDNA differe
853	20	4.1	1734	22	AAH99494	Human protein enco	c 926	20	4.1	5981	22	AAJ06739	Human reproductive
854	20	4.1	1750	22	AAH15943	Human cDNA sequenc	c 927	20	4.1	5981	22	AAJ06739	Human reproductive
855	20	4.1	1761	22	AAK82514	Human immune/haema	c 928	20	4.1	5982	22	AAJ06740	Human breast or ov
856	20	4.1	1765	22	AAH13783	Human cDNA sequenc	c 929	20	4.1	5982	22	AAJ06740	Human breast or ov
857	20	4.1	1772	22	AAH18437	Human cDNA sequenc	c 930	20	4.1	6038	21	AAJ43720	Human FSH-beta DNA
858	20	4.1	1774	24	ABK35166	Human cDNA encodin	c 931	20	4.1	6038	21	AAJ43720	Human FSH-beta DNA
859	20	4.1	1850	22	AAH15266	Human cDNA sequenc	c 932	20	4.1	6120	22	AAK86301	Human follicle sti
860	20	4.1	1867	23	ABV21406	Human prostate exp	c 933	20	4.1	6141	22	ABA07105	Human immune/haema
861	20	4.1	1867	23	ABV27224	Human prostate exp	c 934	20	4.1	6141	22	ABA07105	Human pancreatic c
862	20	4.1	1878	22	AAH14872	Human cDNA sequenc	c 935	20	4.1	6141	22	AAK89317	Human digestive sy
863	20	4.1	1927	23	AAAS71869	DNA encoding novel	c 936	20	4.1	6153	22	AAJ36712	Human musculoskele
864	20	4.1	1984	22	AAH16531	Human cDNA sequenc	c 937	20	4.1	6153	23	ABL97370	Human testicular a
865	20	4.1	1986	22	AAH15683	Human cDNA sequenc	c 938	20	4.1	6162	22	AAK83551	Human immune/haema
866	20	4.1	2097	22	AAK76726	Human immune/haema	c 939	20	4.1	6168	22	AAK83557	Human immune/haema
867	20	4.1	2104	22	AAH14291	Human cDNA sequenc	c 940	20	4.1	6202	22	AAK86314	Human immune/haema
868	20	4.1	2125	21	AAZ43722	Human FSH-beta DNA	c 941	20	4.1	6232	22	AAK83552	Human immune/haema
869	20	4.1	2142	23	ABV22868	Human prostate exp	c 942	20	4.1	6259	22	AAK83559	Human immune/haema
870	20	4.1	2142	23	ABV22868	Human prostate exp	c 943	20	4.1	6261	22	AAK83554	Human immune/haema
871	20	4.1	2261	22	AAH17286	Human cDNA sequenc	c 944	20	4.1	6511	16	AAQ95493	Human Cdn-2 DNA
872	20	4.1	2263	22	AAK68559	Human immune/haema	c 945	20	4.1	6616	22	AAK81014	Human immune/haema
873	20	4.1	2263	22	AAK68559	Human immune/haema	c 946	20	4.1	6743	22	AAJ05842	Human reproductive
874	20	4.1	2297	22	ABA15531	Human immune/haema	c 947	20	4.1	6743	22	AAJ05842	Human reproductive
875	20	4.1	2318	24	AAAS23848	Human protease PRT	c 948	20	4.1	6743	23	ABL98406	Human testicular a
876	20	4.1	2382	23	AAAS80926	DNA encoding novel	c 949	20	4.1	6800	22	AAAS36642	Human cardiovascular
877	20	4.1	2385	22	AAH13908	Human cDNA sequenc	c 950	20	4.1	7156	22	AAK86021	Human immune/haema
878	20	4.1	2497	22	AAH16050	Human cDNA sequenc	c 951	20	4.1	7156	22	AAK86022	Human immune/haema
879	20	4.1	2505	22	AAAS04001	Biomarker UC band	c 952	20	4.1	7622	21	AAJ43718	Human FSH-beta DNA
880	20	4.1	2506	21	AAZ87584	Prostate disease m	c 953	20	4.1	7622	22	AAJ07439	Human follicle sti
881	20	4.1	2513	22	AAH17469	Human cDNA sequenc	c 954	20	4.1	7713	22	AAJ02845	Human reproductive
882	20	4.1	2528	22	AAAS34588	Human DNA for a no	c 955	20	4.1	7760	22	AAK74676	Human immune/haema
883	20	4.1	2530	22	AAAS34588	Human DNA for a no	c 956	20	4.1	8007	22	AAK68751	Human immune/haema
884	20	4.1	2532	24	AAJ32709	Human kinase encod	c 957	20	4.1	8082	22	AAAS28672	Genomic sequence #
885	20	4.1	2532	24	ABA97291	Receptor tyrosine	c 958	20	4.1	8121	22	AAAS36189	Human cardiovascular
	20	4.1	2598	22	ABA08315	Human polycystic d	c 959	20	4.1	8145	22	AAAS30438	DNA encoding novel

c 959 20 4.1 8145 22 AAL06218 Human reproductive
 c 960 20 4.1 8147 22 AAS30437 DNA encoding novel
 c 961 20 4.1 8147 22 AAL06217 Human reproductive
 c 962 20 4.1 8526 22 ABA18356 Human nervous syst
 c 963 20 4.1 8758 24 AAD32710 Human kinase gene.
 c 964 20 4.1 8758 24 ABA97292 Receptor tyrosine
 c 965 20 4.1 8853 22 AAS40657 DNA encoding human
 c 966 20 4.1 8853 22 AAL06545 Human reproductive
 c 967 20 4.1 9133 22 AAK83165 Human immune/haema
 c 968 20 4.1 9745 22 AAS36759 Human cardiovascul
 c 969 20 4.1 9869 22 AAF69947 Human TNFRSF11B ge
 c 970 20 4.1 9898 17 AAV20767 Human OCIF genome
 c 971 20 4.1 10190 19 AAT33183 Fragment of human
 c 972 20 4.1 10867 22 AAL37605 Human musculoskele
 c 973 20 4.1 10867 22 AAS36613 Human cardiovascul
 c 974 20 4.1 10867 22 AAK66345 Human immune/haema
 c 975 20 4.1 10894 22 AAS36611 Human cardiovascul
 c 976 20 4.1 10894 22 AAK66343 Human immune/haema
 c 977 20 4.1 10907 22 AAL37603 Human musculoskele
 c 978 20 4.1 10907 22 AAS36612 Human cardiovascul
 c 979 20 4.1 10907 22 AAK66344 Human immune/haema
 c 980 20 4.1 11172 22 AAS29967 Human lung antigen
 c 981 20 4.1 11446 22 AAK30464 Human digestive sy
 c 982 20 4.1 11453 22 AAK73272 Human immune/haema
 c 983 20 4.1 11553 22 AAK73271 Human immune/haema
 c 984 20 4.1 11598 22 AAS40735 DNA encoding human
 c 985 20 4.1 11598 22 AAL06652 Human reproductive
 c 986 20 4.1 11600 22 AAS40736 DNA encoding human
 c 987 20 4.1 11600 22 AAL06653 Human reproductive
 c 988 20 4.1 11674 22 AAK70965 Human immune/haema
 c 989 20 4.1 11837 22 AAK89070 Human digestive sy
 c 990 20 4.1 11837 22 AAS33429 DNA encoding human
 c 991 20 4.1 11881 22 AAS36624 Human cardiovascul
 c 992 20 4.1 11881 22 AAS27691 DNA encoding novel
 c 993 20 4.1 11881 22 AAS27693 DNA encoding novel
 c 994 20 4.1 12025 22 AAK65230 Human immune/haema
 c 995 20 4.1 12050 22 AAK73194 Human immune/haema
 c 996 20 4.1 12149 22 AAS36758 Human cardiovascul
 c 997 20 4.1 12174 22 AAK30854 Human digestive sy
 c 998 20 4.1 12259 22 AAS36190 Human cardiovascul
 c 999 20 4.1 12718 22 AAL37607 Human musculoskele
 c 1000 20 4.1 12718 22 AAK66346 Human immune/haema

ALIGNMENTS

RESULT 1

AAA64508
 ID AAA64508 standard; cDNA; 5492 BP.

XX AC AAA64508;

XX DT 02-JAN-2001 (first entry)

XX DE cDNA sequence of the wild type human FEZ1 gene.

XX KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
 KW tumour proliferation; tubulin; microtubule; protein EF1-gamma;
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
 KW tumorigenesis; tumour survival; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200050565-A2.

XX PD 31-AUG-2000.

XX PF 25-FEB-2000; 2000WO-US04950.

XX PR 25-FEB-1999; 99US-0121537.

XX XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

PI Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human
 PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
 PT cancer -

XX Example 2; Fig 5B; 255pp; English.

XX The present sequence represents the cDNA sequence of the human FEZ1 gene.
 CC FEZ1 is a tumour suppressor gene, located at chromosome location 8p22.
 CC Decreased or no expression of FEZ1 is detected in a variety of cancer
 CC cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
 CC also interacts with tubulin, with microtubules, and with protein
 CC EF1-gamma. Post-translational phosphorylation and dephosphorylation
 CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
 CC expression are useful for inducing cells to proliferate. Compounds
 CC which modulate FEZ1 association with tubulin are useful for alleviating
 CC tubulin hyper- or hypo- polymerisation disorders, such as those
 CC associated with aberrant initiation of mitosis, modulation of the
 CC initiation and rate of cell proliferation and cell growth, modulation of
 CC cell shape, cell rigidity, cell motility, rate and stage of cellular
 CC DNA replication, intracellular distribution of organelles, metastatic
 CC potential of cell and cellular transformation from a non-cancerous to
 CC cancerous phenotype. Compounds which modulate FEZ1 binding and
 CC phosphorylation are also useful for alleviating a disorder, such as
 CC tumorigenesis, tumour survival, growth and metastasis.

XX SQ Sequence 5492 BP; 1137 A; 1704 C; 1565 G; 1086 T; 0 other;

Query Match 100.0%; Score 486; DB 21; Length 5492;

Best Local Similarity 100.0%; Pred. No. 4.4e-221;

Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCAGATGAGCCACCGCTGCGCCAGATTTCTTTTATTTCTTTCTTTT 60

Db 3557 AGATTCAGATGAGCCACCGCTGCGCCAGATTTCTTTTATTTCTTTT 3616

QY 61 CTTTTCCTGCTTCTGCTTTTTCAGAACGACAGACCTAGCAGGCTGTTCATGTTCT 120

Db 3617 CTTTTCCTGCTTCTGCTTTTTCAGAACGACAGACCTAGCAGGCTGTTCATGTTCT 3676

QY 121 ATTTTTCAGTGTAGCCACAGCTGCTGTTCTCAGGACAGCATCCCTCCACATGCTGCG 180

Db 3677 ATTTTTCAGTGTAGCCACAGCTGCTGTTCTCAGGACAGCATCCCTCCACATGCTGCG 3736

QY 181 CCTGCTGCTGCTGAGATGAGGAGGCGCTGCGGAACCTTGGAGTCCCAAGGCCAGTC 240

Db 3737 CCTGCTGCTGCTGAGATGAGGAGGAGGCGCTGCGGAACCTTGGAGTCCCAAGGCCAGTC 3796

QY 241 CCCATTTTCGCTCGCTCACCGCTGCGCTTAGAGACCCCGAGGTAGGGTGGGAGATG 300

Db 3797 CCCATTTTCGCTCGCTCACCGCTGCGCTTAGAGACCCCGAGGTAGGGTGGGAGATG 3856

QY 301 CTTTCTCTTCGCTGCGCTGAGTGTCTAGGCTTCCCTGAGTGGGCTGAGGC 360

Db 3857 CTTTCTCTTCGCTGCGCTGAGTGTCTAGGCTTCCCTGAGTGGGCTGAGGC 3916

QY 361 CAGAGTACCTTTTCTGTGCTGCTTACCTTCTGCTGCTGAGGTAAACGGTGCCCA 420

Db 3917 CAGAGTACCTTTTCTGTGCTGCTTACCTTCTGCTGCTGAGGTAAACGGTGCCCA 3976

QY 421 TCCTGCCATCCTCAAACGACAGAGGAGCTTTTCTGGAATTTCAACCATTTCTTTAGTC 480

Db 3977 TCCTGCCATCCTCAAACGACAGAGGAGCTTTTCTGGAATTTCAACCATTTCTTTAGTC 4036

QY 481 CCAAGC 486

Db 4037 CCAAGC 4042

Query Match	100.0%;	Score 486;	DB 21;	Length 9048;
Best Local Similarity	100.0%;	Pred. No. 4.4e-221;		
Matches 486;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AGATTGCAGATGTGAGCCACCGTGCCCTGGCCAGATTTTTCTTTTATTCTTCTTCTCTTTT	60	
Db	7148	AGATTGCAGATGTGAGCCACCGTGCCCTGGCCAGATTTTTCTTTTATTCTTCTTCTTTT	7207	
Qy	61	CTTTTTTGCTTTCTTGTCTTTTTCAGAGCAAGCCAGACCTAGCAGGCGTGTTCATGTTCT	120	
Db	7208	CTTTTTTGCTTTCTTGTCTTTTTCAGAGCAAGCCAGACCTAGCAGGCGTGTTCATGTTCT	7267	
Qy	121	ATTTTGTACTGTGTAGCCACAGCTGCTGTTCTCAGGACAGCATCCCTTCCCAACATGCCTCGC	180	

XX PA (FARB) BAYER CORP.
XX PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
XX PI Thiagalingam A, Lewis ME;
XX XX WPI; 2002-426115/45.
XX XX New isolated nucleic acid that is differentially expressed in cancer
XX PT tissues useful for determining the presence of colon cancer in a cell
XX PT or tissue type, and in antisense therapy -
XX PS Claim 1; Fig 1; 796pp; English.
XX CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
XX CC expressed in cancer tissues. ABQ78993 to ABQ79004 represent proteins
XX CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
XX CC used in antisense therapy. An antibody immunoreactive with a polypeptide
XX CC encoded by (I) is useful for detecting cancer in a patient sample, and
XX CC for detecting the presence or absence of a polynucleotide encoded by a
XX CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
XX CC from (I) can be used for determining the presence of a nucleic acid which
XX CC hybridizes to (I), and for determining the phenotype of cells in a sample
XX CC of cells from a patient. (I) is useful for determining the presence of
XX CC colon cancer in a cell or tissue type, for determining the presence or
XX CC state of other type of cancer, in antisense therapy, to generate
XX CC macroarrays on a solid surface, to identify a chromosome on which the
XX CC corresponding gene resides, and in tissue profiling, forensics, genetic
XX CC analysis, mapping and diagnostic applications. (I) can be used to raise
XX CC antibodies, and to screen for peptide analogues and antagonists.
XX SQ Sequence 547 BP; 163 A; 112 C; 127 G; 130 T; 15 other;

Query Match 5.8%; Score 28; DB 24; Length 547;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAGA 34
Db 92 CAGATGTGAGCCACCGTGCCTGGCCAGA 65

RESULT 6
AAH98314
ID AAH98314 standard; cDNA; 1660 BP.
XX AC AAH98314;
XX DE 12-OCT-2001 (first entry)
XX XX Human EST-derived coding sequence SEQ ID NO: 171.
XX XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX KW diagnostics; forensic test; gene mapping; genetic disorder;
XX KW biodiversity; gene therapy; nutrition; ss.
XX OS Homo sapiens.
XX XX WO200154477-A2.
XX XX 02-AUG-2001.
XX XX 25-JAN-2001; 2001WO-US02687.
XX XX 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX XX (HYSE-) HYSEQ INC.
XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
XX DR P-PSDB; AAM23655.
XX XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use -
XX PT Claim 1; Page 293; 1275pp; English.
XX XX The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a cDNA
XX CC of the invention.
XX SQ Sequence 1660 BP; 526 A; 308 C; 270 G; 555 T; 1 other;

Query Match 5.8%; Score 28; DB 22; Length 1660;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAGA 34
Db 1185 CAGATGTGAGCCACCGTGCCTGGCCAGA 1212

RESULT 7
AAH98825
ID AAH98825 standard; cDNA; 1660 BP.
XX AC AAH98825;
XX DE 12-OCT-2001 (first entry)
XX XX Human EST-derived coding sequence SEQ ID NO: 682.
XX XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX KW diagnostics; forensic test; gene mapping; genetic disorder;
XX KW biodiversity; gene therapy; nutrition; ss.
XX OS Homo sapiens.
XX XX WO200154477-A2.
XX XX 02-AUG-2001.
XX XX 25-JAN-2001; 2001WO-US02687.
XX XX 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX XX (HYSE-) HYSEQ INC.
XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
XX DR P-PSDB; AAM24166.
XX XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use -
XX PT Claim 1; Page 629; 1275pp; English.
XX XX The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention.

SQ Sequence 1660 BP; 526 A; 308 C; 270 G; 555 T; 1 other;

Query Match 5.8%; Score 28; DB 22; Length 1660;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CAGATGTGAGCCACCGTGGTGGCCAG 34
 DB 1185 CAGATGTGAGCCACCGTGGTGGCCAG 1212

RESULT 8

AXX22304/c
 ID AAX22304 standard; DNA; 28866 BP.

AC AAX22304;

DT 22-JUN-1999 (first entry)

XX Human IL-1ra BAC contiguous DNA sequence 97.

XX Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition;
 KW interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis;
 KW chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease;
 KW growth factors; treatment; IL-1 receptor complex; BAC; ss.

XX Homo sapiens.

XX W09906426-A1.

XX 11-FEB-1999.

XX 03-AUG-1998; 98WO-US16102.

XX 02-JUL-1998; 98US-0091650.

XX 04-AUG-1997; 97US-0054646.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Pan Y;

XX WPI; 1999-153692/13.

XX New isolated nucleic acid encoding the new human cytokine Tango-77 -
 PT used to inhibit inflammation and to screen for specific modulators

XX Example 5; Figure 4; 226pp; English.

XX AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic
 CC sequences containing alternatively spliced forms of human IL-1ra. Such
 CC fragments are used in the method of the invention which describes the
 CC isolation of a novel human TANGO-77 encoding nucleic acid and protein.
 CC Tango-77 is a member of the cytokine superfamily that is expected to
 CC inhibit inflammation by binding to the interleukin-1 receptor (IL-1R). It
 CC may also bind to a new receptor so could regulate other cellular
 CC processes associated with acute or chronic inflammation, e.g. asthma,
 CC chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and
 CC inflammatory bowel disease. It may also induce or suppress interleukins,
 CC cytokines and growth factors. Modulators of this protein are used to
 CC treat or prevent conditions associated with abnormal levels of
 CC inflammation, or activity of IL-1 or its receptor complex.

SQ Sequence: 28866 BP; 8044 A; 6348 C; 6742 G; 7729 T; 3 other;

Query Match 5.6%; Score 27; DB 20; Length 28866;
 Best Local Similarity 100.0%; Pred. No. 0.0061;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 CAGATGTGAGCCACCGTGGTGGCCAG 33
 DB 21411 CAGATGTGAGCCACCGTGGTGGCCAG 21385

RESULT 9

ABL85166

ID ABL85166 standard; cDNA; 251 BP.

XX ABL85166;

DT 17-MAY-2002 (first entry)

XX Human ovarian cancer related cDNA clone SEQ ID NO:8144.

XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

XX W0200192581-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US17756.

XX 26-MAY-2000; 2000US-207484P.

XX (CORI-) CORIXA CORP.

XX Algate PA, Harlocker SL, Jones R;

XX WPI; 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide

XX Claim 1; SEQ ID 8144; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (III), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
 CC (S1) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumour cDNA library using well known
 CC techniques.

SQ Sequence 251 BP; 59 A; 62 C; 54 G; 76 T; 0 other;

Query Match 5.3%; Score 26; DB 24; Length 251;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGAGCCACCGTGGTGGCCAGATTTT 38

DB 137 TGAGCCACCGTGGTGGCCAGATTTT 162

```

RESULT 10
ABL84945
ID ABL84945 standard; cDNA; 371 BP.
XX
XX ABL84945;
AC
XX 17-MAY-2002 (first entry)
DT
XX
XX Human ovarian cancer related cDNA clone SEQ ID NO:7923.
DE
XX
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
KW
XX Homo sapiens.
OS
XX WO200192581-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 29-MAY-2001; 2001WO-US17756.
PF
XX
XX 26-MAY-2000; 2000US-207484P.
PR
XX (CORI-) CORIXA CORP.
PA
XX
XX Algate PA, Harlocker SL, Jones R;
PI
XX WPI; 2002-122075/16.
DR
XX
XX Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide
XX
XX Claim 1; SEQ ID 7923; 489pp; English.
PS
XX
XX The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.
XX
XX Sequence 371 BP; 100 A; 83 C; 81 G; 107 T; 0 other;
SQ
Query Match 5.3%; Score 26; DB 24; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 TGAGCCACCGTGGCTGCCAGATTTT 38
D6 137 TGAGCCACCGTGGCTGCCAGATTTT 162

```

```

XX AAC75926;
AC
XX 08-FEB-2001 (first entry)
DT
XX
XX Human ORFX ORF1481 polynucleotide sequence SEQ ID NO:2961.
DE
XX
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
XX Homo sapiens.
OS
XX WO200058473-A2.
PN
XX
XX 05-OCT-2000.
PD
XX
XX 31-MAR-2000; 2000WO-US08621.
PF
XX
XX 31-MAR-1999; 99US-0127607.
PR
XX 02-APR-1999; 99US-0127636.
PR
XX 05-APR-1999; 99US-0127728.
PR
XX 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2000-602362/57.
DR
XX P-PSDB; AAB41717.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 5; Page 2198-2199; 5507pp; English.
PS
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; antirheumatic;
CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianemic. The sequences can be used for determining
CC the presence of or predisposition to or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 434 BP; 75 A; 132 C; 123 G; 103 T; 1 other;
SQ
Query Match 5.3%; Score 26; DB 21; Length 434;

```

Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGAGCCACCGTGCTGCCAGATTTT 38
|||||
Db 321 TGAGCCACCGTGCTGCCAGATTTT 346

RESULT 12

AADI6646

ID- AADI6646 standard; DNA; 29449 BP.

XX AC

XX AADI6646;

XX DT

XX 19-NOV-2001 (first entry)

XX DE

XX Human novel protein-encoding gene 22, SEQ ID NO:73.

XX Human; lipid metabolism protein; nootropic; neuroprotective; cardiant;
KW cerebroprotective; hepatotropic; antidiabetic; ophthalmic; nephrotropic;
KW immune disorder; autoimmune disease; rheumatoid arthritis; glossitis;
KW systemic lupus erythematosus; conjunctivitis; inflammatory disorder;
KW respiratory disorder; asthma; allergy; CNS disorder; Alzheimer's disease;
KW Parkinson's disease; atherosclerosis; cardiovascular disorder; cancer;
KW coronary disease; familial hypercholesterolaemia; hyperlipidaemia;
KW haematopoietic disorder; hypolipidaemia; lipodosis; Gaucher's disease;
KW Tay-sach's disease; mental retardation; gene therapy; antisense therapy;
KW ds.

XX OS

XX Homo sapiens.

XX FH Key Location/Qualifiers

FT exon 1..1785

FT FT /*tag= a

FT FT 1786..1847

FT FT /*tag= b

FT FT 1848..1971

FT FT /*tag= c

FT FT 1972..2125

FT FT /*tag= d

FT FT 2126..2475

FT FT /*tag= e

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FT FT /*tag= f

FT FT 2896..2980

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FT FT /*tag= h

FT FT 3326..3786

FT FT /*tag= i

FT FT 3787..5007

FT FT /*tag= j

FT FT 5008..5343

FT FT /*tag= k

FT FT 5344..5789

FT FT /*tag= l

FT FT 5790..5928

FT FT /*tag= m

FT FT 5929..6133

FT FT /*tag= n

FT FT 6134..6205

FT FT /*tag= o

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FT FT 6262..7861

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FT FT 7862..8072

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FT intron /*tag= u
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FT 16880..18110
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FT 27710..29385
FT FT /*tag= av
FT 29386..29449
FT FT /*tag= aw
XX WO200155203-A1.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01327.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.

Query Match 5.3%; Score 26; DB 22; Length 29449;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGTGAGCCACGTCCTGGCCAGATT 36
|||||

Db 8497 TGTGAGCCACGTCCTGGCCAGATT 8522
|||||

RESULT 13
AAS30243/c
ID AAS30243 standard; DNA; 29449 BP.
XX
AC AAS30243;
XX
DT 21-NOV-2001 (first entry)
XX
DE DNA encoding renal and cardiovascular-associated protein, Seq ID 161.
XX
KW Human; antiinflammatory; neuroprotective; immunomodulator; vulnery;
KW cardiovascular; cytostatic; nephrotropic; antianemic; nephritis;
KW immunosuppressive; kidney disorder; renal failure; hypertension;
KW cardiovascular disorder; myocardial infarction; blood disorder; anaemia;
KW blood coagulation disorder; electrolyte imbalance disorder; cancer;
KW hyponatraemia; hyperkalaemia; neoplastic disorder; nephroma;
KW autoimmune disease; inflammatory disease; reproductive system disorder;
KW endocrine disorder; neural activity; neurological disorder;
KW wound healing; respiratory disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200155328-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01359.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216847.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.

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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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PR 14-SEP-2000; 2000US-0232399.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
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PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.

PR 17-NOV-2000; 2000US-0249245.
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PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-488787/53.
DR
XX
XX New polynucleotides and polypeptides, useful for diagnosing, treating,
PT preventing or prognosing e.g. kidney, cardiovascular, blood,
PT electrolyte imbalance or neoplastic disorders, autoimmune diseases,
PT cancers
XX
XX Claim 1; SEQ ID No 161; 506pp; English.
PS
XX
XX The invention relates to novel nucleic acids and polypeptides useful for
CC diagnosing, treating, preventing and/or prognosing disorders related to
CC these polypeptides. The polynucleotides are especially useful in the
CC diagnosis, prognosis, prevention and/or treatment of diseases which
CC include kidney disorders (e.g. renal failure or nephritis),
CC cardiovascular disorders (e.g. hypertension or myocardial infarction),
CC blood disorders (e.g. anaemia or blood coagulation disorders),
CC electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia),
CC neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune
CC diseases, cancers, inflammatory diseases, reproductive system
CC disorders, endocrine disorders, neural activity and neurological
CC disorders, wound healing and respiratory disorders. AAS30165-AAS30251
CC represent the novel human renal and cardiovascular-associated nucleic
CC acid sequences of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at:
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 29449 BP; 9212 A; 6321 C; 5414 G; 8502 T; 0 other;

Query Match 5.3%; Score 26; DB 22; Length 29449;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGTGAGCCACCGTGGCCAGATT 36
Db 20953 TGTGAGCCACCGTGGCCAGATT 20928

RESULT 14
ABQ88186/c
ID ABQ88186 standard; cDNA; 169739 BP.
XX
XX AC ABQ88186;
XX
XX 18-SEP-2002 (first entry)
DT
XX Human osteoblast differentiation related cDNA SEQ ID NO 93.
DE Human; osteoblast; stem cell differentiation; bone tissue deposition;
XX
KW
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osteoporosis; osteopathic; ss.
 OS Homo sapiens.
 XX
 PN WO200250301-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 18-DEC-2001; 2001WO-US48276.
 XX
 PR 18-DEC-2000; 2000US-255882P.
 XX
 PR 24-APR-2001; 2001US-285691P.
 XX
 PA (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 XX
 PI Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
 PI Mertz L;
 XX
 DR WPI; 2002-557663/59.
 XX
 PT Use of genes and their expression profiles associated with osteoblast
 PT differentiation for screening modulators bone formation, for diagnosing
 PT or treating e.g. osteoporosis, or as markers for the differentiation
 PT process -
 XX
 PS Claim 1; SEQ ID NO 93; 78pp + Sequence Listing; English.
 XX
 CC The invention relates to genes and their expression profiles are used
 CC for:
 CC (a) screening modulators of precursor stem cell differentiation into
 CC osteoblasts, or bone tissue deposition;
 CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
 CC osteoblast formation or osteoporosis; or
 CC (c) treating or monitoring treatment of the conditions cited in (b), or
 CC monitoring the progression of bone tissue deposition.
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
 CC drug-induced abnormalities in bone formation or bone loss, conditions
 CC that involve altered bone metabolism (e.g. idiopathic juvenile
 CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
 CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
 CC osteoblast differentiation associated cDNA marker of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
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 DT 17-SEP-2002 (first entry)
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 DE Human prostate expression marker cDNA 51342.
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 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
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 OS Homo sapiens.
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PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
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 PF 20-FEB-2001; 2001WO-US05171.
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 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 9979; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 603 BP; 172 A; 148 C; 149 G; 133 T; 1 other;
 Query Match 5.1%; Score 25; DB 23; Length 603;
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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Job time : 103.798 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 19.0245 Seconds
(without alignments)

Title: US-09-513-888C-1 COPY 7148 7633

Perfect score:

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	25	5.1	819	4	US-09-605-785-571	Sequence 571, Appl	
C 4	25	5.1	36651	4	US-09-738-894-3	Sequence 3, Appli	
C 5	23	4.7	3807	4	US-08-482-918-43	Sequence 43, Appl	
C 6	23	4.7	3807	4	US-09-324-681-43	Sequence 43, Appl	
C 7	23	4.7	3807	4	US-08-336-728A-3	Sequence 43, Appl	
C 8	23	4.7	5864	4	US-08-482-918-47	Sequence 47, Appl	
C 9	23	4.7	5864	4	US-09-242-681-47	Sequence 47, Appl	
C 10	23	4.7	5864	4	US-08-336-728A-3	Sequence 47, Appl	
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396	16	3.3	246240	2	US-08-724-394A-21	Sequence 21, Appl	C 469	15	3.1	396	4	US-09-134-001C-1320	Sequence 1320, Appl
397	16	3.3	246240	2	US-08-724-394A-22	Sequence 22, Appl	C 470	15	3.1	417	3	US-08-714-918-106	Sequence 106, Appl
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399	15	3.1	21	2	US-08-740-215B-4	Sequence 4, Appl	C 472	15	3.1	417	4	US-09-265-315-106	Sequence 106, Appl
400	15	3.1	21	2	US-08-740-215B-4	Sequence 4, Appl	C 473	15	3.1	417	4	US-09-266-417-106	Sequence 106, Appl
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403	15	3.1	35	2	US-08-902-623-34	Sequence 34, Appl	C 476	15	3.1	522	1	US-08-672-569-3	Sequence 3, Appl
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405	15	3.1	39	2	US-08-701-124-44	Sequence 44, Appl	C 478	15	3.1	559	4	US-09-328-111-456	Sequence 456, Appl
406	15	3.1	39	2	US-08-701-124-45	Sequence 45, Appl	C 479	15	3.1	565	4	US-09-385-982-20	Sequence 20, Appl
407	15	3.1	39	3	US-08-130-225-44	Sequence 44, Appl	C 480	15	3.1	600	5	PCT-US93-10418-1	Sequence 1, Appl
408	15	3.1	39	3	US-08-130-225-44	Sequence 44, Appl	C 481	15	3.1	629	4	US-09-328-111-395	Sequence 395, Appl
409	15	3.1	39	4	US-09-455-061-45	Sequence 45, Appl	C 482	15	3.1	670	4	US-09-040-984-7	Sequence 7, Appl
410	15	3.1	39	4	US-09-455-061-45	Sequence 45, Appl	C 483	15	3.1	670	4	US-09-123-912-7	Sequence 7, Appl
411	15	3.1	39	4	US-09-101-751A-68	Sequence 68, Appl	C 484	15	3.1	670	4	US-09-643-597-7	Sequence 7, Appl
412	15	3.1	39	4	US-09-101-751A-79	Sequence 79, Appl	C 485	15	3.1	672	1	US-08-599-252-102	Sequence 102, Appl
413	15	3.1	39	4	US-09-101-751A-80	Sequence 80, Appl	C 486	15	3.1	672	5	PCT-US96-06352-102	Sequence 102, Appl
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419	15	3.1	52	4	US-03-208-966-28	Sequence 28, Appl	C 492	15	3.1	893	4	US-09-535-008-58	Sequence 58, Appl
420	15	3.1	57	4	US-09-101-751A-35	Sequence 35, Appl	C 493	15	3.1	937	3	US-08-860-368B-10	Sequence 10, Appl
421	15	3.1	60	4	US-09-208-966-19	Sequence 19, Appl	C 494	15	3.1	984	4	US-09-583-492-9	Sequence 9, Appl
422	15	3.1	61	5	PCT-US91-03680-8	Sequence 8, Appl	C 495	15	3.1	984	4	US-08-642-274D-53	Sequence 53, Appl
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431	15	3.1	200	3	US-09-065-474-118	Sequence 118, Appl	C 504	15	3.1	1070	1	US-08-441-597-1	Sequence 1, Appl
432	15	3.1	200	3	US-09-065-474-119	Sequence 119, Appl	C 505	15	3.1	1072	4	US-09-088-549-2	Sequence 2, Appl
433	15	3.1	200	4	US-09-557-034-118	Sequence 118, Appl	C 506	15	3.1	1116	1	US-08-672-569-1	Sequence 1, Appl
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435	15	3.1	204	1	US-08-594-031-165	Sequence 165, Appl	C 508	15	3.1	1131	6	5168049-2	Patent No. 5168049
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444	15	3.1	284	2	US-08-902-623-42	Sequence 42, Appl	C 517	15	3.1	1255	4	US-08-765-268A-2	Sequence 2, Appl
445	15	3.1	289	2	US-08-481-658B-63	Sequence 63, Appl	C 518	15	3.1	1278	2	US-08-948-705-3	Sequence 3, Appl
446	15	3.1	289	2	US-08-477-504A-63	Sequence 63, Appl	C 519	15	3.1	1298	3	US-08-580-545B-9	Sequence 9, Appl
447	15	3.1	289	2	US-08-486-756A-63	Sequence 63, Appl	C 520	15	3.1	1312	2	US-09-262-653A-9	Sequence 9, Appl
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449	15	3.1	289	3	US-08-787-739-63	Sequence 63, Appl	C 522	15	3.1	1334	2	US-08-477-504A-44	Sequence 44, Appl
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453	15	3.1	289	4	US-09-178-115-63	Sequence 63, Appl	C 526	15	3.1	1334	3	US-08-487-077A-44	Sequence 44, Appl
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462	15	3.1	370	2	US-08-332-766A-8	Sequence 8, Appl	C 535	15	3.1	1386	2	US-08-687-080-76	Sequence 76, Appl
463	15	3.1	372	2	US-08-454-557C-35	Sequence 35, Appl	C 536	15	3.1	1430	2	US-08-743-130A-1	Sequence 1, Appl
464	15	3.1	372	2	US-08-340-426D-35	Sequence 35, Appl	C 537	15	3.1	1449	4	US-09-695-458-1	Sequence 1, Appl
465	15	3.1	372	2	US-08-450-673C-35	Sequence 35, Appl	C 538	15	3.1				

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c 752	15	3.1	5599	2	US-08-477-451-9	Sequence 9, Appli	c 825	15	3.1	14581	4	US-08-520-373D-4	Sequence 4, Appli
753	15	3.1	5599	2	US-08-477-451-13	Sequence 13, Appli	826	15	3.1	14747	4	US-09-608-285A-42	Sequence 42, Appli
754	15	3.1	5690	2	US-08-447-454-2	Sequence 2, Appli	827	15	3.1	15144	4	US-08-458-434A-6	Sequence 6, Appli
c 755	15	3.1	5690	2	US-08-716-679-2	Sequence 2, Appli	828	15	3.1	15567	4	US-09-627-376-3	Sequence 3, Appli
c 756	15	3.1	6063	1	US-08-195-744-4	Sequence 4, Appli	c 829	15	3.1	15602	4	US-09-844-634-17	Sequence 17, Appli
c 757	15	3.1	6063	2	US-08-788-279-4	Sequence 4, Appli	830	15	3.1	15977	4	US-09-608-285A-59	Sequence 59, Appli

C 831	15	3.1	15977	4	US-09-608-285A-59	Sequence 59, Appl	904	14	2.9	381	1	US-08-041-219A-2	Sequence 2, Appl
C 832	15	3.1	16595	4	US-09-146-053-7	Sequence 7, Appl	905	14	2.9	381	1	US-08-417-122-2	Sequence 2, Appl
C 833	15	3.1	19718	4	US-08-961-527-99	Sequence 99, Appl	c 906	14	2.9	385	4	US-08-729-601A-83	Sequence 83, Appl
C 834	15	3.1	19736	4	US-09-740-035-3	Sequence 3, Appl	907	14	2.9	394	2	US-08-623-906A-7	Sequence 7, Appl
C 835	15	3.1	19932	2	US-08-477-451-25	Sequence 25, Appl	908	14	2.9	414	2	US-08-347-563A-22	Sequence 22, Appl
C 836	15	3.1	20598	4	US-09-593-995-10	Sequence 10, Appl	909	14	2.9	414	3	US-08-485-942A-22	Sequence 22, Appl
C 837	15	3.1	22481	4	US-08-367-841A-43	Sequence 43, Appl	910	14	2.9	414	3	US-08-488-214A-22	Sequence 22, Appl
C 838	15	3.1	22481	5	PCT-US95-07201-43	Sequence 43, Appl	911	14	2.9	414	3	US-08-488-208A-22	Sequence 22, Appl
C 839	15	3.1	22484	4	US-09-875-223-2	Sequence 2, Appl	912	14	2.9	414	4	US-08-483-211A-22	Sequence 22, Appl
C 840	15	3.1	22664	1	US-08-370-975B-1	Sequence 1, Appl	913	14	2.9	414	4	US-08-488-223A-22	GENERAL INFORMA
C 841	15	3.1	28994	3	US-08-884-324-14	Sequence 14, Appl	914	14	2.9	414	4	US-08-438-431A-22	Sequence 22, Appl
C 842	15	3.1	29629	4	US-09-729-995-3	Sequence 3, Appl	915	14	2.9	420	4	US-09-641-638-229	Sequence 229, App
C 843	15	3.1	31571	1	US-08-323-443B-1	Sequence 1, Appl	c 916	14	2.9	422	4	US-09-397-787-186	Sequence 186, App
C 844	15	3.1	32042	4	US-09-245-281-44	Sequence 44, Appl	917	14	2.9	427	4	US-09-556-877-46	Sequence 46, Appl
C 845	15	3.1	35060	3	US-08-814-095-7	Sequence 7, Appl	918	14	2.9	427	4	US-09-620-412C-46	Sequence 46, Appl
C 846	15	3.1	36741	4	US-09-301-665-3	Sequence 3, Appl	c 919	14	2.9	427	4	US-09-397-787-206	Sequence 206, App
C 847	15	3.1	40352	3	US-08-846-111D-15	Sequence 15, Appl	920	14	2.9	432	5	PCT-US94-00545-11	Sequence 11, Appl
C 848	15	3.1	40352	4	US-08-443-077-15	Sequence 15, Appl	c 921	14	2.9	443	4	US-09-397-787-194	Sequence 17, Appl
C 849	15	3.1	48974	4	US-08-920-422-17	Sequence 17, Appl	922	14	2.9	447	4	US-08-875-533-40	Sequence 40, Appl
C 850	15	3.1	49136	4	US-09-422-869-1	Sequence 1, Appl	923	14	2.9	447	4	US-08-875-533-48	Sequence 48, Appl
C 851	15	3.1	51259	3	US-08-781-891-209	Sequence 209, App	924	14	2.9	447	4	US-08-875-533-49	Sequence 49, Appl
C 852	15	3.1	53526	3	US-08-658-136-2	Sequence 2, Appl	925	14	2.9	447	4	US-08-875-533-50	Sequence 50, Appl
C 853	15	3.1	53577	3	US-08-658-136-1	Sequence 1, Appl	c 926	14	2.9	457	1	US-08-039-364-17	Sequence 17, Appl
C 854	15	3.1	81001	4	US-08-750-580-1	Sequence 1, Appl	c 927	14	2.9	457	4	US-09-158-710-17	Sequence 17, Appl
C 855	15	3.1	98844	4	US-08-791-211-10	Sequence 10, Appl	928	14	2.9	459	4	US-08-875-533-58	Sequence 58, Appl
C 856	15	3.1	112132	4	US-09-741-150-3	Sequence 3, Appl	929	14	2.9	465	3	US-08-469-318-180	Sequence 180, App
C 857	14	2.9	20	1	US-08-418-859-22	Sequence 22, Appl	930	14	2.9	465	3	US-08-468-609A-180	Sequence 180, App
C 858	14	2.9	20	2	US-08-643-181-22	Sequence 22, Appl	931	14	2.9	465	3	US-08-471-045-54	Sequence 54, Appl
C 859	14	2.9	21	4	US-08-943-731-328	Sequence 328, App	932	14	2.9	465	3	US-08-469-712A-54	Sequence 54, Appl
C 860	14	2.9	23	3	US-08-975-688A-12	Sequence 12, Appl	933	14	2.9	465	4	US-08-446-871-54	Sequence 54, Appl
C 861	14	2.9	23	4	US-09-417-090-12	Sequence 12, Appl	934	14	2.9	465	4	US-08-446-872A-180	Sequence 180, App
C 862	14	2.9	23	4	US-09-727-578-12	Sequence 12, Appl	935	14	2.9	465	4	US-08-468-910-54	Sequence 54, Appl
C 863	14	2.9	25	1	US-08-469-005A-8	Sequence 8, Appl	936	14	2.9	465	4	US-08-761-907-54	Sequence 54, Appl
C 864	14	2.9	33	1	US-08-591-070A-24	Sequence 24, Appl	937	14	2.9	465	4	US-08-762-227A-180	Sequence 180, App
C 865	14	2.9	33	2	US-08-927-855-24	Sequence 24, Appl	938	14	2.9	465	5	PCT-US95-01185-180	Sequence 180, App
C 866	14	2.9	33	3	US-08-768-859A-3	Sequence 3, Appl	939	14	2.9	466	6	5496550-9	Patent No. 5496550
C 867	14	2.9	33	3	US-08-767-820A-3	Sequence 3, Appl	940	14	2.9	471	4	US-08-875-533-55	Sequence 55, Appl
C 868	14	2.9	33	3	US-08-622-046B-9	Sequence 9, Appl	c 941	14	2.9	471	4	US-09-134-001C-395	Sequence 395, App
C 869	14	2.9	33	5	PCT-US95-06157-3	Sequence 3, Appl	942	14	2.9	471	4	US-08-875-533-56	Sequence 56, Appl
C 870	14	2.9	53	4	US-09-275-850-289	Sequence 289, App	943	14	2.9	474	4	US-09-042-426-2	Sequence 2, Appl
C 871	14	2.9	60	4	US-09-101-751A-33	Sequence 33, Appl	944	14	2.9	490	3	US-09-291-238-2	Sequence 2, Appl
C 872	14	2.9	82	1	US-08-477-530-24	Sequence 24, Appl	c 945	14	2.9	490	4	US-09-330-760-2	Sequence 2, Appl
C 873	14	2.9	82	1	US-08-477-530-24	Sequence 24, Appl	c 946	14	2.9	490	4	US-09-330-760-2	Sequence 2, Appl
C 874	14	2.9	82	1	US-08-477-530-24	Sequence 24, Appl	c 947	14	2.9	490	4	US-09-330-760-2	Sequence 2, Appl
C 875	14	2.9	87	2	US-08-631-751A-4	Sequence 4, Appl	948	14	2.9	490	4	US-09-330-760-2	Sequence 2, Appl
C 876	14	2.9	100	1	US-08-145-705A-5	Sequence 5, Appl	c 949	14	2.9	490	4	US-09-329-169-2	Sequence 2, Appl
C 877	14	2.9	130	2	US-08-631-751A-1	Sequence 1, Appl	c 950	14	2.9	490	4	US-09-330-760-2	Sequence 2, Appl
C 878	14	2.9	137	4	US-08-931-789A-68	Sequence 68, Appl	c 951	14	2.9	490	4	US-09-328-826-2	Sequence 2, Appl
C 879	14	2.9	137	4	US-08-062-451-68	Sequence 68, Appl	952	14	2.9	492	5	PCT-US95-08295-9	Sequence 9, Appl
C 880	14	2.9	137	4	US-09-598-326-68	Sequence 68, Appl	953	14	2.9	494	4	US-09-040-984-54	Sequence 54, Appl
C 881	14	2.9	231	4	US-09-605-990-5	Sequence 5, Appl	954	14	2.9	494	4	US-09-123-912-54	Sequence 54, Appl
C 882	14	2.9	231	4	US-09-420-797B-5	Sequence 5, Appl	955	14	2.9	494	4	US-09-643-597-54	Sequence 54, Appl
C 883	14	2.9	239	5	PCT-US93-06251-50	Sequence 50, Appl	956	14	2.9	511	4	US-09-404-879A-49	Sequence 49, Appl
C 884	14	2.9	240	1	US-08-222-177A-9	Sequence 9, Appl	957	14	2.9	513	4	US-08-642-274D-48	Sequence 48, Appl
C 885	14	2.9	270	4	US-09-530-378A-8	Sequence 8, Appl	c 958	14	2.9	513	4	US-08-642-274D-48	Sequence 48, Appl
C 886	14	2.9	270	4	US-09-404-879A-130	Sequence 130, App	959	14	2.9	513	4	US-08-952-014C-48	Sequence 48, Appl
C 887	14	2.9	272	4	US-09-071-630-439	Sequence 439, App	c 960	14	2.9	513	4	US-08-952-014C-48	Sequence 48, Appl
C 888	14	2.9	279	3	US-08-952-670-5	Sequence 5, Appl	961	14	2.9	513	4	US-09-288-143-31	Sequence 31, Appl
C 889	14	2.9	281	4	US-09-488-295-10	Sequence 10, Appl	c 962	14	2.9	516	4	US-09-134-001C-729	Sequence 729, App
C 890	14	2.9	301	4	US-08-605-785-234	Sequence 234, App	963	14	2.9	531	4	US-09-404-879A-24	Sequence 24, Appl
C 891	14	2.9	301	4	US-09-439-313-234	Sequence 234, App	c 964	14	2.9	532	4	US-09-280-116-137	Sequence 137, App
C 892	14	2.9	301	4	US-09-352-616A-234	Sequence 234, App	965	14	2.9	536	4	US-09-385-982-347	Sequence 347, App
C 893	14	2.9	301	4	US-09-232-149A-234	Sequence 234, App	c 966	14	2.9	541	4	US-09-227-357-23	Sequence 23, Appl
C 894	14	2.9	312	4	US-09-526-935B-9	Sequence 9, Appl	967	14	2.9	544	4	US-09-221-017B-303	Sequence 303, App
C 895	14	2.9	313	1	US-08-365-981-6	Sequence 6, Appl	968	14	2.9	545	4	US-09-397-212-4	Sequence 4, Appl
C 896	14	2.9	321	4	US-08-385-982-366	Sequence 366, App	969	14	2.9	545	4	US-09-948-802-4	Sequence 4, Appl
C 897	14	2.9	333	1	US-08-594-031-57	Sequence 57, Appl	c 970	14	2.9	546	4	US-08-729-601A-84	Sequence 84, Appl
C 898	14	2.9	340	4	US-09-006-353A-17	Sequence 17, Appl	971	14	2.9	549	4	US-09-522-433B-19	Sequence 19, Appl
C 899	14	2.9	340	4	US-09-573-986-17	Sequence 17, Appl	972	14	2.9	573	4	US-08-906-156A-67	Sequence 67, Appl
C 900	14	2.9	361	4	US-09-397-787-165	Sequence 165, App	c 973	14	2.9	579	4	US-09-134-001C-722	Sequence 722, App
C 901	14	2.9	365	4	US-09-071-035-437	Sequence 437, App	974	14	2.9	590	4	US-08-906-156A-19	Sequence 19, Appl
C 902	14	2.9	372	4	US-09-018-584A-15	Sequence 15, Appl	c 975	14	2.9	599	4	US-09-385-982-74	Sequence 74, Appl
C 903	14	2.9	373	4	US-09-535-008A-17	Sequence 17, Appl	976	14	2.9	600	4	US-09-399-913-64	Sequence 64, Appl

977 14 2.9 601 4 US-09-814-951A-13
978 14 2.9 605 1 US-08-388-779A-3
979 14 2.9 605 2 US-08-591-070A-3
980 14 2.9 605 2 US-08-927-855-3
981 14 2.9 606 4 US-09-328-111-132
982 14 2.9 606 4 US-09-328-111-133
983 14 2.9 615 1 US-08-247-946A-5
984 14 2.9 615 5 PCT-US95-06420-5
985 14 2.9 621 4 US-09-643-597-209
986 14 2.9 622 4 US-09-385-982-46
987 14 2.9 624 1 US-07-782-113B-1
988 14 2.9 624 4 US-09-181-974-1
989 14 2.9 624 4 US-09-518-950-1
990 14 2.9 625 4 US-09-328-111-507
991 14 2.9 627 3 US-08-718-904-9
992 14 2.9 628 4 US-09-385-982-383
993 14 2.9 634 4 US-08-642-274D-26
994 14 2.9 634 4 US-08-952-014C-26
995 14 2.9 663 4 US-09-134-001C-2236
996 14 2.9 674 4 US-09-129-030-23
997 14 2.9 675 4 US-08-134-001C-2605
998 14 2.9 692 1 US-08-592-126-123
999 14 2.9 697 4 US-09-488-295-3
c1000 14 2.9 703 4 US-09-071-035-339

ALIGNMENTS

RESULT 1
US-08-909-965C-1
; Sequence 1, Application US/08909965C
; Patent No. 5936078
; GENERAL INFORMATION:
; APPLICANT: Kuga Tetsuo
; APPLICANT: Nakagawa Satoshi
; APPLICANT: Sakaki Yoshiyuki
; APPLICANT: Zhao Nanding
; APPLICANT: Hashida Hideji
; TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
; TITLE OF INVENTION: AND NOVEL ANTIBODY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO
; STREET: 277 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,965C
; FILING DATE: August 12, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 322745/95
; APPLICATION NUMBER: PCT/JP96/03630
; FILING DATE: 12-Dec-1996
; FILING DATE: 12-Dec-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence S. Perry
; REGISTRATION NUMBER: 31865
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-2400
; TELEFAX: 212-758-2982
; TELEX: 236262
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2688 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: human
; IMMEDIATE SOURCE:
; CLONE: F55
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 358 to 486
; LOCATION: 560 to 799
; LOCATION: 1042 to 1182
; LOCATION: 2105 to 2269
; LOCATION: 2370 to 2462
; IDENTIFICATION METHOD: by experiment
; US-08-909-965C-1
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Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 286 GATTGAGATGTGAGCCACCGTGCCTGGCCAGA 318

RESULT 2

US-09-128-155-17/c
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 5.6%; Score 27; DB 3; Length 176373;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAG 33
Db 168918 CAGATGTGAGCCACCGTGCCTGGCCAG 168892

RESULT 3

US-09-605-785-571/c
; Sequence 571, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-571

Query Match 5.1%; Score 25; DB 4; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGGCC 31
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Db 481 CAGATGTGAGCCACCGTGGCC 457

RESULT 4

US-09-738-894A-3/c
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Query Match 5.1%; Score 25; DB 4; Length 36651;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGGCC 31
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Db 29888 CAGATGTGAGCCACCGTGGCC 29864

RESULT 5

US-08-482-918-43/c
; Sequence 43, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.

; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/482,918
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3513..3595)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3513..3595)
US-08-482-918-43

Query Match 4.7%; Score 23; DB 4; Length 3807;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CCACCGTGCTGGCCAGATTTT 39
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Db 2292 CCACCGTGCTGGCCAGATTTT 2270

RESULT 6

US-09-224-681-43/c
; Sequence 43, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
LOCATION: ..3307, 3513..3595)
FEATURE:
NAME/KEY: mat peptide
LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
LOCATION: ..3307, 3513..3595)
US-09-224-681-43

Query Match 4.7%; Score 23; DB 4; Length 3807;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CCACCGTGCCTGGCCAGATTTT 39
Db 2292 CCACCGTGCCTGGCCAGATTTT 2270

RESULT 7

US-08-336-728A-43/c
; Sequence 43, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Krisztina M.

APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 3807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
LOCATION: ..3307, 3512..3597)
FEATURE:
NAME/KEY: mat peptide
LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
LOCATION: ..3307, 3512..3597)
US-08-336-728A-43

Query Match 4.7%; Score 23; DB 4; Length 3807;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CCACCGTGCCTGGCCAGATTTT 39
Db 2292 CCACCGTGCCTGGCCAGATTTT 2270

RESULT 8

US-08-482-918-47/c
; Sequence 47, Application US/08482918

RESULT 10

US-08-336-728A-47/c
; Sequence 47, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Sugrue, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: cds
; LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,
; LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275,
; LOCATION: 5677..5713)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932
; LOCATION: ..4088, 4314..4397, 4778..4887, 5208..5275, 5677
; LOCATION: ..5713)
US-08-336-728A-47

Query Match 4.7%; Score 23; DB 4; Length 5864;
Best Local Similarity 100.0%; Pred.No. 0.038;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

17 CCACCGTGCTGGCCAGATTTTT 39

Db

3071 CCACCGTGCTGGCCAGATTTTT 3049

RESULT 11

US-09-813-133A-3/c
; Sequence 3, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Query Match 4.7%; Score 23; DB 4; Length 55827;
Best Local Similarity 100.0%; Pred.No. 0.043;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

11 TGTGAGCCACCGTGCTGGCCAG 33

Db

10867 TGTGAGCCACCGTGCTGGCCAG 10845

RESULT 12

US-09-750-580-1
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US2 CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: 10946..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
; NAME/KEY: primer_bind
; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
; NAME/KEY: primer_bind
; LOCATION: 12029..12050
; OTHER INFORMATION: 17-42.pu
; NAME/KEY: primer_bind
; LOCATION: 12581..12603
; OTHER INFORMATION: 17-42.rp complement
; NAME/KEY: primer_bind
; LOCATION: 14992..15012
; OTHER INFORMATION: 17-41.pu
; NAME/KEY: primer_bind
; LOCATION: 15460..15482
; OTHER INFORMATION: 17-41.rp complement
; NAME/KEY: primer_bind
; LOCATION: 42070..42090
; OTHER INFORMATION: 20-841.pu
; NAME/KEY: primer_bind
; LOCATION: 45328..45347
; OTHER INFORMATION: 20-842.pu
; NAME/KEY: primer_bind
; LOCATION: 45863..45883
; OTHER INFORMATION: 20-842.rp complement
; NAME/KEY: primer_bind
; LOCATION: 76644..76664
; OTHER INFORMATION: 20-853.pu
; NAME/KEY: primer_bind
; LOCATION: 77166..77185
; OTHER INFORMATION: 20-853.rp complement
; NAME/KEY: primer_bind
; LOCATION: 1220..1238

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; OTHER INFORMATION: 20-828-311.mis
; NAME/KEY: primer_bind
; LOCATION: 1240..1258
; OTHER INFORMATION: 20-828-311.mis complement
; NAME/KEY: primer_bind
; LOCATION: 12328..12346
; OTHER INFORMATION: 17-42-319.mis
; NAME/KEY: primer_bind
; LOCATION: 12348..12366
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15222..15240
; OTHER INFORMATION: 17-41-250.mis
; NAME/KEY: primer_bind
; LOCATION: 15242..15260
; OTHER INFORMATION: 17-41-250.mis complement
; NAME/KEY: primer_bind
; LOCATION: 42199..42217
; OTHER INFORMATION: 20-841-149.mis
; NAME/KEY: primer_bind
; LOCATION: 42219..42237
; OTHER INFORMATION: 20-841-149.mis complement
; NAME/KEY: primer_bind
; LOCATION: 45423..45441
; OTHER INFORMATION: 20-842-115.mis
; NAME/KEY: primer_bind
; LOCATION: 45443..45461
; OTHER INFORMATION: 20-842-115.mis complement
; NAME/KEY: primer_bind
; LOCATION: 77039..77057
; OTHER INFORMATION: 20-853-415.mis
; NAME/KEY: primer_bind
; LOCATION: 77059..77077
; OTHER INFORMATION: 20-853-415.mis complement
; NAME/KEY: misc_binding
; LOCATION: 1227..1251
; OTHER INFORMATION: 20-828-311.probe
; NAME/KEY: misc_binding
; LOCATION: 12335..12359
; OTHER INFORMATION: 17-42-319.probe
; NAME/KEY: misc_binding
; LOCATION: 15229..15253
; OTHER INFORMATION: 17-41-250.probe
; NAME/KEY: misc_binding
; LOCATION: 42206..42230
; OTHER INFORMATION: 20-841-149.probe
; NAME/KEY: misc_binding
; LOCATION: 45430..45454
; OTHER INFORMATION: 20-842-115.probe
; NAME/KEY: misc_binding
; LOCATION: 77046..77070
; OTHER INFORMATION: 20-853-415.probe
; US-09-750-580-1

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Query Match      4.7%; Score 23; DB 4; Length 81001;
Best Local Similarity 100.0%; Pred.No. 0.043;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 12 GTGAGCCACCGTCGCTGCCAGCA 34
Db 30139 GTGAGCCACCGTCGCTGCCAGCA 30161

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RESULT 13

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US-09-092-508-1
; Sequence 1, Application US/09092508
; Patent No. 6291643
; GENERAL INFORMATION:
; APPLICANT: Henzel, William J.
; TITLE OF INVENTION: APAP-1, AN ACTIVATOR OF C ASPASE-3
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

```

STREET: 3100 No. 6291643west Center, 90 South Seventh St
CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/092.508

FILING DATE: 05-JUN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/048,807

FILING DATE: 05-JUN-1997

APPLICATION NUMBER: 60/055,258

FILING DATE: 07-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Kettelberger, Ph.D., Denise M

REGISTRATION NUMBER: 33,924

REFERENCE/DOCKET NUMBER: 11669.6USU1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 7042 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 578...4159

OTHER INFORMATION:

US-09-092-508-1

Query Match 4.5%; Score 22; DB 4; Length 7042;

Best Local Similarity 100.0%; Pred.No. 0.12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGGCCAG 33

Db 5007 GTGAGCCACCGTGGCCAG 5028

RESULT 14

US-09-435-115-1

Sequence 1, Application US/09435115

Patent No. 6346607

GENERAL INFORMATION:

APPLICANT: Henzel, William J.

TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

STREET: 3100 No. 6346607west Center, 90 South Seventh St

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/435,115

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/092,508

FILING DATE:

APPLICATION NUMBER: 60/055,258

FILING DATE: 07-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Kettelberger, Ph.D., Denise M

REGISTRATION NUMBER: 33,924

REFERENCE/DOCKET NUMBER: 11669.6USU1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 7042 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 578...4159

OTHER INFORMATION:

US-09-435-115-1

Query Match 4.5%; Score 22; DB 4; Length 7042;

Best Local Similarity 100.0%; Pred.No. 0.12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGGCCAG 33

Db 5007 GTGAGCCACCGTGGCCAG 5028

RESULT 15

US-09-098-310-1

Sequence 1, Application US/09098310

Patent No. 6403765

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: TRUNCATED APAF-1 AND METHODS OF USE

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 480140.438

CURRENT APPLICATION NUMBER: US/09/098,310

CURRENT FILING DATE: 1998-06-16

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 7042

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: CDS

LOCATION: (578)...(4159)

US-09-098-310-1

Query Match 4.5%; Score 22; DB 4; Length 7042;

Best Local Similarity 100.0%; Pred.No. 0.12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGGCCAG 33

Db 5007 GTGAGCCACCGTGGCCAG 5028

Search completed: June 17, 2003, 06:29:29

Job time : 38.0245 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 51.3786 Seconds
(without alignments)

13697.491 Million cell updates/sec

Title: US-09-513-888C-1 COPY 7148 7633

Perfect score:

Sequence: 1 agattgcagatgtgagccac.....cattgctcttagtcccaagc 486

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1029858 seqs, 724030393 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Minimum DB seq	length: 9
Maximum DB seq	length: 200000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA: *

Line	File	Applicat	Path	Seq.
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3:	/cgn2_6	/ptodata/1/pubnpa/US05	NEW PUB	seq.*
4:	/cgn2_6	/ptodata/1/pubnpa/US06	PUBCOMB	seq.*
5:	/cgn2_6	/ptodata/1/pubnpa/US07	NEW PUB	seq.*
6:	/cgn2_6	/ptodata/1/pubnpa/PCTUS	PUBCOMB	seq.*
7:	/cgn2_6	/ptodata/1/pubnpa/US08	NEW PUB	seq.*
8:	/cgn2_6	/ptodata/1/pubnpa/US08	PUBCOMB	seq.*
9:	/cgn2_6	/ptodata/1/pubnpa/US09	NEW PUB	seq.*
10:	/cgn2_6	/ptodata/1/pubnpa/US09	PUBCOMB	seq.*
11:	/cgn2_6	/ptodata/1/pubnpa/US10	NEW PUB	seq.*
12:	/cgn2_6	/ptodata/1/pubnpa/US10	PUBCOMB	seq.*
13:	/cgn2_6	/ptodata/1/pubnpa/US60	NEW PUB	seq.*
14:	/cgn2_6	/ptodata/1/pubnpa/US60	PUBCOMB	seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	151	31.1	470	9	US-09-918-995-27892	Sequence 27892, A	
c 2	27	5.6	176373	9	US-10-095-407-17	Sequence 17, App	
3	26	5.3	251	10	US-09-867-701-8144	Sequence 8144, A	
4	26	5.3	371	10	US-09-867-701-7923	Sequence 7923, A	
5	26	5.3	29449	9	US-09-389-442-161	Sequence 161, App	
c 6	26	5.3	29449	9	US-10-074-045-73	Sequence 73, App	
7	25	5.1	819	9	US-10-012-896-571	Sequence 571, App	
c 8	25	5.1	819	9	US-09-895-793-571	Sequence 571, App	
9	25	5.1	819	9	US-09-895-814-571	Sequence 571, App	
c 10	25	5.1	819	10	US-09-759-143-571	Sequence 571, App	
c 11	25	5.1	819	10	US-09-780-669-571	Sequence 571, App	
c 12	25	5.1	819	10	US-09-822-827-571	Sequence 571, App	
c 13	25	5.1	2455	9	US-10-012-896-881	Sequence 881, App	
c 14	25	5.1	2455	9	US-10-012-896-882	Sequence 882, App	
c 15	25	5.1	2455	9	US-09-895-793-881	Sequence 881, App	
c 16	25	5.1	2455	9	US-09-895-793-882	Sequence 882, App	
c 17	25	5.1	2455	9	US-09-895-814-881	Sequence 881, App	
c 18	25	5.1	2455	9	US-09-895-814-882	Sequence 882, App	
c 19	25	5.1	2455	10	US-09-759-143-881	Sequence 881, App	

385	22	4.5	3089	9	US-10-197-693-61	Sequence 61, Appl	458	22	4.5	3089	9	US-10-184-641-61	Sequence 61, Appl
386	22	4.5	3089	9	US-10-197-696-61	Sequence 61, Appl	459	22	4.5	3089	9	US-10-187-888-61	Sequence 61, Appl
387	22	4.5	3089	9	US-10-197-698-61	Sequence 61, Appl	460	22	4.5	3089	9	US-10-194-360-61	Sequence 61, Appl
388	22	4.5	3089	9	US-10-197-703-61	Sequence 61, Appl	461	22	4.5	3089	9	US-10-194-365-61	Sequence 61, Appl
389	22	4.5	3089	9	US-10-197-711-61	Sequence 61, Appl	462	22	4.5	3089	9	US-10-195-895-61	Sequence 61, Appl
390	22	4.5	3089	9	US-10-198-757-61	Sequence 61, Appl	463	22	4.5	3089	9	US-10-195-898-61	Sequence 61, Appl
391	22	4.5	3089	9	US-10-198-761-61	Sequence 61, Appl	464	22	4.5	3089	9	US-10-196-759-61	Sequence 61, Appl
392	22	4.5	3089	9	US-10-198-762-61	Sequence 61, Appl	465	22	4.5	3089	9	US-10-199-302-61	Sequence 61, Appl
393	22	4.5	3089	9	US-10-198-763-61	Sequence 61, Appl	466	22	4.5	3089	9	US-10-201-323-61	Sequence 61, Appl
394	22	4.5	3089	9	US-10-198-767-61	Sequence 61, Appl	467	22	4.5	3089	9	US-10-205-510-61	Sequence 61, Appl
395	22	4.5	3089	9	US-10-199-301-61	Sequence 61, Appl	468	22	4.5	3089	9	US-10-205-891-61	Sequence 61, Appl
396	22	4.5	3089	9	US-10-199-307-61	Sequence 61, Appl	469	22	4.5	3089	9	US-10-205-904-61	Sequence 61, Appl
397	22	4.5	3089	9	US-10-199-312-61	Sequence 61, Appl	470	22	4.5	3089	9	US-10-206-917-61	Sequence 61, Appl
398	22	4.5	3089	9	US-10-199-315-61	Sequence 61, Appl	471	22	4.5	3089	9	US-10-207-923-61	Sequence 61, Appl
399	22	4.5	3089	9	US-10-199-316-61	Sequence 61, Appl	472	22	4.5	3089	9	US-10-207-924-61	Sequence 61, Appl
400	22	4.5	3089	9	US-10-199-457-61	Sequence 61, Appl	473	22	4.5	3089	9	US-10-208-028-61	Sequence 61, Appl
401	22	4.5	3089	9	US-10-199-459-61	Sequence 61, Appl	474	22	4.5	3089	9	US-09-989-328-46	Sequence 46, Appl
402	22	4.5	3089	9	US-10-199-460-61	Sequence 61, Appl	475	22	4.5	3089	9	US-09-993-583-46	Sequence 46, Appl
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405	22	4.5	3089	9	US-10-199-673-61	Sequence 61, Appl	478	22	4.5	3089	9	US-10-180-553-61	Sequence 61, Appl
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412	22	4.5	3089	9	US-10-201-769-61	Sequence 61, Appl	485	22	4.5	3089	9	US-09-997-333-46	Sequence 46, Appl
413	22	4.5	3089	9	US-10-201-771-61	Sequence 61, Appl	486	22	4.5	3089	9	US-09-997-384-46	Sequence 46, Appl
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415	22	4.5	3089	9	US-10-202-410-61	Sequence 61, Appl	488	22	4.5	3089	9	US-10-176-491-61	Sequence 61, Appl
416	22	4.5	3089	9	US-10-202-473-61	Sequence 61, Appl	489	22	4.5	3089	9	US-10-176-979-61	Sequence 61, Appl
417	22	4.5	3089	9	US-10-202-474-61	Sequence 61, Appl	490	22	4.5	3089	9	US-10-187-592-61	Sequence 61, Appl
418	22	4.5	3089	9	US-10-205-503-61	Sequence 61, Appl	491	22	4.5	3089	9	US-10-197-691-61	Sequence 61, Appl
419	22	4.5	3089	9	US-10-205-512-61	Sequence 61, Appl	492	22	4.5	3089	9	US-10-198-771-61	Sequence 61, Appl
420	22	4.5	3089	9	US-10-205-892-61	Sequence 61, Appl	493	22	4.5	3089	9	US-10-174-575A-61	Sequence 61, Appl
421	22	4.5	3089	9	US-10-205-894-61	Sequence 61, Appl	494	22	4.5	3089	9	US-10-179-520-61	Sequence 61, Appl
422	22	4.5	3089	9	US-10-205-896-61	Sequence 61, Appl	495	22	4.5	3089	9	US-10-201-325-61	Sequence 61, Appl
423	22	4.5	3089	9	US-10-205-898-61	Sequence 61, Appl	496	22	4.5	3089	9	US-10-202-941-61	Sequence 61, Appl
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425	22	4.5	3089	9	US-10-205-903-61	Sequence 61, Appl	498	22	4.5	3089	9	US-10-179-526-61	Sequence 61, Appl
426	22	4.5	3089	9	US-10-206-909-61	Sequence 61, Appl	499	22	4.5	3089	9	US-10-173-701-61	Sequence 61, Appl
427	22	4.5	3089	9	US-10-206-910-61	Sequence 61, Appl	500	22	4.5	3089	9	US-10-179-511-61	Sequence 61, Appl
428	22	4.5	3089	9	US-10-206-911-61	Sequence 61, Appl	501	22	4.5	3089	9	US-10-179-518-61	Sequence 61, Appl
429	22	4.5	3089	9	US-10-206-912-61	Sequence 61, Appl	502	22	4.5	3089	9	US-10-183-018-61	Sequence 61, Appl
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431	22	4.5	3089	9	US-10-206-914-61	Sequence 61, Appl	504	22	4.5	3089	9	US-10-184-657-61	Sequence 61, Appl
432	22	4.5	3089	9	US-10-206-920-61	Sequence 61, Appl	505	22	4.5	3089	9	US-10-197-701-61	Sequence 61, Appl
433	22	4.5	3089	9	US-10-206-921-61	Sequence 61, Appl	506	22	4.5	3089	9	US-10-197-706-61	Sequence 61, Appl
434	22	4.5	3089	9	US-10-206-923-61	Sequence 61, Appl	507	22	4.5	3089	9	US-10-201-857-61	Sequence 61, Appl
435	22	4.5	3089	9	US-10-206-925-61	Sequence 61, Appl	508	22	4.5	3089	9	US-10-202-413-61	Sequence 61, Appl
436	22	4.5	3089	9	US-10-206-926-61	Sequence 61, Appl	509	22	4.5	3089	9	US-10-202-938-61	Sequence 61, Appl
437	22	4.5	3089	9	US-10-206-927-61	Sequence 61, Appl	510	22	4.5	3089	9	US-10-202-940-61	Sequence 61, Appl
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439	22	4.5	3089	9	US-10-207-917-61	Sequence 61, Appl	512	22	4.5	3089	9	US-10-205-905-61	Sequence 61, Appl
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443	22	4.5	3089	9	US-10-207-925-61	Sequence 61, Appl	516	22	4.5	3089	10	US-09-989-723-46	Sequence 46, Appl
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445	22	4.5	3089	9	US-10-208-022-61	Sequence 61, Appl	518	22	4.5	3089	10	US-09-989-727-46	Sequence 46, Appl
446	22	4.5	3089	9	US-10-208-023-61	Sequence 61, Appl	519	22	4.5	3089	10	US-09-989-731-46	Sequence 46, Appl
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452	22	4.5	3089	9	US-09-990-439-46	Sequence 46, Appl	525	22	4.5	3089	10	US-09-990-456-46	Sequence 46, Appl
453	22	4.5	3089	9	US-10-173-593-61	Sequence 61, Appl	526	22	4.5	3089	10	US-09-989-721-46	Sequence 46, Appl
454	22	4.5	3089	9	US-10-174-578-61	Sequence 61, Appl	527	22	4.5	3089	10	US-10-052-586-61	Sequence 61, Appl
455	22	4.5	3089	9	US-10-175-741-61	Sequence 61, Appl	528	22	4.5	7042	9	US-10-171-581-264	Sequence 264, App
456	22	4.5	3089	9	US-10-175-750-61	Sequence 61, Appl	529	22	4.5	7042	10	US-09-876-667-1	Sequence 1, Appl
457	22	4.5	3089	9	US-10-176-986-61	Sequence 61, Appl	530	22	4.5	7075	10	US-09-876-667-15	Sequence 15, Appl

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532	22	4.5	8095	9	US-09-989-920-73	Sequence 73, Appl	605	21	4.3	4407	9	US-10-175-752-351	Sequence 351, App
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534	22	4.5	11076	9	US-09-764-891-9421	Sequence 9421, Ap	607	21	4.3	4407	9	US-10-176-757-351	Sequence 351, App
535	22	4.5	12970	9	US-09-764-891-7689	Sequence 7689, Ap	608	21	4.3	4407	9	US-10-176-913-351	Sequence 351, App
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537	22	4.5	14040	9	US-09-764-891-10205	Sequence 10205, A	610	21	4.3	4407	9	US-10-180-557-351	Sequence 351, App
538	22	4.5	20444	9	US-09-764-891-9422	Sequence 9422, Ap	611	21	4.3	4407	9	US-10-173-700-351	Sequence 351, App
539	22	4.5	21724	10	US-09-764-864-1603	Sequence 1603, Ap	612	21	4.3	4407	9	US-10-174-572-351	Sequence 351, App
540	22	4.5	21727	10	US-09-764-864-1604	Sequence 1604, Ap	613	21	4.3	4407	9	US-10-174-579-351	Sequence 351, App
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543	22	4.5	23378	9	US-10-092-154-1514	Sequence 1514, Ap	616	21	4.3	4407	9	US-10-175-739-351	Sequence 351, App
544	22	4.5	23378	10	US-09-764-847-1514	Sequence 1514, Ap	617	21	4.3	4407	9	US-10-175-740-351	Sequence 351, App
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547	22	4.5	32170	10	US-09-764-860-1108	Sequence 1108, Ap	620	21	4.3	4407	9	US-10-176-492-351	Sequence 351, App
548	22	4.5	56737	10	US-09-782-378A-17	Sequence 17, Appl	621	21	4.3	4407	9	US-10-176-747-351	Sequence 351, App
549	22	4.5	83450	9	US-09-811-469-3	Sequence 3, Appl	622	21	4.3	4407	9	US-10-176-750-351	Sequence 351, App
550	22	4.5	88191	10	US-09-799-799-3	Sequence 3, Appl	623	21	4.3	4407	9	US-10-176-985-351	Sequence 351, App
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558	21	4.3	319	10	US-09-764-877-3895	Sequence 3895, Ap	631	21	4.3	4407	9	US-10-173-705-351	Sequence 351, App
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567	21	4.3	401	9	US-09-946-807-1465	Sequence 1465, Ap	640	21	4.3	4407	9	US-10-176-756-351	Sequence 351, App
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584	21	4.3	546	9	US-09-918-995-14987	Sequence 14987, A	657	21	4.3	4407	9	US-10-184-623-351	Sequence 351, App
585	21	4.3	631	9	US-09-871-161-354	Sequence 354, App	658	21	4.3	4407	9	US-10-184-635-351	Sequence 351, App
586	21	4.3	745	9	US-09-796-753-37	Sequence 37, Appl	659	21	4.3	4407	9	US-10-184-637-351	Sequence 351, App
587	21	4.3	978	10	US-09-888-623-15	Sequence 15, Appl	660	21	4.3	4407	9	US-10-184-646-351	Sequence 351, App
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593	21	4.3	1672	10	US-09-764-847-1183	Sequence 1183, Ap	666	21	4.3	4407	9	US-10-187-885-351	Sequence 351, App
594	21	4.3	2092	9	US-10-091-504-1930	Sequence 1930, Ap	667	21	4.3	4407	9	US-10-187-886-351	Sequence 351, App
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596	21	4.3	2209	9	US-09-819-994-1	Sequence 1, Appl	669	21	4.3	4407	9	US-10-176-751-351	Sequence 351, App
597	21	4.3	2394	9	US-10-198-846-11746	Sequence 11746, A	670	21	4.3	4407	9	US-10-176-760-351	Sequence 351, App
598	21	4.3	3011	9	US-10-103-313-630	Sequence 630, App	671	21	4.3	4407	9	US-10-176-990-351	Sequence 351, App
599	21	4.3	4106	9	US-09-764-891-7739	Sequence 7739, Ap	672	21	4.3	4407	9	US-10-180-541-351	Sequence 351, App
600	21	4.3	4407	9	US-10-174-590-351	Sequence 351, App	673	21	4.3	4407	9	US-10-180-542-351	Sequence 351, App
601	21	4.3	4407	9	US-10-176-758-351	Sequence 351, App	674	21	4.3	4407	9	US-10-180-548-351	Sequence 351, App
602	21	4.3	4407	9	US-10-175-737-351	Sequence 351, App	675	21	4.3	4407	9	US-10-180-551-351	Sequence 351, App
603	21	4.3	4407	9	US-10-173-706-351	Sequence 351, App	676	21	4.3	4407	9	US-10-180-998-351	Sequence 351, App

677	21	4.3	4407	9	US-10-180-999-351	Sequence 351, App	750	21	4.3	4407	9	US-10-176-753-351	Sequence 351, App
678	21	4.3	4407	9	US-10-183-013-351	Sequence 351, App	751	21	4.3	4407	9	US-10-176-917-351	Sequence 351, App
679	21	4.3	4407	9	US-10-184-612-351	Sequence 351, App	752	21	4.3	4407	9	US-10-176-982-351	Sequence 351, App
680	21	4.3	4407	9	US-10-184-616-351	Sequence 351, App	753	21	4.3	4407	9	US-10-179-506-351	Sequence 351, App
681	21	4.3	4407	9	US-10-184-617-351	Sequence 351, App	754	21	4.3	4407	9	US-10-179-513-351	Sequence 351, App
682	21	4.3	4407	9	US-10-184-622-351	Sequence 351, App	755	21	4.3	4407	9	US-10-179-514-351	Sequence 351, App
683	21	4.3	4407	9	US-10-184-628-351	Sequence 351, App	756	21	4.3	4407	9	US-10-179-522-351	Sequence 351, App
684	21	4.3	4407	9	US-10-184-629-351	Sequence 351, App	757	21	4.3	4407	9	US-10-180-556-351	Sequence 351, App
685	21	4.3	4407	9	US-10-184-630-351	Sequence 351, App	758	21	4.3	4407	9	US-10-180-560-351	Sequence 351, App
686	21	4.3	4407	9	US-10-184-631-351	Sequence 351, App	759	21	4.3	4407	9	US-10-183-015-351	Sequence 351, App
687	21	4.3	4407	9	US-10-184-632-351	Sequence 351, App	760	21	4.3	4407	9	US-10-184-615-351	Sequence 351, App
688	21	4.3	4407	9	US-10-184-636-351	Sequence 351, App	761	21	4.3	4407	9	US-10-184-620-351	Sequence 351, App
689	21	4.3	4407	9	US-10-184-640-351	Sequence 351, App	762	21	4.3	4407	9	US-10-184-643-351	Sequence 351, App
690	21	4.3	4407	9	US-10-184-650-351	Sequence 351, App	763	21	4.3	4407	9	US-10-184-656-351	Sequence 351, App
691	21	4.3	4407	9	US-10-184-651-351	Sequence 351, App	764	21	4.3	4407	9	US-10-192-010-351	Sequence 351, App
692	21	4.3	4407	9	US-10-187-588-351	Sequence 351, App	765	21	4.3	4407	9	US-10-195-894-351	Sequence 351, App
693	21	4.3	4407	9	US-10-187-597-351	Sequence 351, App	766	21	4.3	4407	9	US-10-205-908-351	Sequence 351, App
694	21	4.3	4407	9	US-10-187-598-351	Sequence 351, App	767	21	4.3	4407	9	US-10-186-855-351	Sequence 351, App
695	21	4.3	4407	9	US-10-187-600-351	Sequence 351, App	768	21	4.3	4407	9	US-10-187-599-351	Sequence 351, App
696	21	4.3	4407	9	US-10-187-601-351	Sequence 351, App	769	21	4.3	4407	9	US-10-187-750-351	Sequence 351, App
697	21	4.3	4407	9	US-10-187-602-351	Sequence 351, App	770	21	4.3	4407	9	US-10-188-780-351	Sequence 351, App
698	21	4.3	4407	9	US-10-187-603-351	Sequence 351, App	771	21	4.3	4407	9	US-10-192-015-351	Sequence 351, App
699	21	4.3	4407	9	US-10-187-741-351	Sequence 351, App	772	21	4.3	4407	9	US-10-194-394-351	Sequence 351, App
700	21	4.3	4407	9	US-10-187-743-351	Sequence 351, App	773	21	4.3	4407	9	US-10-194-425-351	Sequence 351, App
701	21	4.3	4407	9	US-10-187-746-351	Sequence 351, App	774	21	4.3	4407	9	US-10-194-485-351	Sequence 351, App
702	21	4.3	4407	9	US-10-187-747-351	Sequence 351, App	775	21	4.3	4407	9	US-10-195-885-351	Sequence 351, App
703	21	4.3	4407	9	US-10-187-751-351	Sequence 351, App	776	21	4.3	4407	9	US-10-195-890-351	Sequence 351, App
704	21	4.3	4407	9	US-10-187-753-351	Sequence 351, App	777	21	4.3	4407	9	US-10-195-899-351	Sequence 351, App
70													


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US-09-867-701-7923
; Sequence 7923, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7923
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-7923

Query Match      5.3%; Score 26; DB 10; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TGAGCCACCGTGGCTGCCAGATTTT 38
Db      137 TGAGCCACCGTGGCTGCCAGATTTT 162

RESULT 5
US-09-989-442-161/c
; Sequence 161, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
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; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-12-08
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; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
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; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/249,216
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,210
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/226,681
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/235,759
 ; PRIOR FILING DATE: 2000-08-14
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 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/227,182
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,214
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/235,836
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/230,438
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/215,135
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 60/225,266
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/249,218
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,208
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,213
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,212
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,207
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,245
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,244
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,217
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,211
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 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,297
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/232,400
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/231,242
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/232,081
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 ; PRIOR APPLICATION NUMBER: 60/232,080
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/231,414
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/231,244
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/233,064
 ; PRIOR FILING DATE: 2000-09-14
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 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/232,397
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/232,399
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/232,401
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/241,808
 ; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/241,826
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/241,786
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/241,221
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/246,475
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/231,243
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/233,065
 ; PRIOR FILING DATE: 2000-09-14

Query Match 5.3%; Score 26; DB 9; Length 29449;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGTGAGCCACCGTGCCTGGCCAGATT 36
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 Db 20953 TGTGAGCCACCGTGCCTGGCCAGATT 20928

RESULT 6

US-10-074-045-73
 ; Sequence 73, Application US/10074045
 ; Publication No. US20030092102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT221C1
 ; CURRENT APPLICATION NUMBER: US/10/074,045
 ; CURRENT FILING DATE: 2002-02-14
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 73
 ; LENGTH: 29449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-074-045-73

Query Match 5.3%; Score 26; DB 9; Length 29449;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGTGAGCCACCGTGCCTGGCCAGATT 36
 |||||
 Db 8497 TGTGAGCCACCGTGCCTGGCCAGATT 8522

RESULT 7

US-10-012-896-571/c
 ; Sequence 571, Application US/10012896
 ; Publication No. US20020183251A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.


```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-571

Query Match          5.1%; Score 25; DB 9; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 8
US-09-895-793-571/c
; Sequence 571, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-571

Query Match          5.1%; Score 25; DB 9; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 9
US-09-895-814-571/c
; Sequence 571, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-571

Query Match          5.1%; Score 25; DB 9; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 10
US-09-759-143-571/c
; Sequence 571, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun

```

; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-571

Query Match 5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCC 31
|||||
Db 481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 11

US-09-780-669-571/c
; Sequence 571, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-571

Query Match 5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCC 31
|||||
Db 481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 12

US-09-822-827-571/c

; Sequence 571, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-571

Query Match 5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCC 31
|||||
Db 481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 13

US-10-012-896-881/c
; Sequence 881, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeline Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-881

Query Match 5.1%; Score 25; DB 9; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCC 31

Db 481 CAGATGTGAGCCACCGTGGCC 457

RESULT 14

US-10-012-896-882/c

; Sequence 882, Application US/10012896

; Publication No. US20020183251A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; APPLICANT: Wantanabe, Yoshihiro

; APPLICANT: Meagher, Madeleine Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C27

; CURRENT APPLICATION NUMBER: US/10/012.896

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 1011

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 882

; LENGTH: 2455

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-012-896-882

Query Match 5.1%; Score 25; DB 9; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGGCC 31

Db 481 CAGATGTGAGCCACCGTGGCC 457

RESULT 15

US-09-895-793-881/c

; Sequence 881, Application US/09895793

; Publication No. US20020192763A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 552.273 Seconds
(without alignments)

14252.028 Million cell updates/sec

Title: US-09-513-888C-1_COPY_7148_7633

Perfect score: 486

Sequence: 1 agattgcagatgtgagccac.....cattgtcttagtcccaagc 486

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_estc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	240	49.4	294	13	BI059493
3	240	49.4	294	13	BI061867
4	239	49.2	331	12	BF819430
5	200	41.2	713	13	BI226587
6	155	31.9	319	14	BQ345812

BF934192	CM3-NT024	204	12	BF934192	17.9	87	7	C
BF947854	CM2-NN021	306	12	BF947854	13.2	64	8	C
T65465	YC73b09_r1	435	14	T65465	13.2	64	9	C
F11822	HSC32A091_n	302	14	F11822	9.5	46	10	C
AI684794	wa73g05_x	362	9	AI684794	5.8	28	11	C
AA651660	ns89d03.s	399	9	AA651660	5.8	28	12	C
AW974922	EST387027	449	10	AW974922	5.8	28	13	C
BE826708	OVI-EN004	344	12	BE826708	5.6	27	14	C
AQ043261	CIT-HSP-2	350	17	AQ043261	5.6	27	15	C
BE826581	OVI-EN004	364	12	BE826581	5.6	27	16	C
AQ19687	RFC11-10	508	17	AQ19687	5.6	27	17	C
AQ723378	HS-5333_A	527	17	AQ723378	5.6	27	18	C
BE014383	125972_MA	541	10	BE014383	5.6	27	19	C
AA847103	oe09e09.s	351	9	AA847103	5.3	26	20	C
AQ008494	CIT-HSP-2	351	9	AQ008494	5.3	26	21	C
AA837683	oe05h06.s	371	9	AA837683	5.3	26	22	C
AW265498	xq70d07_x	426	10	AW265498	5.3	26	23	C
EG977956	PM1-C1015	464	13	EG977956	5.3	26	24	C
B33966	HS-1023-B2-	466	17	B33966	5.3	26	25	C
AQ818128	HS-5254_B	471	17	AQ818128	5.3	26	26	C
AQ384959	RFC11-13	486	17	AQ384959	5.3	26	27	C
AQ193515	CIT-HSP-2	489	17	AQ193515	5.3	26	28	C
AQ473430	CITBI-E1-	520	17	AQ473430	5.3	26	29	C
AA682840	zj4911.s	554	9	AA682840	5.3	26	30	C
AQ892343	HS-2205_B	562	17	AQ892343	5.3	26	31	C
AW979242	EST391352	641	10	AW979242	5.3	26	32	C
AG049716	Pan trogl	647	17	AG049716	5.3	26	33	C
AG065702	Pan trogl	662	17	AG065702	5.3	26	34	C
BQ216612	AGENCOURT	899	14	BQ216612	5.3	26	35	C
EG104754	602311895	931	12	EG104754	5.3	26	36	C
N84001	KK4277F_Hum	126	14	N84001	5.1	25	37	C
AA657396	nt64f10.s	249	9	AA657396	5.1	25	38	C
BI010653	CM3-EN011	286	13	BI010653	5.1	25	39	C
AW326884	20061_MAR	321	10	AW326884	5.1	25	40	C
B80341	CIT-HSP-204	342	17	B80341	5.1	25	41	C
BE072026	PM0-BT053	346	10	BE072026	5.1	25	42	C
BF858962	MRO-FT019	361	12	BF858962	5.1	25	43	C
AA626829	ab52g10.r	396	9	AA626829	5.1	25	44	C
AQ593490	HS-5445_B	412	17	AQ593490	5.1	25	45	C
AQ675803	HS-2145_A	437	17	AQ675803	5.1	25	46	C
BG230544	ns44g01	440	12	BG230544	5.1	25	47	C
AQ476459	CITBI-E1-	451	17	AQ476459	5.1	25	48	C
AQ695146	HS-5485_B	466	17	AQ695146	5.1	25	49	C
AQ494356	HS-5155_B	527	17	AQ494356	5.1	25	50	C
AQ210269	HS-3251_B	531	17	AQ210269	5.1	25	51	C
AQ382242	RFC11-13	563	17	AQ382242	5.1	25	52	C
BM029691	488021_MA	568	13	BM029691	5.1	25	53	C
BQ777619	il38g01.x	604	14	BQ777619	5.1	25	54	C
AG119978	Pan trogl	659	17	AG119978	5.1	25	55	C
AG000721	Homo sapi	718	17	AG000721	5.1	25	56	C
AG000135	Homo sapi	757	17	AG000135	5.1	25	57	C
AG000136	Homo sapi	758	17	AG000136	5.1	25	58	C
AG000154	Homo sapi	775	17	AG000154	5.1	25	59	C
AG000153	Homo sapi	776	17	AG000153	5.1	25	60	C
AQ383311	RFC11-13	180	17	AQ383311	4.9	24	61	C
AQ081806	RFC11-55	320	17	AQ081806	4.9	24	62	C
AI037914	ox23c07.x	425	9	AI037914	4.9	24	63	C
AQ134180	HS-3057_A	447	17	AQ134180	4.9	24	64	C
T67519	yd12g04.s1	452	14	T67519	4.9	24	65	C
BI124335	RFC1-24-3	474	17	BI124335	4.9	24	66	C
BM667147	UI-E-DX0-	481	13	BM667147	4.9	24	67	C
AW996821	QV3-BN004	498	10	AW996821	4.9	24	68	C
AV707864	AV707864	505	10	AV707864	4.9	24	69	C
AQ485774	RPCI-11-2	525	17	AQ485774	4.9	24	70	C
AQ511433	HS-5214_A	533	17	AQ511433	4.9	24	71	C
AQ666891	HS-2108_A	543	17	AQ666891	4.9	24	72	C
AQ576617	ndxb0089D	579	17	AQ576617	4.9	24	73	C
AZ055831	RPCI-23-4	614	17	AZ055831	4.9	24	74	C
BM991838	UI-H-DF1-	654	14	BM991838	4.9	24	75	C
AG039054	Pan trogl	657	17	AG039054	4.9	24	76	C
AG160445	Pan trogl	683	17	AG160445	4.9	24	77	C
AQ690721	ndxb0082J	945	17	AQ690721	4.9	24	78	C
AQ554471	RPCI-11-4	195	17	AQ554471	4.7	23	79	C

C	80	23	4.7	199	13	BI039464	BI039464 IL3-NT028	153	23	4.7	628	17	AG165879	AG165879 Pan trogl
	81	23	4.7	253	12	BF736236	BF736236 PM4-KT000	154	23	4.7	629	17	AG022087	AG022087 Pan trogl
	82	23	4.7	260	12	BF795628	BF795628 602260315	C 155	23	4.7	630	14	BM932802	BM932802 UI-H-DT0-
	83	23	4.7	271	12	BF795628	BF795628 602260315	C 156	23	4.7	631	14	BM932802	BM932802 UI-H-DT0-
	84	23	4.7	270	12	BF795628	BF795628 602260315	C 157	23	4.7	632	14	BM932802	BM932802 UI-H-DT0-
	85	23	4.7	271	14	H27289	H27289 y116f01.s1	C 158	23	4.7	642	17	AQ012852	AQ012852 CIT-HSP-2
	86	23	4.7	273	17	AQ633853	AQ633853 RPCI-11-4	C 159	23	4.7	643	10	BB217077	BB217077 BB217077
	87	23	4.7	279	10	BE505213	BE505213 dc19c12.x	C 160	23	4.7	645	17	AZ361301	AZ361301 IM0104L24
	88	23	4.7	296	9	AA888097	AA888097 am38g07.s	C 161	23	4.7	645	17	AA126814	AA126814 zn87C10.f
	89	23	4.7	298	9	AA434120	AA434120 zw24d02.s	C 162	23	4.7	652	17	AQ055741	AQ055741 CIT-HSP-2
	90	23	4.7	330	9	AA455282	AA455282 zx80b09.s	C 163	23	4.7	656	17	AQ069900	AQ069900 Pan trogl
	91	23	4.7	330	10	AA856425	AA856425 PM0-CT028	C 164	23	4.7	666	17	AQ471009	AQ471009 CITBI-E1-
	92	23	4.7	335	10	AV688511	AV688511 AV688511	C 165	23	4.7	667	17	AG131706	AG131706 Pan trogl
	93	23	4.7	354	10	AW078821	AW078821 xa99h09.x	C 166	23	4.7	685	17	AG096721	AG096721 Pan trogl
	94	23	4.7	355	10	AW511507	AW511507 x057a01.x	C 167	23	4.7	686	12	EG481182	EG481182 602528502
	95	23	4.7	359	14	H39839	H39839 yP01f12.s1	C 168	23	4.7	698	12	EG480433	EG480433 602529652
	96	23	4.7	363	10	AW390284	AW390284 CM2-ST018	C 169	23	4.7	709	17	AG111647	AG111647 Pan trogl
	97	23	4.7	366	9	A1347665	A1347665 qp01c06.x	C 170	23	4.7	776	12	BG209884	BG209884 RST29412
	98	23	4.7	373	17	AQ521750	AQ521750 HS 5239.A	C 171	23	4.7	776	12	BF107316	BF107316 601823721
	99	23	4.7	376	9	AA644223	AA644223 ab63e10.s	C 172	23	4.7	813	12	BF674925	BF674925 602138003
	100	23	4.7	381	9	A1581433	A1581433 to71h07.x	C 173	23	4.7	813	9	AA195059	AA195059 z135e11.s
	101	23	4.7	381	9	AA581498	AA581498 nd8f02.s	C 174	23	4.7	831	12	EG702736	EG702736 602684289
	102	23	4.7	382	17	AQ0207950	AQ0207950 HS 3145.B	C 175	23	4.7	884	17	AQ740017	AQ740017 HS 5503.A
	103	23	4.7	382	17	AQ041505	AQ041505 CIT-HSP-2	C 176	23	4.7	883	14	BQ653001	BQ653001 AGENCOURT
	104	23	4.7	393	9	A1472736	A1472736 tal3c04.x	C 177	23	4.7	911	14	BQ708999	BQ708999 AGENCOURT
	105	23	4.7	399	9	AA079350	AA079350 zm96d01.s	C 178	23	4.7	1000	14	BQ721541	BQ721541 AGENCOURT
	106	23	4.7	407	10	AW103674	AW103674 x882d07.x	C 179	23	4.7	1025	13	BM547130	BM547130 AGENCOURT
	107	23	4.7	411	14	BQ101225	BQ101225 1j25f02.y	C 180	23	4.7	1034	14	BM904665	BM904665 AGENCOURT
	108	23	4.7	416	13	BM667496	BM667496 UI-E-DX0-	C 181	22	4.5	1258	14	BQ646064	BQ646064 AGENCOURT
	109	23	4.7	420	10	AW316599	AW316599 xW09604.x	C 182	22	4.5	1119	12	BF918856	BF918856 QV0-NT015
	110	23	4.7	421	10	AW440568	AW440568 xt15e04.x	C 183	22	4.5	142	12	BF945953	BF945953 CM0-NN115
	111	23	4.7	421	17	AQ187918	AQ187918 HS 3138.B	C 184	22	4.5	145	10	BE173452	BE173452 RC2-HT056
	112	23	4.7	422	12	BE826611	BE826611 601433420	C 185	22	4.5	169	10	AW380926	AW380926 CM2-HT028
	113	23	4.7	429	9	AA614449	AA614449 nm89d09.s	C 186	22	4.5	175	9	AA318209	AA318209 EST20530
	114	23	4.7	429	14	BQ184116	BQ184116 UI-E-EJ1-	C 187	22	4.5	197	13	BI017658	BI017658 PM1-ET025
	115	23	4.7	438	9	AA678932	AA678932 ah08g03.s	C 188	22	4.5	202	12	BF924053	BF924053 QV4-NT024
	116	23	4.7	440	12	BG611079	BG611079 602612028	C 189	22	4.5	206	9	AA678616	AA678616 ah03c11.s
	117	23	4.7	442	17	AQ836262	AQ836262 HS 5511.A	C 190	22	4.5	208	12	BF767054	BF767054 RC4-CN008
	118	23	4.7	446	17	AZ110237	AZ110237 RPCI-23-4	C 191	22	4.5	215	14	BQ376042	BQ376042 RC0-TN007
	119	23	4.7	449	10	AW081610	AW081610 xc32b10.x	C 192	22	4.5	223	17	AZ808053	AZ808053 2M0071B22
	120	23	4.7	453	12	BF846122	BF846122 QV0-EN005	C 193	22	4.5	226	10	BE141341	BE141341 MR0-HT007
	121	23	4.7	455	9	AA181700	AA181700 zp55h01.s	C 194	22	4.5	227	9	AA654485	AA654485 nt62h05.s
	122	23	4.7	456	14	BM679390	BM679390 UI-E-E00-	C 195	22	4.5	239	14	BQ376041	BQ376041 RC0-TN007
	123	23	4.7	460	10	BE301610	BE301610 bb75e09.x	C 196	22	4.5	256	12	BF950271	BF950271 CM3-NN118
	124	23	4.7	463	14	BQ024670	BQ024670 UI-1-BBP	C 197	22	4.5	263	12	BF912838	BF912838 IL3-UT011
	125	23	4.7	465	9	AA283753	AA283753 zt19g06.s	C 198	22	4.5	263	12	BF915805	BF915805 IL3-UT011
	126	23	4.7	471	10	BE677244	BE677244 7d82d09.x	C 199	22	4.5	275	14	AW802845	AW802845 IL2-UM007
	127	23	4.7	476	14	N67313	N67313 yz51e02.s1	C 200	22	4.5	279	10	AW972743	AW972743 EST384837
	128	23	4.7	483	17	AQ193028	AQ193028 HS 3055.B	C 201	22	4.5	284	12	BF812870	BF812870 CM2-CI018
	129	23	4.7	495	10	AW080160	AW080160 xc49c05.x	C 202	22	4.5	284	14	BQ185176	BQ185176 UI-E-EJ1-
	130	23	4.7	495	14	N42784	N42784 yz25g12.r1	C 203	22	4.5	288	12	BE932779	BE932779 CM4-HT086
	131	23	4.7	498	14	BM995211	BM995211 UI-H-ED0-	C 204	22	4.5	293	12	BF944142	BF944142 CM0-NN015
	132	23	4.7	500	17	AQ216864	AQ216864 HS 3253.B	C 205	22	4.5	293	12	BF944224	BF944224 CM0-NN115
	133	23	4.7	505	14	BM716303	BM716303 UI-E-COI-	C 206	22	4.5	298	12	BF945947	BF945947 CM0-NN115
	134	23	4.7	511	10	BE464585	BE464585 h85a05.x	C 207	22	4.5	300	13	BM110091	BM110091 EST557627
	135	23	4.7	511	17	AQ379061	AQ379061 RPCI11-13	C 208	22	4.5	304	14	BQ187986	BQ187986 UI-E-EJ1-
	136	23	4.7	512	17	AQ568405	AQ568405 HS 5239.B	C 209	22	4.5	306	14	F07193	F07193 HSCIYD091.n
	137	23	4.7	520	10	AV718743	AV718743 AV718743	C 210	22	4.5	307	9	AA834891	AA834891 oeo2e08.s
	138	23	4.7	521	17	AQ172248	AQ172248 HS 3179.B	C 211	22	4.5	310	14	T11629	T11629 AI342F Hear
	139	23	4.7	527	17	AQ564404	AQ564404 HS 5355.A	C 212	22	4.5	317	10	AA805449	AA805449 QV1-UM010
	140	23	4.7	527	17	AQ564404	AQ564404 HS 5355.A	C 213	22	4.5	318	9	AA321595	AA321595 EST24203
	141	23	4.7	536	17	AQ122660	AQ122660 HS 3086.A	C 214	22	4.5	319	9	AI538236	AI538236 tp37h08.x
	142	23	4.7	536	17	AQ628374	AQ628374 CITBI-E1-	C 215	22	4.5	331	12	BG005999	BG005999 PM4-GN023
	143	23	4.7	537	17	B52287	B52287 CIT-HSP-387	C 216	22	4.5	337	9	AA865144	AA865144 oh48c04.s
	144	23	4.7	544	12	BE701335	BE701335 MR0-NN015	C 217	22	4.5	340	10	AW023515	AW023515 df56a09.y
	145	23	4.7	546	9	AI889995	AI889995 wm80c03.x	C 218	22	4.5	343	9	AA836097	AA836097 odi5b01.s
	146	23	4.7	556	17	AQ589258	AQ589258 CITBI-E1-	C 219	22	4.5	344	9	AA975915	AA975915 oo33d01.s
	147	23	4.7	557	12	BF817600	BF817600 MR3-CI018	C 220	22	4.5	347	17	AQ177372	AQ177372 HS 2208.A
	148	23	4.7	561	9	AA439758	AA439758 LD14406.5	C 221	22	4.5	349	17	AQ263599	AQ263599 CITBI-E1-
	149	23	4.7	576	9	AUI55117	AUI55117 AUI55117	C 222	22	4.5	351	13	BM662212	BM662212 UI-E-CL0-
	150	23	4.7	581	17	AQ377968	AQ377968 RPCI-11-1	C 223	22	4.5	360	17	AQ347796	AQ347796 RPCI11-13
	151	23	4.7	589	9	AA483043	AA483043 ne71b09.s	C 224	22	4.5	362	17	AQ965225	AQ965225 LERIB10TF
	152	23	4.7	606	14	BQ778458	BQ778458 i131d07.x	C 225	22	4.5	364	9	AI233155	AI233155 EST229843

c 226	22	4.5	364	9	AA341813	AA341813 EST47225	c 299	22	4.5	499	17	AQ298446	AQ298446 HS 2231.B
c 227	22	4.5	364	9	AA525293	AA525293 ni53b03.s	c 300	22	4.5	503	17	AQ244830	AQ244830 CITBI-EI-
c 228	22	4.5	366	14	T70937	T70937 yc49a12.r1	c 301	22	4.5	510	17	AQ228412	AQ228412 HS 2014.B
c 229	22	4.5	371	9	AA626404	AA626404 ab49c03.r	c 302	22	4.5	513	13	BI754824	BI754824 603025281
c 230	22	4.5	376	9	AA49460	AA49460 zx05f03.s	c 303	22	4.5	513	14	BM978885	BM978885 UI-CF-DU1
c 231	22	4.5	376	9	AA508036	AA508036 ng92c08.s	c 304	22	4.5	513	12	BF187711	BF187711 EST443998
c 232	22	4.5	377	10	BE062321	BE062321 RCL-BT025	c 305	22	4.5	519	14	BM690164	BM690164 UI-E-CLO-
c 233	22	4.5	386	10	AW961477	AW961477 EST373549	c 306	22	4.5	520	17	AQ127555	AQ127555 HS 3062.B
c 234	22	4.5	388	17	AV691147	AV691147 AV691147	c 307	22	4.5	526	9	AL603305	AL603305 DKF2p6861
c 235	22	4.5	389	10	AQ032744	AQ032744 HS 2213.B	c 308	22	4.5	528	17	B37130	B37130 HS-1042-BI-
c 236	22	4.5	390	12	BF842141	BF842141 RC6-HT084	c 309	22	4.5	528	17	AQ380439	AQ380439 RFC111-16
c 237	22	4.5	392	12	EG057631	EG057631 nan93h05.	c 310	22	4.5	529	17	AQ111124	AQ111124 CIT-HSP-2
c 238	22	4.5	392	17	AQ171543	AQ171543 HS 5429.B	c 311	22	4.5	531	10	AW961606	AW961606 EST373678
c 239	22	4.5	396	9	AI273675	AI273675 ql61h01.x	c 312	22	4.5	535	17	AG020061	AG020061 Homo sapi
c 240	22	4.5	397	9	AI887797	AI887797 wml18h12.x	c 313	22	4.5	536	10	AW170332	AW170332 xn59g03.x
c 241	22	4.5	399	10	AW271071	AW271071 xt48c12.x	c 314	22	4.5	538	12	BG776152	BG776152 602663107
c 242	22	4.5	400	14	M77950	M77950 EST01534.Fe	c 315	22	4.5	539	10	AV685047	AV685047 AV685047
c 243	22	4.5	401	9	AA593535	AA593535 nm28b04.s	c 316	22	4.5	540	10	AW090261	AW090261 xc85h08.x
c 244	22	4.5	402	9	AA318481	AA318481 EST20562	c 317	22	4.5	540	17	AQ477094	AQ477094 CITBI-EI-
c 245	22	4.5	405	17	B40586	B40586 HS-1051-B2-	c 318	22	4.5	542	17	AQ628282	AQ628282 CITBI-EI-
c 246	22	4.5	406	9	AI360521	AI360521 qx18d10.x	c 319	22	4.5	544	17	AQ189519	AQ189519 HS 3203.B
c 247	22	4.5	409	14	BM792401	BM792401 K-EST0072	c 320	22	4.5	546	17	AQ382744	AQ382744 RFC111-16
c 248	22	4.5	410	9	AI278211	AI278211 ql83d09.x	c 321	22	4.5	550	10	BE159081	BE159081 MR0-HT040
c 249	22	4.5	410	17	AQ630370	AQ630370 RPL1-11-4	c 322	22	4.5	550	10	BE548885	BE548885 601073327
c 250	22	4.5	413	9	AI268564	AI268564 qo37e08.x	c 323	22	4.5	551	17	AQ626960	AQ626960 CITBI-EI-
c 251	22	4.5	413	9	AI475798	AI475798 tcl2c07.x	c 324	22	4.5	552	14	N79258	N79258 za63h10.s1
c 252	22	4.5	414	9	AI560073	AI560073 tcl2c07.x	c 325	22	4.5	552	17	AQ406908	AQ406908 HS 5113.A
c 253	22	4.5	414	9	BE173615	BE173615 RC2-HT056	c 326	22	4.5	554	17	AQ386113	AQ386113 RFC111-14
c 254	22	4.5	415	9	AA618451	AA618451 nm27f08.s	c 327	22	4.5	556	17	AQ569873	AQ569873 HS-5357.A
c 255	22	4.5	416	12	BG474043	BG474043 602516603	c 328	22	4.5	557	17	AQ611081	AQ611081 HS 5100.B
c 256	22	4.5	417	17	AQ695151	AQ695151 HS 5485.B	c 329	22	4.5	560	17	AQ392493	AQ392493 CITBI-EI-
c 257	22	4.5	419	10	BE173511	BE173511 RC2-HT056	c 330	22	4.5	561	9	AL697074	AL697074 DKF2p6860
c 258	22	4.5	424	9	AI821595	AI821595 nc39a08.x	c 331	22	4.5	561	10	BE300991	BE300991 ba82a12.x
c 259	22	4.5	424	12	BF900891	BF900891 IL2-WT017	c 332	22	4.5	562	17	AQ111084	AQ111084 CIT-HSP-2
c 260	22	4.5	428	9	AI859219	AI859219 wl34c12.x	c 333	22	4.5	563	10	BE674238	BE674238 7877c01.x
c 261	22	4.5	428	10	AW276933	AW276933 xp57g10.x	c 334	22	4.5	573	17	AQ774558	AQ774558 HS 3142.A
c 262	22	4.5	430	9	AL041013	AL041013 DKF2p4340	c 335	22	4.5	575	10	AW817814	AW817814 PMO-ST026
c 263	22	4.5	432	10	AW818004	AW818004 CM3-ST027	c 336	22	4.5	575	13	BM503226	BM503226 i973c09.x
c 264	22	4.5	434	12	BG483361	BG483361 602503270	c 337	22	4.5	578	10	BE252421	BE252421 601108224
c 265	22	4.5	435	14	N69462	N69462 za18a08.s1	c 338	22	4.5	578	12	BF694257	BF694257 602082888
c 266	22	4.5	438	17	AQ167966	AQ167966 HS 2232.B	c 339	22	4.5	578	12	BE869668	BE869668 60145770
c 267	22	4.5	444	17	AZ626797	AZ626797 IM0467E13	c 340	22	4.5	578	17	AQ679563	AQ679563 HS 5346.A
c 268	22	4.5	444	17	AQ569912	AQ569912 HS 5328.A	c 341	22	4.5	587	17	B68220	B68220 CIT978SK-A-
c 269	22	4.5	445	17	AQ020367	AQ020367 CIT-HSP-2	c 342	22	4.5	592	17	AQ509373	AQ509373 nbxb0096K
c 270	22	4.5	445	17	AZ773462	AZ773462 UP 500-4C	c 343	22	4.5	594	9	AL598913	AL598913 DKF2p313D
c 271	22	4.5	445	17	AQ594759	AQ594759 HS 5413.A	c 344	22	4.5	594	10	BE180543	BE180543 RC3-HT062
c 272	22	4.5	446	9	AA225034	AA225034 nc34b07.F	c 345	22	4.5	596	9	AL707906	AL707906 DKF2p686B
c 273	22	4.5	448	17	AQ734927	AQ734927 HS 3051.A	c 346	22	4.5	597	9	AL134457	AL134457 DKF2p547J
c 274	22	4.5	450	12	BG170524	BG170524 602322914	c 347	22	4.5	597	10	BE148631	BE148631 MR0-HT024
c 275	22	4.5	451	17	AQ129984	AQ129984 HS 2170.A	c 348	22	4.5	597	17	AQ965227	AQ965227 LBR1B10TR
c 276	22	4.5	452	10	AW974897	AW974897 EST387002	c 349	22	4.5	600	9	AL138218	AL138218 DKF2p547A
c 277	22	4.5	453	10	BE173455	BE173455 RC2-HT056	c 350	22	4.5	600	13	BI509736	BI509736 BBI70019B
c 278	22	4.5	456	17	AQ790067	AQ790067 HS 3193.B	c 351	22	4.5	600	17	AQ478963	AQ478963 RPL1-11-2
c 279	22	4.5	456	17	B30904	B30904 HS-1003-A2-	c 352	22	4.5	606	17	AQ632815	AQ632815 RPL1-11-4
c 280	22	4.5	458	17	AQ114900	AQ114900 CIT-HSP-2	c 353	22	4.5	609	10	AW817810	AW817810 PMO-ST026
c 281	22	4.5	459	17	B59129	B59129 CIT-HSP-201	c 354	22	4.5	609	12	BE929451	BE929451 MR0-GN002
c 282	22	4.5	461	13	BM312512	BM312512 iq75e03.y	c 355	22	4.5	613	14	BM722009	BM722009 UI-E-E00
c 283	22	4.5	466	9	AI138918	AI138918 qc56g02.x	c 356	22	4.5	616	10	AW949748	AW949748 EST361818
c 284	22	4.5	469	12	BF955438	BF955438 MK4-NM119	c 357	22	4.5	618	17	AQ543062	AQ543062 RPL1-11-3
c 285	22	4.5	472	14	BM997236	BM997236 UI-H-DHO-	c 358	22	4.5	623	14	BQ778000	BQ778000 il139g03.y
c 286	22	4.5	473	10	AW102811	AW102811 xdg8e05.x	c 359	22	4.5	630	17	AG152294	AG152294 Pan trogl
c 287	22	4.5	476	9	AA741020	AA741020 ny99b11.s	c 360	22	4.5	630	17	AQ515606	AQ515606 HS 5237.A
c 288	22	4.5	477	14	BQ018445	BQ018445 UI-H-DH1-	c 361	22	4.5	632	17	AG083897	AG083897 Pan trogl
c 289	22	4.5	477	17	AQ348428	AQ348428 RPL11-13	c 362	22	4.5	640	9	AL044041	AL044041 DKF2p434K
c 290	22	4.5	478	9	AL598189	AL598189 DKF2p313H	c 363	22	4.5	641	17	AG090402	AG090402 Pan trogl
c 291	22	4.5	480	9	AI091282	AI091282 ow62c02.x	c 364	22	4.5	643	17	AG078779	AG078779 Pan trogl
c 292	22	4.5	485	9	AI371804	AI371804 tai2a04.x	c 365	22	4.5	647	12	BE888431	BE888431 601512802
c 293	22	4.5	485	12	BF897789	BF897789 QV1-WT022	c 366	22	4.5	647	14	BM791560	BM791560 K-EST0071
c 294	22	4.5	490	17	AQ893312	AQ893312 HS 3175.A	c 367	22	4.5	648	10	AQ387105	AQ387105 MR0-ST002
c 295	22	4.5	494	17	AQ588960	AQ588960 CITBI-EI-	c 368	22	4.5	648	17	AQ266668	AQ266668 RPL11-74
c 296	22	4.5	496	14	BM720112	BM720112 UI-E-E00-	c 369	22	4.5	652	17	AG064845	AG064845 Pan trogl
c 297	22	4.5	497	9	AA488898	AA488898 aa55h05.s	c 370	22	4.5	656	17	AG142083	AG142083 Pan trogl
c 298	22	4.5	497	17	AQ233463	AQ233463 HS 2045.B	c 371	22	4.5				

C 372	22	4.5	658	12	BG530359	602559296	445	21	4.3	148	12	BG003545	CM0-GN010
C 373	22	4.5	660	17	AG045026	Pan trogl	446	21	4.3	153	12	BF830860	CM1-HT087
C 374	22	4.5	663	10	AG045026	Pan trogl	C 447	21	4.3	189	9	AA337750	EST42522
C 375	22	4.5	664	10	BE351155	RFC111-12	C 448	21	4.3	189	12	BF994645	CM0-GN009
C 376	22	4.5	665	17	AG157485	Pan trogl	C 449	21	4.3	205	12	BF841886	RC6-HT084
C 377	22	4.5	672	10	BE541778	601063746	C 450	21	4.3	208	12	BF810994	CM2-CI017
C 378	22	4.5	672	17	AG134171	Pan trogl	C 451	21	4.3	208	12	BF818609	MR3-CI018
C 379	22	4.5	673	17	AG051795	Pan trogl	C 452	21	4.3	215	12	BF928054	IL5-NT022
C 380	22	4.5	677	17	AG183516	Pan trogl	C 453	21	4.3	216	9	AL601789	DKFZp313G
C 381	22	4.5	681	17	AG129457	Pan trogl	C 454	21	4.3	217	10	AW862049	RC3-CT034
C 382	22	4.5	685	17	AG129457	Pan trogl	C 455	21	4.3	220	10	AW814200	MR3-ST020
C 383	22	4.5	687	12	AG123897	CITBI-E1	C 456	21	4.3	220	10	AW814200	MR3-ST020
C 384	22	4.5	688	17	AG107615	Pan trogl	C 457	21	4.3	225	14	T10591	hbc623 Huma
C 385	22	4.5	691	14	AG107615	Pan trogl	C 458	21	4.3	231	12	BF929538	OV3-NT021
C 386	22	4.5	693	10	AV733710	AV733710	C 459	21	4.3	232	12	BE743332	601573249
C 387	22	4.5	694	17	AZ354813	IM0094D16	C 460	21	4.3	233	14	H86067	YS93C06.s1
C 388	22	4.5	695	17	AG171499	Pan trogl	C 461	21	4.3	234	14	T10583	hbc332 Huma
C 389	22	4.5	696	17	AG169302	Pan trogl	C 462	21	4.3	236	10	AW089809	kd13C03.X
C 390	22	4.5	706	17	AZ970121	2M0243H09	C 463	21	4.3	242	13	AG951696	MR1-CT073
C 391	22	4.5	707	17	AG096186	Pan trogl	C 464	21	4.3	248	9	AA669059	ab92f03.s
C 392	22	4.5	708	14	EQ004148	UT-H-E10	C 465	21	4.3	248	10	BE155313	PM1-HT035
C 393	22	4.5	711	17	AG098953	Pan trogl	C 466	21	4.3	248	10	BE160803	PM1-HT042
C 394	22	4.5	717	13	AG965738	602830594	C 467	21	4.3	249	10	AW895905	QV4-NN003
C 395	22	4.5	718	17	AG012676	Homo sapi	C 468	21	4.3	253	17	AO281285	RPC111-80
C 396	22	4.5	719	17	AG012678	Homo sapi	C 469	21	4.3	262	9	AI612032	tt63e01.x
C 397	22	4.5	720	17	AG012683	Homo sapi	C 470	21	4.3	263	14	Z21052	HSAADKIG H
C 398	22	4.5	721	14	BQ512442	EST619857	C 471	21	4.3	264	17	AO063244	CIT-HSP-2
C 399	22	4.5	724	17	AG012682	Homo sapi	C 472	21	4.3	265	9	AA381775	EST94893
C 400	22	4.5	725	17	AG172854	Pan trogl	C 473	21	4.3	268	10	BE152573	CM2-HT032
C 401	22	4.5	733	10	AV706448	AV706448	C 474	21	4.3	268	12	BF935802	IL2-NT020
C 402	22	4.5	738	12	AV703460	AV703460	C 475	21	4.3	270	12	BF767026	RC5-CS002
C 403	22	4.5	739	12	BG850644	1024028H1	C 476	21	4.3	272	14	BF997339	OV3-GN020
C 404	22	4.5	746	12	BG288816	602387914	C 477	21	4.3	272	14	R19542	Y926f03.x1
C 405	22	4.5	746	13	BM013316	603635233	C 478	21	4.3	276	12	BF834158	RC1-HT022
C 406	22	4.5	753	14	BM997063	UT-H-ED0	C 479	21	4.3	277	10	AW370083	MR0-BT024
C 407	22	4.5	754	12	BG326602	602410833	C 480	21	4.3	278	17	B57322	CIT-HSP-200
C 408	22	4.5	776	17	AG091643	HS 3203 B	C 481	21	4.3	281	10	AW370055	MR0-BT024
C 409	22	4.5	786	17	BH024116	Gm_UMB001	C 482	21	4.3	283	14	N74177	za76f08.s1
C 410	22	4.5	788	17	AG029909	Pan trogl	C 483	21	4.3	284	17	AZ317123	IN0035F07
C 411	22	4.5	800	12	BG402348	602465934	C 484	21	4.3	285	17	AQ284723	RPC111-89
C 412	22	4.5	812	13	B1116317	602869057	C 485	21	4.3	285	17	AW370099	MR0-BT024
C 413	22	4.5	825	12	BG109294	60281132	C 486	21	4.3	288	10	AW576658	MR0-BT024
C 414	22	4.5	834	17	AQ746306	HS 2277 A	C 487	21	4.3	288	10	AW805113	QV1-UM009
C 415	22	4.5	843	17	BH560119	BOGWH70TF	C 488	21	4.3	288	17	AQ391637	CITBI-E1
C 416	22	4.5	844	17	AQ891345	HS_5263 A	C 489	21	4.3	288	10	BE069109	OV3-BT037
C 417	22	4.5	844	17	AZ175714	SP_0133 A	C 490	21	4.3	290	10	BE069196	QV3-BT037
C 418	22	4.5	853	10	BE470416	IPRk0146	C 491	21	4.3	291	12	BF927262	CM1-NT024
C 419	22	4.5	854	13	B1912717	603176374	C 492	21	4.3	291	13	BI050929	CM4-GN036
C 420	22	4.5	854	17	AQ900581	HS 2087 B	C 493	21	4.3	294	12	BF741047	QV1-HB003
C 421	22	4.5	913	12	BG108218	602280101	C 494	21	4.3	294	12	BF741050	QV1-HB003
C 422	22	4.5	920	12	BF982222	60236273	C 495	21	4.3	294	14	BQ301850	QV1-HB003
C 423	22	4.5	921	14	BQ425349	AGENCOURT	C 496	21	4.3	295	9	AA831801	oe21b02.s
C 424	22	4.5	927	12	BF983588	60236578	C 497	21	4.3	297	12	BF766735	RC5-CS002
C 425	22	4.5	931	14	BQ942350	AGENCOURT	C 498	21	4.3	298	17	B78904	CIT-HSP-292
C 426	22	4.5	940	12	BE787771	601482347	C 499	21	4.3	299	9	AA338204	EST43100
C 427	22	4.5	952	14	BQ674594	AGENCOURT	C 500	21	4.3	299	9	AA338204	EST43100
C 428	22	4.5	1002	17	AG031839	Pan trogl	C 501	21	4.3	299	9	AA338204	EST43100
C 429	22	4.5	1010	13	BM465334	AGENCOURT	C 502	21	4.3	300	17	AQ106944	HS_3086_A
C 430	22	4.5	1015	12	BF206123	601869480	C 503	21	4.3	300	17	AQ554436	RPC1-11-4
C 431	22	4.5	1042	12	BG683708	602651731	C 504	21	4.3	302	13	BI051239	CM4-GN036
C 432	22	4.5	1078	13	BM415532	OP20608 M	C 505	21	4.3	304	10	AW935933	QV3-BT001
C 433	22	4.5	1082	12	BG620534	601483796	C 506	21	4.3	305	14	N75715	YV31b02.x1
C 434	22	4.5	1108	12	BG387308	602456058	C 507	21	4.3	306	12	BF848613	IL5-EN008
C 435	22	4.5	1124	12	BF981559	602309437	C 508	21	4.3	307	12	EG059365	nah50c11.
C 436	22	4.5	1133	14	BQ050855	AGENCOURT	C 509	21	4.3	310	9	AA832016	oe22b10.s
C 437	22	4.5	1201	17	CNS016FT	AGENCOURT	C 510	21	4.3	310	10	BE138504	xt76c01.x
C 438	22	4.5	1282	12	BG111360	602281721	C 511	21	4.3	311	17	AQ303086	RPC1-11-3
C 439	22	4.5	1371	12	BG035008	602325282	C 512	21	4.3	312	10	AW203108	f108109.x
C 440	22	4.5	1522	13	BM478753	AGENCOURT	C 513	21	4.3	313	13	BI115748	602866202
C 441	22	4.3	102	10	AW843450	CM0-CN003	C 514	21	4.3	314	9	AA856950	oe03d01.s
C 442	21	4.3	109	17	AQ537311	RPC1-11-3	C 515	21	4.3	316	9	AI886432	wm94902.x
C 443	21	4.3	122	13	BI024994	CM4-MT028	C 516	21	4.3	319	9	AA669647	ac20f02.s
C 444	21	4.3	145	9	AA320448	EST23157	C 517	21	4.3	319	10	BB085179	BB085179

518	21	4.3	320	12	BF927045	BF927045 CM2-NT019	c 591	21	4.3	378	17	AQ486453	AQ486453 RPCI-11-2
519	21	4.3	326	10	AW339970	AW339970 ha61910.x	c 592	21	4.3	379	13	BI052200	BI052200 CM4-GN031
520	21	4.3	326	9	AA345399	AA345399 EST51412	c 593	21	4.3	379	13	BI052200	BI052200 CM4-GN031
521	21	4.3	326	17	AQ264626	AQ264626 CITBI-E1-	c 594	21	4.3	381	14	R83702	R83702 YQ14309.r1
522	21	4.3	328	9	AA502688	AA502688 ng63a04.b	c 595	21	4.3	382	17	AQ080883	AQ080883 GSGT0101
523	21	4.3	329	9	AA908540	AA908540 o982910.8	c 596	21	4.3	382	17	AQ122945	AQ122945 HS_3094_B
524	21	4.3	329	17	AQ594641	AQ594641 HS_2120_B	c 597	21	4.3	383	9	AI417675	AI417675 tg80h05.x
525	21	4.3	331	10	BE150331	BE150331 QV4-HT026	c 598	21	4.3	384	12	BE934245	BE934245 CM0-HT091
526	21	4.3	333	17	AQ094318	AQ094318 HS_3025_B	c 599	21	4.3	384	12	BE934245	BE934245 CM0-HT091
527	21	4.3	334	14	H59346	H59346 Yr2701.r1	c 600	21	4.3	384	17	AQ062048	AQ062048 CIT-HSP-2
528	21	4.3	335	17	AQ393389	AQ393389 CITBI-E1-	c 601	21	4.3	387	9	AA418048	AA418048 zv97h12.s
529	21	4.3	336	9	AI922115	AI922115 wn88f01.x	c 602	21	4.3	388	9	AI648670	AI648670 tx63h05.x
530	21	4.3	336	13	BG957884	BG957884 IL3-CT067	c 603	21	4.3	389	12	BF897633	BF897633 RCI-MT016
531	21	4.3	337	13	BG953731	BG953731 MR4-CT053	c 604	21	4.3	390	12	BF896026	BF896026 CM2-MT015
532	21	4.3	338	12	BF771418	BF771418 IL5-IT002	c 605	21	4.3	391	14	N44678	N44678 YV22b03.r1
533	21	4.3	338	13	BI032335	BI032335 CM3-NN025	c 606	21	4.3	391	14	N44678	N44678 YV22b03.r1
534	21	4.3	339	17	AQ081573	AQ081573 RPCI11-54	c 607	21	4.3	392	17	AQ243921	AQ243921 HS_2058_B
535	21	4.3	340	9	AA601930	AA601930 np02e04.s	c 608	21	4.3	392	14	HA0536	HA0536 YP63f02.s1
536	21	4.3	340	14	F09292	F09292 HSC2ZF032.n	c 609	21	4.3	393	9	AI146725	AI146725 qb2b07.x
537	21	4.3	341	17	AQ113312	AQ113312 CIT-HSP-2	c 610	21	4.3	395	10	BE178609	BE178609 PM3-HT060
538	21	4.3	343	10	AW149882	AW149882 XG30e09.x	c 611	21	4.3	396	9	AI825372	AI825372 wb17f08.x
539	21	4.3	343	13	BG956712	BG956712 MR4-CT053	c 612	21	4.3	397	9	AI572560	AI572560 tx59a10.x
540	21	4.3	343	14	N51140	N51140 YV96a10.r1	c 613	21	4.3	398	9	AI224481	AI224481 qx06d09.x
541	21	4.3	346	10	AW370188	AW370188 RC5-BT025	c 614	21	4.3	398	9	AA620292	AA620292 af04h06.s
542	21	4.3	346	17	AQ610097	AQ610097 HS_5092_A	c 615	21	4.3	398	10	AW889796	AW889796 XG08d07.x
543	21	4.3	347	12	BF773101	BF773101 CM3-IT004	c 616	21	4.3	398	10	BE181228	BE181228 CM2-HT063
544	21	4.3	348	9	AI002398	AI002398 or78b03.s	c 617	21	4.3	398	17	AQ082856	AQ082856 RPCI11-55
545	21	4.3	348	17	AQ042012	AQ042012 CIT-HSP-2	c 618	21	4.3	399	17	AA877143	AA877143 oh79e03.s
546	21	4.3	348	17	AQ554433	AQ554433 RPCI-11-4	c 619	21	4.3	399	17	AQ207824	AQ207824 HS_3028_A
547	21	4.3	349	9	AI769210	AI769210 wg35c02.x	c 620	21	4.3	401	12	BF855695	BF855695 RC6-FN020
548	21	4.3	349	12	BF732461	BF732461 nael0b06.	c 621	21	4.3	401	12	BF855695	BF855695 RC6-FN020
549	21	4.3	351	9	AI393740	AI393740 tg60c09.x	c 622	21	4.3	401	13	BI005157	BI005157 PM3-HN007
550	21	4.3	352	9	AI801690	AI801690 to94a02.x	c 623	21	4.3	401	17	AQ354491	AQ354491 CITBI-E1-
551	21	4.3	352	10	AW088763	AW088763 xd29h02.x	c 624	21	4.3	402	12	BF771450	BF771450 CM1-IT003
552	21	4.3	352	12	BF946793	BF946793 CM0-NN115	c 625	21	4.3	402	17	AZ755944	AZ755944 ex04c09.r
553	21	4.3	352	17	AQ905998	AQ905998 GSGT0657	c 626	21	4.3	403	9	AA468575	AA468575 ne07f03.s
554	21	4.3	354	9	AA641435	AA641435 nr93c01.s	c 627	21	4.3	403	9	AA508040	AA508040 ng32d03.s
555	21	4.3	354	12	BG006166	BG006166 RC5-GN019	c 628	21	4.3	403	17	BE609578	BE609578 H1V12C10
556	21	4.3	355	9	AI217536	AI217536 qd43a09.x	c 629	21	4.3	404	17	AQ043406	AQ043406 CIT-HSP-2
557	21	4.3	355	17	AQ068284	AQ068284 HS_2240_B	c 630	21	4.3	405	17	AQ037934	AQ037934 CIT-RSP-2
558	21	4.3	356	17	AQ0817094	AQ0817094 HS_5553_A	c 631	21	4.3	405	17	AQ685494	AQ685494 HS_5528_B
559	21	4.3	357	9	AA666066	AA666066 ac41c04.s	c 632	21	4.3	405	17	AQ182308	AQ182308 HS_2233_B
560	21	4.3	357	14	D45476	D45476 HUMGS02649	c 633	21	4.3	407	10	AV762816	AV762816 AV762816
561	21	4.3	357	17	AQ816076	AQ816076 HS_5484_A	c 634	21	4.3	408	13	BI002174	BI002174 PM3-HN007
562	21	4.3	358	9	AI923135	AI923135 wn29a09.x	c 635	21	4.3	408	13	W32430	W32430 zc05d10.s1
563	21	4.3	358	12	BG010509	BG010509 PM4-GN030	c 636	21	4.3	409	13	BI034926	BI034926 QV2-NN200
564	21	4.3	359	17	AQ584200	AQ584200 RPCI-11-4	c 637	21	4.3	409	13	BI513745	BI513745 BS160013B
565	21	4.3	360	9	AI218171	AI218171 qh28c06.x	c 638	21	4.3	410	13	BI036617	BI036617 RC5-NT018
566	21	4.3	360	13	BG956714	BG956714 MR4-CT053	c 639	21	4.3	410	17	AQ220064	AQ220064 HS_3251_B
567	21	4.3	361	9	AI982522	AI982522 wt21e01.x	c 640	21	4.3	411	9	B63919	B63919 RPCI11-5F24
568	21	4.3	361	12	BG012513	BG012513 IL5-GN023	c 641	21	4.3	411	9	AA837607	AA837607 od68c10.s
569	21	4.3	362	10	AW591402	AW591402 XG35h09.x	c 642	21	4.3	411	9	AI678879	AI678879 tu70d04.x
570	21	4.3	364	14	N47882	N47882 YV96a10.s1	c 643	21	4.3	411	9	AI738813	AI738813 wi36h07.x
571	21	4.3	364	17	AQ242624	AQ242624 CITBI-E1-	c 644	21	4.3	411	10	AV744364	AV744364 AV744364
572	21	4.3	364	17	AQ472259	AQ472259 CITBI-E1-	c 645	21	4.3	411	10	AW074223	AW074223 x509e11.x
573	21	4.3	365	9	AA837709	AA837709 oe06c10.s	c 646	21	4.3	412	10	AW074223	AW074223 x509e11.x
574	21	4.3	365	9	AA601680	AA601680 no01f11.s	c 647	21	4.3	412	10	B30650	B30650 HS-1003-A1-
575	21	4.3	365	10	AW905130	AW905130 QV0-NN107	c 648	21	4.3	412	17	AQ527907	AQ527907 RPCI-11-3
576	21	4.3	367	9	AA634013	AA634013 ac74b02.s	c 649	21	4.3	413	10	AV735885	AV735885 AV735885
577	21	4.3	368	10	BE086702	BE086702 QV1-BT026	c 650	21	4.3	413	10	AW512739	AW512739 XG06g04.x
578	21	4.3	368	14	H65994	H65994 Yr73b11.r1	c 651	21	4.3	413	13	BG950830	BG950830 CM4-CT066
579	21	4.3	369	12	BG012998	BG012998 IL5-GN023	c 652	21	4.3	414	9	AI619953	AI619953 ty45d03.x
580	21	4.3	369	13	BI10741	BI10741 iq90b01.y	c 653	21	4.3	414	12	BF771409	BF771409 IL5-IT002
581	21	4.3	370	9	AA594510	AA594510 nl94e10.s	c 654	21	4.3	415	10	AW516975	AW516975 XG05e08.x
582	21	4.3	370	14	H58688	H58688 Yr20904.s1	c 655	21	4.3	417	17	AQ264160	AQ264160 CITBI-E1-
583	21	4.3	370	17	AQ192909	AQ192909 HS_3045_B	c 656	21	4.3	418	9	AA418231	AA418231 zv97h12.r
584	21	4.3	371	9	AA084726	AA084726 zn06f08.s	c 657	21	4.3	418	12	BF821769	BF821769 MR1-RT004
585	21	4.3	372	12	BG012983	BG012983 IL5-GN023	c 658	21	4.3	419	9	AI672778	AI672778 we73a03.x
586	21	4.3	372	14	R08853	R08853 Yf21c04.s1	c 659	21	4.3	420	14	N55508	N55508 YV50e05.s1
587	21	4.3	372	12	R08853	R08853 Yf21c04.s1	c 660	21	4.3	422	17	B85693	B85693 RPCI11-20J2
588	21	4.3	373	9	AI660629	AI660629 wf23a02.x	c 661	21	4.3	423	10	AW593635	AW593635 X193b03.x
589	21	4.3	373	17	AQ778733	AQ778733 HS_2174_B	c 662	21	4.3	423	14	H94410	H94410 YV18a12.r1
590	21	4.3	377	17	BI3935	BI3935 A-423E9.TP	c 663	21	4.3	423	17	AQ334428	AQ334428 HS_5005_A

C 664	21	4.3	424	9	AA780046	AA780046 zj24f02.s	C 737	21	4.3	467	10	BE504930
C 665	21	4.3	424	14	R87078	R87078 yq31f04.r1	738	21	4.3	467	17	AQ178246
C 666	21	4.3	425	9	AI538779	AI538779 tp66d11.x	739	21	4.3	468	9	AA115656
C 667	21	4.3	425	17	AQ825042	AQ825042 HS_5253.A	740	21	4.3	468	9	AI951698
C 668	21	4.3	426	12	BF963838	BF963838 QV2-NN004	741	21	4.3	469	10	AW517716
C 669	21	4.3	426	10	AW008093	AW008093 wv49h04.x	742	21	4.3	469	12	BF034813
C 670	21	4.3	427	14	R73294	R73294 yj92e02.r1	743	21	4.3	470	14	W45229
C 671	21	4.3	427	14	R73294	R73294 yj92e02.r1	744	21	4.3	470	14	W45229
C 672	21	4.3	428	9	AA789350	AA789350 v93b11.x	745	21	4.3	470	17	AQ110647
C 673	21	4.3	430	17	AQ333433	AQ333433 CITBI-EI-	746	21	4.3	471	10	AW473537
C 674	21	4.3	434	17	AQ380968	AQ380968 RPI111-16	747	21	4.3	471	13	BI015807
C 675	21	4.3	435	14	N79243	N79243 za63c09.s1	748	21	4.3	472	13	BI715111
C 676	21	4.3	436	12	BF771348	BF771348 RC3-TT002	749	21	4.3	472	14	BM710409
C 677	21	4.3	437	17	AQ589705	AQ589705 HS_2117.B	750	21	4.3	472	17	AQ933785
C 678	21	4.3	438	14	R66831	R66831 y125h06.r1	751	21	4.3	474	10	AW812117
C 679	21	4.3	439	17	AQ331997	AQ331997 HS_5011.A	752	21	4.3	474	10	AW812124
C 680	21	4.3	440	17	AQ609456	AQ609456 HS_5078.B	753	21	4.3	476	9	AI889356
C 681	21	4.3	440	14	W01078	W01078 za56b10.r1	754	21	4.3	476	14	BQ581554
C 682	21	4.3	441	9	AI928406	AI928406 w096h08.x	755	21	4.3	476	17	AQ708398
C 683	21	4.3	441	10	BE162414	BE162414 PM1-HT045	756	21	4.3	478	9	AQ229829
C 684	21	4.3	442	9	AI278896	AI278896 q051b07.x	757	21	4.3	479	9	AI814767
C 685	21	4.3	442	9	AI278896	AI278896 q051b07.x	758	21	4.3	479	12	BF589833
C 686	21	4.3	442	17	AQ080562	AQ080562 CIT-HSP-2	759	21	4.3	479	17	AQ191881
C 687	21	4.3	442	17	AQ550371	AQ550371 RPI11-4	760	21	4.3	479	17	AQ496317
C 688	21	4.3	443	10	AW117936	AW117936 x639d08.x	761	21	4.3	480	9	AI249735
C 689	21	4.3	444	14	BM988988	BM988988 UT-H-D10-	762	21	4.3	480	9	AI924095
C 690	21	4.3	444	14	R72145	R72145 yj87f08.r1	763	21	4.3	480	14	H98660
C 691	21	4.3	444	17	AQ706405	AQ706405 HS_5354.A	764	21	4.3	481	12	BF900598
C 692	21	4.3	445	9	AI217123	AI217123 qf47b12.x	765	21	4.3	481	14	R95838
C 693	21	4.3	446	9	AI559114	AI559114 tq31d12.x	766	21	4.3	481	17	AQ424515
C 694	21	4.3	446	17	AQ691848	AQ691848 HS_5385.A	767	21	4.3	482	14	BQ581877
C 695	21	4.3	447	9	AI799444	AI799444 tw56e03.x	768	21	4.3	482	14	N54909
C 696	21	4.3	447	17	AQ383758	AQ383758 RPI11-12	769	21	4.3	484	17	AQ404036
C 697	21	4.3	448	9	AI346528	AI346528 qp46a05.x	770	21	4.3	485	9	AI523316
C 698	21	4.3	448	12	BF880775	BF880775 QV3-ET017	771	21	4.3	485	17	AQ432176
C 699	21	4.3	448	17	AQ030084	AQ030084 RPI111-38	772	21	4.3	485	17	AQ441297
C 700	21	4.3	450	9	AI079823	AI079823 ox50b05.x	773	21	4.3	485	17	AQ454625
C 701	21	4.3	450	9	AL708173	AL708173 DKZP686H	774	21	4.3	486	9	AI889361
C 702	21	4.3	450	10	AW889893	AW889893 RC5-NT003	775	21	4.3	486	13	BI792314
C 703	21	4.3	450	12	BF771353	BF771353 RC3-IT002	776	21	4.3	488	10	AW058407
C 704	21	4.3	450	12	BQ06892	BQ06892 IL5-GN023	777	21	4.3	489	17	AI080473
C 705	21	4.3	450	17	AQ536523	AQ536523 RPI11-3	778	21	4.3	489	17	AQ143334
C 706	21	4.3	452	9	AI027760	AI027760 ov93h09.x	779	21	4.3	489	17	AQ537845
C 707	21	4.3	452	9	AI970474	AI970474 wq93c07.x	780	21	4.3	490	17	BI152886
C 708	21	4.3	453	9	AI633021	AI633021 tz33e07.x	781	21	4.3	491	9	AA642887
C 709	21	4.3	453	10	BE675381	BE675381 7F08b04.x	782	21	4.3	491	9	AI624234
C 710	21	4.3	454	17	AQ627764	AQ627764 CITBI-EI-	783	21	4.3	492	17	AQ753098
C 711	21	4.3	455	10	AW192325	AW192325 x144a02.x	784	21	4.3	492	17	AQ475870
C 712	21	4.3	455	17	AQ079438	AQ079438 CIT-HSP-2	785	21	4.3	494	17	B80382
C 713	21	4.3	455	17	AQ392348	AQ392348 CITBI-EI-	786	21	4.3	496	17	B42111
C 714	21	4.3	456	9	AI758805	AI758805 ty24f04.x	787	21	4.3	497	9	AI540107
C 715	21	4.3	456	12	BF919890	BF919890 QV2-NT014	788	21	4.3	497	12	BF434329
C 716	21	4.3	456	14	H00788	H00788 yj30e02.r1	789	21	4.3	497	14	BQ380108
C 717	21	4.3	456	17	B85450	B85450 RPI111-17J5	790	21	4.3	498	9	AA573209
C 718	21	4.3	457	9	AA021616	AA021616 ze69c08.x	791	21	4.3	499	14	BM990819
C 719	21	4.3	457	17	AQ232321	AQ232321 HS_2009.A	792	21	4.3	500	10	AW889901
C 720	21	4.3	458	9	AI935684	AI935684 w099e04.x	793	21	4.3	500	17	AW996768
C 721	21	4.3	458	17	AQ232316	AQ232316 HS_2009.A	794	21	4.3	501	17	AQ452933
C 722	21	4.3	460	9	AA988666	AA988666 q08e10.s	795	21	4.3	501	17	AQ470357
C 723	21	4.3	460	9	AA565826	AA565826 nj32a09.s	796	21	4.3	503	12	BF903930
C 724	21	4.3	461	10	AW673426	AW673426 bb35f08.x	797	21	4.3	504	17	BF533093
C 725	21	4.3	461	14	N73439	N73439 yz31g10.r1	798	21	4.3	505	9	AA126271
C 726	21	4.3	462	13	BI061800	BI061800 PM4-UT010	799	21	4.3	505	9	AA126271
C 727	21	4.3	462	14	BM983733	BM983733 UT-CF-DU1	800	21	4.3	505	17	AQ062744
C 728	21	4.3	462	17	AQ460432	AQ460432 HS_5141.A	801	21	4.3	505	17	AQ43943
C 729	21	4.3	463	12	BF821941	BF821941 MRI-RT004	802	21	4.3	507	14	R24296
C 730	21	4.3	463	14	BM729198	BM729198 UT-E-BO1-	803	21	4.3	507	17	AQ792017
C 731	21	4.3	464	9	AI793119	AI793119 oo31a01.y	804	21	4.3	507	17	AQ120179
C 732	21	4.3	465	9	AI986134	AI986134 wr30g05.x	805	21	4.3	508	9	AI863203
C 733	21	4.3	465	14	BM672735	BM672735 UT-E-CQ0-	806	21	4.3	510	9	AI814771
C 734	21	4.3	465	17	AQ754647	AQ754647 HS_5537.B	807	21	4.3	510	14	BM993150
C 735	21	4.3	466	9	AI248623	AI248623 qh77b09.x	808	21	4.3	510	17	AZ516419
C 736	21	4.3	466	13	BI015804	BI015804 PM2-ET025	809	21	4.3	511	17	AQ651681

BE504930	hz32g08.x
AQ178246	HS_2217.B
AA115656	z186c09.s
AI951698	wv38d07.x
AW517716	xs86h03.x
BF034813	601457319
W45229	zc23d10.r1
AQ110647	CIT-HSP-2
AW473537	hb05e08.x
BI015807	PM2-ET025
BI715111	ic29a09.y
BM710409	UT-E-CQ1-
AQ933785	RPI1-23-2
AW812117	RC1-ST017
AW812124	RC1-ST017
AI889356	wm98a12.x
BQ581554	1110c03.x
AQ708398	HS_5568.A
AQ229829	HS_2027.A
AI814767	wk65e05.x
BF589833	rac25f08
AQ191881	HS_3223.B
AQ496317	HS_5108.A
AI249735	qj64e10.x
AI924095	wn78g10.x
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BF900598	MR1-MT028
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AQ424515	CITBI-EI-
BQ581877	1110c03.y
N54909	yv34e04.s1
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AQ040336	CIT-HSP-2
AI523316	ar71f11.x
AQ432176	HS_5050.A
AQ441297	HS_5129.B
AQ546425	CITBI-EI-
AI889361	wm98b08.x
BI792314	ic29a09.x
AW058407	wx20c11.x
AI080473	os71c08.x
AQ143334	HS_3067.B
AQ537845	RPI1-11-3
BI152886	UP_331-18
AA642887	nr34a01.s
AI624234	ts28b03.x
AQ753098	HS_5303.A
AQ475870	CITBI-EI-
B80382	CIT-HSP-204
B42111	HS-1055-A2-
AI540107	td09e01.x
BF434329	7095g03.x
BQ380108	RC1-UT001
AA573209	nj42g03.s
BM990819	UT-H-D10-
AW889901	RC5-NT003
AW996768	QV3-BN004
AQ152933	HS_2322.A
AQ470357	CITBI-EI-
BF903930	MR1-MT028
AQ553093	RPI1-11-4
AA126271	z186g03.s
AA126271	MR2-OT007
AW886400	CIT-HSP-2
AQ062744	CIT-HSP-2
AQ143943	HS_3074.A
R24296	yq32b03.r1
AQ120179	HS_5270.A
AI863203	tz44f04.x
AI814771	wk65e12.x
BM993150	UT-H-DT0-
AZ516419	RPI1-11-1
AQ651681	Sheared D

C 810	21	4.3	512	10	AW995494	QV0-BN004	C 883	21	4.3	570	17	AQ514720	HS_5215_A
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C 812	21	4.3	513	12	AW141233	HS_3145_B	885	21	4.3	572	12	BG474875	602490938
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C 814	21	4.3	514	17	AQ131786	HS_2254_A	887	21	4.3	576	10	BE147135	PM2-HT022
C 815	21	4.3	515	10	BE170758	HS_2254_A	888	21	4.3	581	17	B66212	CIT-HSP-202
C 816	21	4.3	515	12	BF897535	RC1-MT015	889	21	4.3	581	17	AQ483978	RFCI-11-2
C 817	21	4.3	515	14	BM971275	UI-CF-DUI	890	21	4.3	582	17	AQ472461	CITBI-E1
C 818	21	4.3	515	17	AQ187230	HS_3126_B	891	21	4.3	583	10	BE245280	TCBAP1E24
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C 822	21	4.3	519	10	BE158823	IL2-HT039	895	21	4.3	586	17	BH260463	CH230-29J
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C 826	21	4.3	520	17	AQ387974	RFCI-11-4	899	21	4.3	598	10	AV740809	AV740809
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C 828	21	4.3	521	17	AQ707763	HS_5560_A	901	21	4.3	598	17	AQ347819	RFCI-11-11
C 829	21	4.3	522	12	BE927955	MR3-CT046	902	21	4.3	598	17	BE384697	601276980
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C 831	21	4.3	523	17	AQ019769	CIT-HSP-2	904	21	4.3	598	17	AQ373685	RFCI-11-15
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C 841	21	4.3	535	17	AQ599248	HS_5361_A	914	21	4.3	604	17	AQ07891	HS_5055_B
C 842	21	4.3	536	10	BE012629	12262_MA	915	21	4.3	604	17	AQ637008	RFCI-11-4
C 843	21	4.3	536	17	AQ439789	HS_5075_B	916	21	4.3	609	12	BF530337	602071617
C 844	21	4.3	541	17	AQ507788	RFCI-11-3	917	21	4.3	609	17	AG129657	PM4-KT000
C 845	21	4.3	543	10	AW129741	x23306.x	918	21	4.3	609	17	AQ386609	RFCI-11-3
C 846	21	4.3	543	17	AQ551756	RFCI-11-3	919	21	4.3	616	13	BM478467	603065789
C 847	21	4.3	544	17	AQ891472	HS_3063_A	920	21	4.3	617	17	BI94632	CIT-HSP-216
C 848	21	4.3	545	10	AW517695	x86604.x	921	21	4.3	619	9	AI982994	wt46e02.x
C 849	21	4.3	546	17	AQ486753	RFCI-11-2	922	21	4.3	621	17	AQ374906	RFCI-11-15
C 850	21	4.3	547	17	AQ829732	HS_4862_A	923	21	4.3	623	12	BF818471	MR1-CI018
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C 854	21	4.3	551	17	AQ536274	RFCI-11-4	927	21	4.3	624	10	AW816505	PM4-KT000
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C 856	21	4.3	552	17	AQ265642	CITBI-E1	929	21	4.3	626	12	BF913251	IL3-UT011
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C 858	21	4.3	554	12	BG291634	602385760	931	21	4.3	627	17	AQ587997	CITBI-E1
C 859	21	4.3	555	9	AA760867	n214h08.s	932	21	4.3	631	17	AQ035581	CIT-HSP-2
C 860	21	4.3	555	9	AA760867	n214h08.s	933	21	4.3	631	17	AQ035581	CIT-HSP-2
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C 862	21	4.3	556	17	AQ312166	RFCI-11-11	935	21	4.3	637	14	BQ379723	MR3-UT010
C 863	21	4.3	558	12	BG008492	PM4-GN030	936	21	4.3	640	17	AQ536737	RFCI-11-3
C 864	21	4.3	558	17	AQ438812	HS_5077_B	937	21	4.3	640	17	AQ536737	RFCI-11-3
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C 867	21	4.3	560	17	AQ764816	HS_3118_A	940	21	4.3	644	17	AG057657	PM4-KT000
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C 869	21	4.3	563	9	AL709136	602385760	942	21	4.3	645	17	AG033429	RFCI-11-59
C 870	21	4.3	563	14	BM831465	K-EST0105	943	21	4.3	645	17	AG033429	RFCI-11-59
C 871	21	4.3	564	12	BF846742	nfs1d02.s	944	21	4.3	645	17	AQ391374	CITBI-E1
C 872	21	4.3	564	12	BF846742	nfs1d02.s	945	21	4.3	647	17	AG176477	PM4-KT000
C 873	21	4.3	564	17	AQ358231	HS_5029_A	946	21	4.3	648	17	AQ083477	RFCI-23-3
C 874	21	4.3	566	17	AQ012743	CIT-HSP-2	947	21	4.3	648	17	AQ083477	RFCI-23-3
C 875	21	4.3	566	17	AQ346062	RFCI-11-12	948	21	4.3	649	14	BM998914	UI-H-DI0-
C 876	21	4.3	566	17	AQ427700	CITBI-E1	949	21	4.3	649	14	BM998914	UI-H-DI0-
C 877	21	4.3	567	10	AV720723	AV720723	950	21	4.3	651	17	AG047653	PM4-KT000
C 878	21	4.3	568	13	BI857080	603383657	951	21	4.3	653	17	AG106495	PM4-KT000
C 879	21	4.3	568	17	AQ531625	RFCI-11-3	952	21	4.3	653	17	AG106495	PM4-KT000
C 880	21	4.3	570	17	BH552938	BOHQ622R	953	21	4.3	654	13	BM009397	603629880
C 881	21	4.3	570	17	AQ391603	CITBI-E1	954	21	4.3	655	17	AZ839675	2M0135121
C 882	21	4.3	570	17	AQ425937	CITBI-E1	955	21	4.3	655	17	AQ544656	CITBI-E1

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM11761 row: m column: 02
 High quality sequence stop: 684.
 Location/Qualifiers
 1. .734
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 /clone_lib="NIH MGC 96"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTITTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 135 a 222 c 179 g 198 t
 ORIGIN

Query Match 75.3%; Score 366; DB 13; Length 734;
 Best Local Similarity 99.8%; Pred. No. 4.9e-157;
 Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGATTGCAGATGTGAGCCACCGCTGCTGCGCAGATTTTCTTTATTTCTTTCTTTT 60
 DB 29 AGATTGCAGATGTGAGCCACCGCTGCTGCGCAGATTTTCTTTATTTCTTTT 88
 QY 61 CTTTCT 120
 DB 89 CTTTCT 148
 QY 121 ATTTTTCAGTGTAGCCACAGCTGCTGCTCTCAGACAGATCCCTTCCACATGCTGCG 180
 DB 149 ATTTTTCAGTGTAGCCACAGCTGCTGCTCTCAGACAGATCCCTTCCACATGCTGCG 208
 QY 181 CTTCTGCT 240
 DB 209 CTTCTGCT 268
 QY 241 CCATTTCTGCT 300
 DB 269 CCATTTCTGCT 328
 QY 301 CTTTCT 360
 DB 329 CTTTCT 388
 QY 361 CAGAGTCACCTTTTCTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
 DB 389 CAGAGTCACCTTTTCTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 445

RESULT 2
 BI059493
 LOCUS
 DEFINITION PM4-UT0102-040101-002-f03 UT0102 Homo sapiens cdna, mRNA sequence.
 ACCESSION BI059493
 VERSION BI059493.1 GI:14467020
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 294)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

ALIGNMENTS

RESULT 1
 BI02493
 LOCUS
 DEFINITION 603248907F1 NIH_MGC_96 Homo sapiens cdna clone IMAGE:5300905 5', mRNA sequence.
 ACCESSION BI02493
 VERSION BI02493.1 GI:15495432
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 734)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1kt2-MR1-RT0028-091100-001-f02&t3=2000-11-09&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 331.
Location/Qualifiers

FEATURES
source

1. 331
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/db_xref="taxon:9606"
/clone_lib="RT0028"
/dev_stages="Adult"
/note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 81 a 86 c 103 g 61 t
ORIGIN

Query Match 49.2%; Score 239; DB 12; Length 331;
Best Local Similarity 99.7%; Pred. No. 7.4e-99;
Matches 289; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 331 ATGAGGAGGAGCGCTCGGAACTTGGAGTCCCAAGCCAGTCCCAATTTCTGCTCGC 272
Db |||||||
Qy 257 TCACCGCTGGCCCTTAGAGACCCGAGGTAGGGGTGGGAGATGCTTCTCTCTTGCCCC 316
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Qy 271 TCACCGCTGGCCCTTAGAGACCCGAGGTAGGGGTGGGAGATGCTTCTCTCTTGCCCC 212
Db |||||||
Qy 317 CGGCCCTCATGGTCTTAGCTTCCCTGAGTGGGGCTGAGGGCAGAGTCACTTTCT 376
Db |||||||
Qy 211 CGGCCCTCATGGTCTTAGCTTCCCTGAGTGGGGCTGAGGGCAGAGTCACTTTCT 152
Db |||||||
Qy 377 GTGGTGGCTCTACCTTCTCTGCTGAGTTAAACGTTGCCATCTGCGCATCTCAAA 436
Db |||||||
Qy 151 GTGGTGGCTCTACCTTCTCTGCTGAGTTAAACGTTGCCATCTGCGCATCTCAAA 92
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Qy 437 CGACAGAGGAGCTTTTCTGGAATTTCAACACCATGCTCTTAGTCCCAAGC 486
Db |||||||
Qy 91 CGACAGAGGAGCTTTTCTGGAATTTCAACACCATGCTCTTAGTCCCAAGC 42
Db |||||||

RESULT 5
LOCUS B1226587 713 bp mRNA linear EST 11-JUL-2001
DEFINITION 602951569F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5095793 5', mRNA sequence.
ACCESSION B1226587
VERSION B1226587.1 GI:14680031
KEYWORDS EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

human.
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs@email.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI866 row: j column: 18
High quality sequence start: 56
High quality sequence stop: 687.
Location/Qualifiers

FEATURES
source

1. 713
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/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 127 a 216 c 168 g 202 t
ORIGIN

Query Match 41.2%; Score 200; DB 13; Length 713;
Best Local Similarity 100.0%; Pred. No. 5.5e-81;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 TTTTGTCTTCTGTCTTTTCAGAACCAAGCAGCTAGCAGCTCTTCCATGTTCTAT 122
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Qy 130 TTTTGTCTTCTGTCTTTTCAGAACCAAGCAGCTAGCAGCTCTTCCATGTTCTAT 189
Db |||||||
Qy 123 TTTGACTGTAGCACAGCTGCTGTCTTCAGGACAGCATCCCTTCCACATGCTCGCC 182
Db |||||||
Qy 190 TTTGACTGTAGCACAGCTGCTGTCTTCAGGACAGCATCCCTTCCACATGCTCGCC 249
Db |||||||
Qy 183 TGCTGCTCTGATGAGGAGGGAGCGTCTGGAACTTGGAGTCCAAAGGCCAGTCCC 242
Db |||||||
Qy 250 TGCTGCTCTGATGAGGAGGGAGCGTCTGGAACTTGGAGTCCAAAGGCCAGTCCC 309
Db |||||||
Qy 243 CATTTCTGCTCGCTCACCG 262
Db |||||||
Qy 310 CATTTCTGCTCGCTCACCG 329
Db |||||||

RESULT 6
LOCUS BQ345812 319 bp mRNA linear EST 20-MAY-2002
DEFINITION PMO-NT0314-280501-004-d08 NT0314 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ345812
VERSION BQ345812.1 GI:21009873
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 319)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., deOliveira,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE
JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

CONTACT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&t2=PM0-NT0314-280501-004-d08&t3=2001-05-28&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 15

High quality sequence stop: 319.

Location/Qualifiers

1. .319

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone lib="NT0314"

/dev stage="Adult"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

68 a 108 c 64 g 78 t 1 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 31.9%; Score 155; DB 14; Length 319;

Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 CTACCCCTTCCCTGAGTGGGGCTGAGCCAGAGTCACTTTTCTGTGGCTGTCTACC 391

Db 16 CTAGCCCTTCCCTGAGTGGGGCTGAGCCAGAGTCACTTTTCTGTGGCTGTCTACC 75

Qy 392 TTCTGTCCCTGAGTTAAACGGTGGCCATCTCCATCTCAACACGAGAGGCTTT 451

Db 76 TTCTGTCCCTGAGTTAAACGGTGGCCATCTCCATCTCAACACGAGAGGCTTT 135

Qy 452 TCTGGAATTTCAACACCTGCTCTAGTCCCAAGC 486

Db 136 TCTGGAATTTCAACACCTGCTCTAGTCCCAAGC 170

RESULT 7

BF9341192/c

LOCUS

BF9341192

DEFINITION

CM3-NT0245-211200-585-b05 NT0245 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF9341192

VERSION

BF9341192.1 GI:12351516

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 204)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

CONTACT

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-NT0245-211200-585-b05&t3=2000-12-21&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 46

High quality sequence stop: 204.

Location/Qualifiers

1. .204

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone lib="NT0245"

/dev stage="Adult"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

59 a 46 c 65 g 34 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 17.9%; Score 87; DB 12; Length 204;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 295 GAGATGTTCTCTCTTGGCCCGCCCTCATGGTCTAGCCCTTCCCTGAGTGGCGC 354

Db 204 GAGATGTTCTCTCTTGGCCCGCCCTCATGGTCTAGCCCTTCCCTGAGTGGCGC 145

Qy 355 TGAGGCCAGAGTCACCTTTTCTGTGGC 381

Db 144 TGAGGCCAGAGTCACCTTTTCTGTGGC 118

RESULT 8

BF947854

LOCUS

BF947854

DEFINITION

CM2-NN0212-301000-440-a07 NN0212 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF947854

VERSION

BF947854.1 GI:12365129

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 306)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

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Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

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Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

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 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpeoneludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN0212-
 301000-440-a07&t3=2000-10-30&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 22
 High quality sequence stop: 306.
 Location/Qualifiers
 1. 306
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN0212"
 /dev_stage="Adult"
 /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 65 a 97 c 63 g 81 t
 BASE COUNT
 ORIGIN
 Query Match 13.2%; Score 64; DB 12; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 423 CTGCCATCTCTCAACGACAGAGGAGCTTTCTGGAATTTCAAAACCATTTGCTCTTAGTCCC 482
 Db 81 CTGCCATCTCTCAACGACAGAGGAGCTTTCTGGAATTTCAAAACCATTTGCTCTTAGTCCC 140
 Qy 483 AAGC 486
 Db 141 AAGC 144
 RESULT 9
 T65465
 LOCUS
 DEFINITION
 T65465
 T65465
 T65465.1 GI:674510
 EST.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 435)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
 R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1734
 High quality sequence stops: 336 Source: IMAGE Consortium, LLNL This
 clone is available royalty-free through LLNL; contact the IMAGE
 Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1734 Std Error: 0.00

Seq primer: M13RP1
 High quality sequence stop: 336.
 Location/Qualifiers
 1. 435
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:21528"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(dT) primer; 15'
 AACTGAAGAATTCCGGCCGCGAGGAATTTTCTTTTCTTTT 3';
 double-stranded cDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the Lafmid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."
 94 a 130 c 105 g 103 t 3 others
 BASE COUNT
 ORIGIN
 Query Match 13.2%; Score 64; DB 14; Length 435;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 423 CTGCCATCTCTCAACGACAGAGGAGCTTTCTGGAATTTCAAAACCATTTGCTCTTAGTCCC 482
 Db 32 CTGCCATCTCTCAACGACAGAGGAGCTTTCTGGAATTTCAAAACCATTTGCTCTTAGTCCC 91
 Qy 483 AAGC 486
 Db 92 AAGC 95
 RESULT 10
 F11822
 LOCUS
 DEFINITION
 F11822
 F11822
 F11822.1 GI:706134
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 302)
 Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes
 M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F.,
 Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
 Sebastiani-Kabakchis, C. and Tessier, A.
 IMAGE: molecular integration of the analysis of the human genome
 and its expression
 C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
 95277534
 Contact: Genethon
 Genexpress-Genethon
 Genethon Centre de recherche sur le Genome Humain
 1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
 Tel: 33169472800
 Fax: 33160778698
 Email: genexpress@genethon.fr
 Single read.
 Genexpress library id: C; Genexpress_sequence_id: y1c-32a09
 Seq primer: (-21)M13 universal.
 Location/Qualifiers
 1. 302
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="C-32a09"

/clone_lib="normalized infant brain cDNA"
 /sex="Female"
 /tissue_type="total brain"
 /dev_stages="3 months old"
 /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
 Site_2: NotI; sex:female; dev_stage=3 months old;
 isolate-muscular atrophy patient; tissue_type=total brain
 ; total mRNA was oligo-(dT) primed and directionally
 cloned 5' -> 3' into the HindIII -> NotI sites of the
 lafmid BA vector. Clone library from B.Soaress, Psychiatry
 Dept. Columbia University, USA. Normalization_method:
 Bento Soares, P.N.A.S in press"

BASE COUNT 67 a 97 c 65 g 72 t 1 others
 ORIGIN

Query Match 9.5%; Score 46; DB 14; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2e-10;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 441 AGAGAGCTTTCTGGAATTTCAAACCAATCTCTTAGTCCCAAGC 486
 |||||||
 Db 52 AGAGAGCTTTCTGGAATTTCAAACCAATCTCTTAGTCCCAAGC 97

RESULT 11
 A1684794
 LOCUS
 DEFINITION wa73905.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:2301848 3' similar to contains Alu repetitive element; mRNA
 sequence.

ACCESSION A1684794
 VERSION A1684794.1 GI:4896088
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 362)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco
 High quality sequence stop: 252.

FEATURES

Location/Qualifiers
 1..362
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2301848"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CGAP_GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 90 a 86 c 69 g 116 t 1 others
 ORIGIN

Query Match 5.8%; Score 28; DB 9; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAGA 34
 |||||||
 Db 232 CAGATGTGAGCCACCGTGCCTGGCCAGA 259

RESULT 12

AA651660/c
 LOCUS
 DEFINITION ns89d03.e1 NCI-CGAP Pr3 Homo sapiens cDNA clone IMAGE:1190789
 similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AA651660
 VERSION AA651660.1 GI:2583312
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 399)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
 , Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 503 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham.

Location/Qualifiers
 1..399

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1190789"
 /clone_lib="NCI-CGAP_Pr3"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"

/note="vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10
 ,000 microdissected cells histologically-determined to be
 fully malignant prostate cancer cells. Double-stranded
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
 applied to the cDNA with an adaptor-specific primer, and
 the resulting PCR product subcloned into pAMP10 by the
 UDG-cloning method (life technologies). Average insert
 size is 600 bp. NOTE: Not directionally cloned. This
 library was constructed by David Krizman."

BASE COUNT 116 a 93 c 113 g 77 t

ORIGIN

Query Match 5.8%; Score 28; DB 9; Length 399;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGACCCACCGTGCCTGGCCAGATTTT 39
 |||||||
 Db 122 GTGACCCACCGTGCCTGGCCAGATTTT 95

RESULT 13

AW974922/c
 LOCUS
 DEFINITION EST387027 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW974922
 VERSION AW974922.1 GI:8166125

```

KEYWORDS EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 499)
AUTHORS     Hegde,P., Oi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            T.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
TITLE       Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL     Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 341
            Seq primer: Forward.
FEATURES    Location/Qualifiers
            1..499
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="MAGE resequences, MAGN"
            /note="Vector: pbluescriptSKm"
BASE COUNT 139 a 116 c 138 g 106 t
ORIGIN
Query Match      5.8%; Score 28; DB 10; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGCCTGCCAGATTTT 39
    |||||||||||||||||||||||||||
Db 236 GTGAGCCACCGTGCCTGCCAGATTTT 209

RESULT 14
BE826708/c
LOCUS        BE826708             344 bp    mRNA    linear    EST 22-SEP-2000
DEFINITION   QV1-EN0042-130600-237-b05 EN0042 Homo sapiens cDNA, mRNA sequence.
ACCESSION    BE826708
VERSION      BE826708.1 GI:10259086
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE     1 (bases 1 to 344)
AUTHORS       Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zagro,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.J.
TITLE         Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE       20202663
COMMENT       Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QV1-EN0042-130
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            Seq primer: puc 18 forward

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VERSION      AQ043261.1 GI:3312188
KEYWORDS     GSS.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE     1 (bases 1 to 350)
AUTHORS       Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
            Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
            Simon,M. and Venter,J.C.
TITLE         Use of a random BAC End Sequence Database for Sequence-Ready Map
            Building (1998)
JOURNAL       Unpublished (1998)
COMMENT       Other_GSSs: CIT-HSP-2329A1.TF
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Search completed: June 17, 2003, 06:26:24
Job time : 594.523 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 1317.49 Seconds
(without alignments)
15794.017 Million cell updates/sec

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Perfect score: 715
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

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2: gb_hgt.*

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16: em_fun.*

17: em_hum.*

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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	715	100.0	9108	9	AF123653 Homo sapi
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4	22	3.1	113331	2	AC107283 Rattus no
5	22	3.1	159838	9	AC073991 Homo sapi
6	22	3.1	251905	2	AC093682 Homo sapi
7	21	2.9	11215	1	AE001783 Thormotog
8	21	2.9	84661	9	AL353695 Human DNA
9	21	2.9	147968	2	AC114256 Rattus no
10	21	2.9	155334	2	AC011156 Homo sapi
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14	21	2.9	230879	9	AP003465 Homo sapi
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21	20	2.8	92095	2	AC107548 Rattus no
22	20	2.8	108605	2	AC103501 Rattus no
23	20	2.8	131570	9	AP002495 Homo sapi
24	20	2.8	133084	2	AC099208 Rattus no
25	20	2.8	135734	2	AC002346 Homo sapi
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27	20	2.8	143968	2	AC108404 Mus muscu
28	20	2.8	166379	9	AC074121 Homo sapi
29	20	2.8	169873	2	AC079881 Homo sapi
30	20	2.8	173269	2	AC068357 Homo sapi
31	20	2.8	178785	9	AC068139 Homo sapi
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44	20	2.8	201642	2	AC124727 Mus muscu
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67	19	2.7	52614	2	AC090899	AC090899 Mus muscu	c 140	19	2.7	194520	10	AL691424	AL691424 Mouse DNA
68	19	2.7	52752	9	AL157773	AL157773 Human DNA	c 141	19	2.7	196496	2	AL805910	AL805910 Mus muscu
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96	19	2.7	155111	2	AC119639	AC119639 Rattus no	c 169	19	2.7	340000	9	HS21C102	HS21C102 Homo sapi
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106	19	2.7	166134	2	AC117059	AC117059 Rattus no	c 179	18	2.5	801	10	RATTH	MI6473 Rat tyrosin
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126	19	2.7	186947	9	AC026998	AC026998 Homo sapi	c 199	18	2.5	3105	10	RATTHA	M23598 Rattus norv
127	19	2.7	187114	2	AC026998	AC026998 Rattus no	c 200	18	2.5	3483	9	HSM802181	AL137465 Homo sapi
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134	19	2.7	190243	2	AC102729	AC102729 Mus muscu	c 207	18	2.5	5319	9	AB028953	AB028953 Homo sapi
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138	19	2.7	194246	9	AL627230	AL627230 Human DNA	c 211	18	2.5	6842	10	AF014956	AF014956 Rattus no

212	18	2.5	7851	10	RNU09357	U09357 Rattus norv	c 285	18	2.5	96132	2	AC017927	AC017927 Drosophil
c 213	18	2.5	11149	1	AE004587	AE004587 Pseudomon	c 286	18	2.5	97218	9	AC092385	AC092385 Homo sapi
214	18	2.5	11986	9	U77616	U77616 Human achae	287	18	2.5	97375	9	AL353898	AL353898 Human DNA
c 215	18	2.5	12931	9	HS358H9	AL023576 Human DNA	288	18	2.5	97451	2	AC068603	AC068603 Homo sapi
c 216	18	2.5	13161	1	AE000093	AE000093 Rhizobium	c 289	18	2.5	98853	2	AL130929	AL130929 Rattus no
217	18	2.5	15523	1	AE000705	AE000705 Aquifex a	c 290	18	2.5	99109	9	AL805934	AL805934 Human DNA
c 218	18	2.5	25406	9	AL513313	AL513313 Human DNA	c 291	18	2.5	100000	2	AP000505	AP000505 Homo sapi
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c 220	18	2.5	36886	9	AP001238	AP001238 Homo sapi	293	18	2.5	100836	2	AC087298	AC087298 Homo sapi
c 221	18	2.5	37918	9	AP005232	AP005232 Homo sapi	294	18	2.5	101445	2	AL133411	AL133411 Human DNA
c 222	18	2.5	39640	1	SCL2	AL137778 Streptomy	295	18	2.5	103196	9	AL589847	AL589847 Human DNA
c 223	18	2.5	39042	9	AP001224	AP001224 Homo sapi	c 296	18	2.5	103822	9	AL353639	AL353639 Human DNA
c 224	18	2.5	41589	9	AC020955	AC020955 Homo sapi	c 297	18	2.5	104785	9	AP001465	AP001465 Homo sapi
c 225	18	2.5	41630	3	U97592	U97592 Caenorhabdi	298	18	2.5	106216	9	AL161908	AL161908 Human DNA
c 226	18	2.5	43470	9	AP001216	AP001216 Homo sapi	c 299	18	2.5	107568	2	AF212832	AF212832 Homo sapi
c 227	18	2.5	44235	9	AC005262	AC005262 Homo sapi	c 300	18	2.5	107714	2	AL356306	AL356306 Homo sapi
c 228	18	2.5	44985	9	AC110781	AC110781 Homo sapi	c 301	18	2.5	110000	2	AC079625	AC079625 2 of
c 229	18	2.5	47625	2	AC1117803	AC1117803 Mus muscu	c 302	18	2.5	110000	2	AC091288	AC091288 2 of
c 230	18	2.5	49910	2	AC011689	AC011689 Homo sapi	c 303	18	2.5	110000	2	AC098773	AC098773 1 of
231	18	2.5	51411	2	AC101008	AC101008 Mus muscu	304	18	2.5	110000	2	AC108448	AC108448 0 of
c 232	18	2.5	54554	9	AC009500	AC009500 Homo sapi	305	18	2.5	110000	2	AC108448	AC108448 1 of
c 233	18	2.5	54787	9	AL355803	AL355803 Human DNA	306	18	2.5	110000	2	AC108448	AC108448 2 of
c 234	18	2.5	55832	2	AC124326	AC124326 Mus muscu	c 307	18	2.5	110000	2	HSS171M	HSS171M 0 of
c 235	18	2.5	56825	2	AC113044	AC113044 Mus muscu	c 308	18	2.5	110937	2	AC129054	AC129054 Rattus no
c 236	18	2.5	56861	2	AC068509	AC068509 Homo sapi	c 309	18	2.5	112293	2	AC129410	AC129410 Rattus no
c 237	18	2.5	57729	9	AL449284	AL449284 Human DNA	310	18	2.5	112620	2	AC131439	AC131439 Rattus no
c 238	18	2.5	58434	2	AC108446	AC108446 Homo sapi	c 311	18	2.5	112295	9	AC084337	AC084337 Homo sapi
c 239	18	2.5	58434	2	AC108446	AC108446 Homo sapi	312	18	2.5	112361	9	AC027316	AC027316 Homo sapi
c 240	18	2.5	58970	2	AC101231	AC101231 Mus muscu	313	18	2.5	112365	9	AC027317	AC027317 Homo sapi
c 241	18	2.5	59302	2	AC111339	AC111339 Rattus no	c 314	18	2.5	112793	2	AC098438	AC098438 Rattus no
c 242	18	2.5	59352	2	AC061983	AC061983 Homo sapi	315	18	2.5	114642	9	AL357033	AL357033 Human DNA
c 243	18	2.5	59396	2	AC009799	AC009799 Homo sapi	316	18	2.5	114835	9	AP001628	AP001628 Homo sapi
c 244	18	2.5	59999	9	AL499627	AL499627 Human DNA	317	18	2.5	116012	2	AC096210	AC096210 Rattus no
c 245	18	2.5	60269	9	AL512490	AL512490 Human DNA	318	18	2.5	116683	2	AC095543	AC095543 Rattus no
c 246	18	2.5	60612	2	AC079212	AC079212 Homo sapi	c 319	18	2.5	116836	2	AC098503	AC098503 Rattus no
c 247	18	2.5	61962	2	AC123616	AC123616 Mus muscu	c 320	18	2.5	116857	9	HSDJ655K7	HSDJ655K7
c 248	18	2.5	62197	9	AL589939	AL589939 Human DNA	c 321	18	2.5	118280	9	HSDDJ73D5	HSDDJ73D5
c 249	18	2.5	64244	2	AC101546	AC101546 Mus muscu	322	18	2.5	119660	2	AC123101	AC123101 Rattus no
c 250	18	2.5	64529	2	AC108449	AC108449 Homo sapi	323	18	2.5	119707	2	AL773521	AL773521 Sus scrof
c 251	18	2.5	64586	2	AC011279	AC011279 Homo sapi	c 324	18	2.5	119842	9	AC108537	AC108537 Rattus no
c 252	18	2.5	64953	2	AC015569	AC015569 Homo sapi	c 325	18	2.5	119847	9	AF064866	AF064866 Homo sapi
c 253	18	2.5	65302	2	AC119951	AC119951 Mus muscu	c 326	18	2.5	120480	9	AP000806	AP000806 Homo sapi
c 254	18	2.5	66066	2	AC126400	AC126400 Homo sapi	c 327	18	2.5	120637	10	CNS07YF1	CNS07YF1
c 255	18	2.5	66104	2	AC123880	AC123880 Mus muscu	c 328	18	2.5	121982	9	HS1107C24	HS1107C24
c 256	18	2.5	66789	2	AC103807	AC103807 Homo sapi	329	18	2.5	122432	2	AL390073	AL390073 Homo sapi
c 257	18	2.5	68567	9	AL389916	AL389916 Human DNA	c 330	18	2.5	123219	6	AX195073	AX195073 Sequence
c 258	18	2.5	68875	9	AC096559	AC096559 Homo sapi	c 331	18	2.5	123302	2	AC095135	AC095135 Rattus no
c 259	18	2.5	70297	2	AC118615	AC118615 Mus muscu	332	18	2.5	124687	9	AL592164	AL592164 Human DNA
c 260	18	2.5	70474	9	AC109483	AC109483 Homo sapi	333	18	2.5	125000	9	AB017602	AB017602 Homo sapi
c 261	18	2.5	70642	2	AC099870	AC099870 Mus muscu	334	18	2.5	125110	9	AL450267	AL450267 Human DNA
c 262	18	2.5	72229	2	AC101639	AC101639 Homo sapi	c 335	18	2.5	125254	2	AC087399	AC087399 Homo sapi
c 263	18	2.5	72245	9	HS93C23	AL008713 Human DNA	336	18	2.5	125376	9	AP001627	AP001627 Homo sapi
c 264	18	2.5	74188	2	AC021315	AC021315 Homo sapi	337	18	2.5	125949	9	AC025442	AC025442 Homo sapi
c 265	18	2.5	75192	2	AC009215	AC009215 Drosophil	c 338	18	2.5	125959	2	AC122086	AC122086 Rattus no
c 266	18	2.5	76410	2	AC016093	AC016093 Homo sapi	c 339	18	2.5	126243	2	AL773562	AL773562 Sus scrof
c 267	18	2.5	77175	2	AC105650	AC105650 Rattus no	c 340	18	2.5	126895	2	AL356913	AL356913 Human DNA
c 268	18	2.5	77396	2	AC021779	AC021779 Homo sapi	341	18	2.5	128495	9	AL33499	AL33499 Homo sapi
c 269	18	2.5	77790	9	AC026108	AC026108 Homo sapi	c 342	18	2.5	128868	9	HSB211023	HSB211023
c 270	18	2.5	78467	9	AC008078	AC008078 Homo sapi	343	18	2.5	131002	2	AC024392	AC024392 Homo sapi
c 271	18	2.5	79043	9	HS93614	AC009614 Homo sapi	344	18	2.5	132994	2	AL119046	AL119046 Rattus no
c 272	18	2.5	86131	2	AC108349	AC108349 Rattus no	345	18	2.5	133135	2	AL113970	AL113970 Homo sapi
c 273	18	2.5	87753	2	AC117852	AC117852 Rattus no	c 346	18	2.5	133141	2	AC128876	AC128876 Rattus no
c 274	18	2.5	88111	2	AC105556	AC105556 Rattus no	347	18	2.5	133730	2	AC104294	AC104294 Rattus no
c 275	18	2.5	90785	2	AC097694	AC097694 Rattus no	c 348	18	2.5	134213	9	CNS05TEV	CNS05TEV
c 276	18	2.5	90788	2	AC005442	AC005442 Drosophil	349	18	2.5	135784	9	AL662847	AL662847 Human chr
c 277	18	2.5	91783	9	AL160006	AL160006 Human DNA	c 350	18	2.5	136232	2	AC024006	AC024006 Homo sapi
c 278	18	2.5	91842	9	AC008392	AC008392 Homo sapi	c 351	18	2.5	136372	9	AL103828	AL103828 Homo sapi
c 279	18	2.5	92347	2	AC103053	AC103053 Rattus no	c 352	18	2.5	139111	9	AL158048	AL158048 Human DNA
c 280	18	2.5	93179	9	AL356272	AL356272 Human DNA	353	18	2.5	139399	9	AL662801	AL662801 Human DNA
c 281	18	2.5	94629	2	AL139806	AL139806 Human DNA	c 354	18	2.5	139655	2	AC125152	AC125152 Mus muscu
c 282	18	2.5	94703	2	AC008563	AC008563 Homo sapi	355	18	2.5	139982	2	AC113500	AC113500 Mus muscu
c 283	18	2.5	95283	9	HS599F21	AL035662 Human DNA	356	18	2.5	140257	9	HSDDJ551D2	HSDDJ551D2
c 284	18	2.5	96128	10	AL663077	AL663077 Mouse DNA	357	18	2.5	141669	2	AC121194	AC121194 Rattus no

358	18	2.5	142121	9	AC078980	AC078980 Homo sapi	431	18	2.5	164008	2	AC024064	AC024064 Homo sapi
359	18	2.5	142155	10	AC092479	Mus muscu	C 432	18	2.5	164028	9	AC004890	AC004890 Homo sapi
360	18	2.5	142326	2	AC024047	AC024047 Homo sapi	C 433	18	2.5	164248	2	AC074248	AC074248 Homo sapi
C 361	18	2.5	142616	2	AC028646	AC028646 Homo sapi	C 434	18	2.5	164352	2	AC024008	AC024008 Homo sapi
362	18	2.5	143200	9	AC008413	AC008413 Homo sapi	435	18	2.5	164378	2	AC111675	AC111675 Rattus no
363	18	2.5	143620	9	AC0117425	AC0117425 Homo sapi	C 436	18	2.5	164655	9	AC007687	AC007687 Homo sapi
364	18	2.5	145882	2	AL139131	AL139131 Homo sapi	C 437	18	2.5	164790	2	AC068858	AC068858 Homo sapi
C 365	18	2.5	146001	2	AC112747	AC112747 Rattus no	C 438	18	2.5	164838	2	AL691479	AL691479 Homo sapi
366	18	2.5	146614	2	AC118967	AC118967 Rattus no	C 439	18	2.5	165007	9	AC019047	AC019047 Homo sapi
367	18	2.5	146715	9	AL355795	AL355795 Human DNA	C 440	18	2.5	165240	2	AC011040	AC011040 Homo sapi
C 368	18	2.5	147029	2	AC098249	AC098249 Rattus no	C 441	18	2.5	165501	2	AC037468	AC037468 Homo sapi
369	18	2.5	147109	9	AL591043	AL591043 Human DNA	C 442	18	2.5	165509	2	AC009886	AC009886 Homo sapi
370	18	2.5	147780	9	AP001979	AP001979 Homo sapi	C 443	18	2.5	165841	2	AC021409	AC021409 Homo sapi
C 371	18	2.5	148270	2	AC027579	AC027579 Homo sapi	C 444	18	2.5	165968	2	AC094158	AC094158 Rattus no
372	18	2.5	148663	2	AC120088	AC120088 Rattus no	C 445	18	2.5	166418	2	AC020990	AC020990 Homo sapi
C 373	18	2.5	148769	2	AC128968	AC128968 Rattus no	C 446	18	2.5	166600	9	AL391121	AL391121 Human DNA
374	18	2.5	148996	9	AC102953	AC102953 Homo sapi	C 447	18	2.5	166996	10	AL606470	AL606470 Mouse DNA
375	18	2.5	148996	9	AC102953	AC102953 Homo sapi	C 448	18	2.5	167130	2	AC114229	AC114229 Rattus no
376	18	2.5	149045	2	AC118440	AC118440 Rattus no	C 449	18	2.5	167348	2	AC027780	AC027780 Homo sapi
377	18	2.5	149363	2	AC109657	AC109657 Rattus no	C 450	18	2.5	167568	2	AC111734	AC111734 Rattus no
C 378	18	2.5	149437	2	AC027218	AC027218 Homo sapi	C 451	18	2.5	167687	2	AC023476	AC023476 Homo sapi
379	18	2.5	149532	2	AC123515	AC123515 Oryza sat	C 452	18	2.5	167732	9	AC091092	AC091092 Papio cyn
380	18	2.5	150011	2	AC068232	AC068232 Homo sapi	C 453	18	2.5	168182	2	AC068338	AC068338 Homo sapi
381	18	2.5	150145	9	AC069216	AC069216 Homo sapi	C 454	18	2.5	168310	2	AC010775	AC010775 Homo sapi
382	18	2.5	150494	2	AC078879	AC078879 Homo sapi	C 455	18	2.5	168318	2	AC024042	AC024042 Homo sapi
C 383	18	2.5	150573	2	AC102252	AC102252 Mus muscu	C 456	18	2.5	168435	2	AC098629	AC098629 Rattus no
384	18	2.5	150599	9	AL591504	AL591504 Human DNA	C 457	18	2.5	168505	2	AC080010	AC080010 Homo sapi
C 385	18	2.5	151834	9	AC005399	AC005399 Homo sapi	C 458	18	2.5	168614	9	AL357672	AL357672 Human DNA
386	18	2.5	151840	2	AL691446	AL691446 Mus muscu	C 459	18	2.5	168778	2	AC115743	AC115743 Mus muscu
C 387	18	2.5	152983	2	AC113733	AC113733 Rattus no	C 460	18	2.5	168906	2	AC129800	AC129800 Rattus no
388	18	2.5	153015	2	AC010442	AC010442 Homo sapi	C 461	18	2.5	168949	9	AC046134	AC046134 Homo sapi
389	18	2.5	153327	9	AC096636	AC096636 Homo sapi	C 462	18	2.5	168988	2	AC106979	AC106979 Rattus no
C 390	18	2.5	153468	9	AC113208	AC113208 Homo sapi	C 463	18	2.5	169289	2	AC026491	AC026491 Homo sapi
391	18	2.5	153836	8	AP005344	AP005344 Homo sapi	C 464	18	2.5	169341	2	AC017753	AC017753 Mus muscu
C 392	18	2.5	153865	8	AP002744	AP002744 Oryza sat	C 465	18	2.5	169824	2	AP001854	AP001854 Homo sapi
393	18	2.5	154064	9	AC022394	AC022394 Homo sapi	C 466	18	2.5	169939	2	AC117053	AC117053 Rattus no
394	18	2.5	154176	2	AC118829	AC118829 Rattus no	C 467	18	2.5	170000	2	AC006564	AC006564 Homo sapi
C 395	18	2.5	154283	2	AC112229	AC112229 Homo sapi	C 468	18	2.5	170255	2	AC120712	AC120712 Rattus no
396	18	2.5	154461	2	AC025711	AC025711 Homo sapi	C 469	18	2.5	170362	3	AC009250	AC009250 Drosophila
C 397	18	2.5	154737	9	AC078834	AC078834 Homo sapi	C 470	18	2.5	170670	2	AC121758	AC121758 Homo sapi
C 398	18	2.5	155065	9	HSJ659119	HSJ659119 Human DNA	C 471	18	2.5	170703	2	AC113391	AC113391 Homo sapi
399	18	2.5	155206	2	AC125884	AC125884 Rattus no	C 472	18	2.5	170725	2	AC087675	AC087675 Homo sapi
C 400	18	2.5	155488	2	AC008373	AC008373 Homo sapi	C 473	18	2.5	170880	2	AC128397	AC128397 Rattus no
C 401	18	2.5	155711	2	AC048335	AC048335 Homo sapi	C 474	18	2.5	170880	2	AC128397	AC128397 Rattus no
402	18	2.5	155843	2	AC106772	AC106772 Homo sapi	C 475	18	2.5	170928	9	AL356740	AL356740 Human DNA
403	18	2.5	156089	2	AC013750	AC013750 Homo sapi	C 476	18	2.5	170934	2	AL354684	AL354684 Homo sapi
C 404	18	2.5	156490	10	AL603709	AL603709 Mouse DNA	C 477	18	2.5	171142	9	AC069026	AC069026 Homo sapi
C 405	18	2.5	156814	9	AC006484	AC006484 Homo sapi	C 478	18	2.5	171146	2	AC117933	AC117933 Papio cyn
406	18	2.5	156957	9	AP001977	AP001977 Homo sapi	C 479	18	2.5	171200	9	AP000864	AP000864 Homo sapi
C 407	18	2.5	157183	9	AC011731	AC011731 Homo sapi	C 480	18	2.5	171261	9	AC129286	AC129286 Rattus no
C 408	18	2.5	157236	2	AC117068	AC117068 Rattus no	C 481	18	2.5	171539	9	CNS07EPB	AL512362 Human chr
C 409	18	2.5	157328	2	AC122990	AC122990 Rattus no	C 482	18	2.5	172238	9	AC090942	AC090942 Homo sapi
410	18	2.5	157566	9	AC022517	AC022517 Homo sapi	C 483	18	2.5	172261	2	AC111840	AC111840 Rattus no
C 411	18	2.5	158414	2	AC095422	AC095422 Rattus no	C 484	18	2.5	172360	2	AC024552	AC024552 Homo sapi
C 412	18	2.5	158519	9	AL135926	AL135926 Human DNA	C 485	18	2.5	172452	9	AC106332	AC106332 Rattus no
C 413	18	2.5	158653	9	AC105217	AC105217 Homo sapi	C 486	18	2.5	172465	9	AC110080	AC110080 Homo sapi
C 414	18	2.5	158910	9	AC007607	AC007607 Homo sapi	C 487	18	2.5	172693	2	AC074246	AC074246 Homo sapi
415	18	2.5	158944	9	AC096746	AC096746 Homo sapi	C 488	18	2.5	172847	2	AC116211	AC116211 Rattus no
C 416	18	2.5	159135	9	AC090060	AC090060 Homo sapi	C 489	18	2.5	172873	2	AC117799	AC117799 Mus muscu
417	18	2.5	159142	2	AC110680	AC110680 Rattus no	C 490	18	2.5	173277	2	AC120914	AC120914 Rattus no
C 418	18	2.5	159360	2	AC122607	AC122607 Rattus no	C 491	18	2.5	173488	2	AC078887	AC078887 Homo sapi
C 419	18	2.5	159926	9	AC007653	AC007653 Homo sapi	C 492	18	2.5	173742	2	AC114507	AC114507 Rattus no
C 420	18	2.5	160040	2	AC105674	AC105674 Rattus no	C 493	18	2.5	173751	2	AL590292	AL590292 Homo sapi
C 421	18	2.5	160279	2	AC019024	AC019024 Homo sapi	C 494	18	2.5	174253	2	AC068590	AC068590 Homo sapi
C 422	18	2.5	160800	2	AP002011	AP002011 Homo sapi	C 495	18	2.5	174303	2	AC099104	AC099104 Rattus no
C 423	18	2.5	161773	2	AC103491	AC103491 Rattus no	C 496	18	2.5	174535	9	AC106872	AC106872 Homo sapi
C 424	18	2.5	161988	2	AC009129	AC009129 Homo sapi	C 497	18	2.5	174547	9	AC006445	AC006445 Homo sapi
C 425	18	2.5	162267	2	AC095266	AC095266 Rattus no	C 498	18	2.5	174588	9	AC011841	AC011841 Homo sapi
C 426	18	2.5	163203	2	AC121206	AC121206 Rattus no	C 499	18	2.5	174659	2	AC128119	AC128119 Rattus no
C 427	18	2.5	163387	2	AC130912	AC130912 Rattus no	C 500	18	2.5	174705	2	AC101958	AC101958 Homo sapi
C 428	18	2.5	163613	9	AC078983	AC078983 Homo sapi	C 501	18	2.5	175026	2	AL512409	AL512409 Mus muscu
C 429	18	2.5	163871	9	HS115841	HS115841 Human DNA	C 502	18	2.5	175249	9	AC119038	AC119038 Homo sapi
C 430	18	2.5	163995	2	AC095112	AC095112 Rattus no	C 503	18	2.5	175271	2	AC116500	AC116500 Mus muscu

C 504	18	2.5	175776	2	AC112511	Homo sapi
C 505	18	2.5	175916	9	AC007861	Homo sapi
C 506	18	2.5	176123	9	AL390718	Human DNA
C 507	18	2.5	176209	9	AC009518	Homo sapi
C 508	18	2.5	176360	2	AC129633	Homo sapi
C 509	18	2.5	176644	9	AP002982	Homo sapi
C 510	18	2.5	177034	9	AP002840	Homo sapi
C 511	18	2.5	177250	2	AP000778	Homo sapi
C 512	18	2.5	177286	9	AC008085	Homo sapi
C 513	18	2.5	177300	2	AC102453	Mus muscu
C 514	18	2.5	177447	2	AC104687	Homo sapi
C 515	18	2.5	177521	2	AL161438	Homo sapi
C 516	18	2.5	177541	2	AC129140	Homo sapi
C 517	18	2.5	177801	2	AC114391	Homo sapi
C 518	18	2.5	177818	2	AC120701	Homo sapi
C 519	18	2.5	177941	9	AL445423	Human DNA
C 520	18	2.5	177976	2	AC090755	Homo sapi
C 521	18	2.5	178080	2	AC011919	Homo sapi
C 522	18	2.5	178168	2	AC024412	Homo sapi
C 523	18	2.5	178171	2	AC026961	Homo sapi
C 524	18	2.5	178410	2	AC125148	Homo sapi
C 525	18	2.5	178478	2	AP002834	Homo sapi
C 526	18	2.5	178481	3	AC090872	Drosophila
C 527	18	2.5	178716	2	AC099216	Rattus no
C 528	18	2.5	178908	2	AC110206	Mus muscu
C 529	18	2.5	178916	2	AP002874	Homo sapi
C 530	18	2.5	179357	9	AC074191	Homo sapi
C 531	18	2.5	179443	2	AC079051	Homo sapi
C 532	18	2.5	179610	2	AC018445	Homo sapi
C 533	18	2.5	179720	2	AC131436	Rattus no
C 534	18	2.5	179756	2	AC130143	Rattus no
C 535	18	2.5	180588	2	AL807398	Mus muscu
C 536	18	2.5	180859	2	AC098994	Rattus no
C 537	18	2.5	181047	2	AC016765	Homo sapi
C 538	18	2.5	181075	10	CNS07YP2	AL713885 Mus muscu
C 539	18	2.5	181182	2	AC084832	Homo sapi
C 540	18	2.5	181254	2	AP000825	Homo sapi
C 541	18	2.5	181589	9	AP000868	Homo sapi
C 542	18	2.5	181648	2	AC027094	Homo sapi
C 543	18	2.5	181672	2	AC119327	Rattus no
C 544	18	2.5	181683	2	AC021618	Homo sapi
C 545	18	2.5	181991	9	AC025882	Homo sapi
C 546	18	2.5	182214	2	AC067869	Homo sapi
C 547	18	2.5	182302	9	AC009145	Homo sapi
C 548	18	2.5	182760	2	AC123803	Mus muscu
C 549	18	2.5	182896	2	AC011043	Homo sapi
C 550	18	2.5	183309	2	AC018968	Homo sapi
C 551	18	2.5	183358	9	AC013041	Homo sapi
C 552	18	2.5	183584	9	AP003126	Homo sapi
C 553	18	2.5	183584	30	AL360171	AL360171 Human DNA
C 554	18	2.5	183619	2	AC111069	Mus muscu
C 555	18	2.5	183674	2	AC016996	Homo sapi
C 556	18	2.5	183685	2	AC099199	Rattus no
C 557	18	2.5	184007	2	AC120614	Rattus no
C 558	18	2.5	184321	2	AC025890	Homo sapi
C 559	18	2.5	184525	2	AC127614	Rattus no
C 560	18	2.5	184598	9	AL139406	Human DNA
C 561	18	2.5	184666	9	DJ201G24	AF129756 Homo sapi
C 562	18	2.5	185147	2	AP002388	Homo sapi
C 563	18	2.5	185967	9	CNS01DVR	AL136001 Human chr
C 564	18	2.5	186048	2	AC074190	Homo sapi
C 565	18	2.5	186076	2	AC127664	Rattus no
C 566	18	2.5	186388	9	AP001189	Homo sapi
C 567	18	2.5	186980	2	AC130961	Rattus no
C 568	18	2.5	187004	9	AC023154	Homo sapi
C 569	18	2.5	187254	2	AC124649	Homo sapi
C 570	18	2.5	187490	2	AC048378	Homo sapi
C 571	18	2.5	187492	2	AC129260	Rattus no
C 572	18	2.5	188868	9	AC023232	Homo sapi
C 573	18	2.5	188936	2	AC110238	Mus muscu
C 574	18	2.5	189123	2	AC093998	Rattus no
C 575	18	2.5	189339	2	AC123548	Mus muscu
C 576	18	2.5	189639	2	AC008246	Homo sapi
C 577	18	2.5	189747	2	AC087791	Homo sapi
C 578	18	2.5	189927	10	AC116588	Mus muscu
C 579	18	2.5	190180	2	AC105339	Mus muscu
C 580	18	2.5	190185	2	AC102050	Mus muscu
C 581	18	2.5	190189	2	AC107477	Rattus no
C 582	18	2.5	190357	2	AC012259	Homo sapi
C 583	18	2.5	190651	9	AL353811	Human DNA
C 584	18	2.5	190832	2	AC098161	Rattus no
C 585	18	2.5	190882	9	AL133355	Human DNA
C 586	18	2.5	191020	2	AC111129	Mus muscu
C 587	18	2.5	191410	10	AC083814	Mus muscu
C 588	18	2.5	191525	9	AC103830	Homo sapi
C 589	18	2.5	192086	2	AC117634	Mus muscu
C 590	18	2.5	192239	9	AC009796	Homo sapi
C 591	18	2.5	192370	2	AC016857	Homo sapi
C 592	18	2.5	192383	2	AC129753	Rattus no
C 593	18	2.5	192565	9	AC098935	Homo sapi
C 594	18	2.5	192724	2	AC073825	Mus muscu
C 595	18	2.5	193134	2	AC016702	Homo sapi
C 596	18	2.5	193358	9	AL135960	Human DNA
C 597	18	2.5	193400	2	AC090669	Homo sapi
C 598	18	2.5	193471	9	HSAL31016	Homo sapi
C 599	18	2.5	194630	2	AC128412	Rattus no
C 600	18	2.5	194973	9	AP002008	Homo sapi
C 601	18	2.5	195197	9	AC020911	Homo sapi
C 602	18	2.5	195270	9	AC096534	Homo sapi
C 603	18	2.5	195290	2	AC074364	Homo sapi
C 604	18	2.5	195538	9	AC092733	Homo sapi
C 605	18	2.5	195579	2	AC118087	Rattus no
C 606	18	2.5	195792	2	AC118087	Rattus no
C 607	18	2.5	196274	2	AL645797	Mus muscu
C 608	18	2.5	196319	2	AL115268	Rattus no
C 609	18	2.5	196377	2	AL691432	Homo sapi
C 610	18	2.5	196378	2	AC117504	Homo sapi
C 611	18	2.5	197061	10	AL606914	Mouse DNA
C 612	18	2.5	197738	2	AC096146	Rattus no
C 613	18	2.5	197924	2	AC120771	Rattus no
C 614	18	2.5	198079	2	AC044917	Homo sapi
C 615	18	2.5	198464	2	AC022764	Homo sapi
C 616	18	2.5	198647	2	AL845157	Mus muscu
C 617	18	2.5	198719	2	AC015176	Homo sapi
C 618	18	2.5	199254	2	AC021144	Homo sapi
C 619	18	2.5	199347	2	AL805952	Mus muscu
C 620	18	2.5	199371	2	AC110515	Mus muscu
C 621	18	2.5	199806	2	AC025580	Homo sapi
C 622	18	2.5	200000	2	AC004689	Homo sapi
C 623	18	2.5	200098	2	AC091161	Homo sapi
C 624	18	2.5	200203	2	AC104890	Mus muscu
C 625	18	2.5	200218	2	AC117248	Mus muscu
C 626	18	2.5	200340	9	AC009997	Homo sapi
C 627	18	2.5	200581	2	AC102652	Mus muscu
C 628	18	2.5	200589	2	AC127735	Rattus no
C 629	18	2.5	200627	2	AC019225	Homo sapi
C 630	18	2.5	200709	9	AC007317	Homo sapi
C 631	18	2.5	200882	2	AC112377	Rattus no
C 632	18	2.5	201157	2	AC079189	Homo sapi
C 633	18	2.5	201190	9	AC022256	Homo sapi
C 634	18	2.5	201412	9	AC096921	Homo sapi
C 635	18	2.5	201477	2	AC102653	Mus muscu
C 636	18	2.5	201570	2	AC095868	Rattus no
C 637	18	2.5	202086	10	AC080015	Mus muscu
C 638	18	2.5	202231	2	AC113244	Mus muscu
C 639	18	2.5	202235	2	AC117378	Homo sapi
C 640	18	2.5	202358	10	AL596187	Mouse DNA
C 641	18	2.5	202634	2	AC114771	Homo sapi
C 642	18	2.5	202686	10	AL589870	Mouse DNA
C 643	18	2.5	203010	9	AC006530	Homo sapi
C 644	18	2.5	203131	2	AL831780	Mus muscu
C 645	18	2.5	203481	30	AC023470	Homo sapi
C 646	18	2.5	204038	2	AC121821	Mus muscu
C 647	18	2.5	204045	2	AL805918	Mus muscu
C 648	18	2.5	204166	2	AC129385	Rattus no
C 649	18	2.5	204641	2	AC016056	Homo sapi

c 650	18	2.5	204720	2	AC008052	AC008052 Homo sapi	c 723	18	2.5	340000	9	HS21C083	AL163283 Homo sapi
c 651	18	2.5	205397	2	AC124366	AC124366 Mus muscu	c 724	18	2.5	340000	9	HS21C101	AL163301 Homo sapi
c 652	18	2.5	205673	2	AC073131	AC073131 Homo sapi	c 725	18	2.5	344000	1	TAC1D1	AL445063 Thermopla
c 653	18	2.5	205796	2	AL713891	AL713891 Mus muscu	c 726	18	2.5	347310	2	AC018743	AC018743 Homo sapi
c 654	18	2.5	205873	2	AC073147	AC073147 Homo sapi	c 727	18	2.5	350000	10	AC091453	AC091453 Mus muscu
c 655	18	2.5	206457	9	AC013268	AC013268 Homo sapi	c 728	17	2.4	151	9	HSACEINT3	AF022146 Homo sapi
c 656	18	2.5	206804	2	AC113474	AC113474 Mus muscu	c 729	17	2.4	202	9	HS36D8R	258347 H.sapiens C
c 657	18	2.5	207374	2	CNS078FU	AL583722 Human chr	c 730	17	2.4	224	9	HSU52699	252659 Human tenas
c 658	18	2.5	207593	2	AC023474	AC023474 Homo sapi	c 731	17	2.4	232	6	AX310198	AX310198 Sequence
c 659	18	2.5	207706	2	AC116393	AC116393 Mus muscu	c 732	17	2.4	270	9	AB00905S14	AB009070 Homo sapi
c 660	18	2.5	208315	1	AP003017	AP003017 Mesorhizo	c 733	17	2.4	278	9	HSA010550	AFJ01050 Homo sapi
c 661	18	2.5	208817	2	AC094908	AC094908 Rattus no	c 734	17	2.4	278	9	AF485427	AF485427 Homo sapi
c 662	18	2.5	208844	2	AC125070	AC125070 Mus muscu	c 735	17	2.4	290	9	HS33B9F	Z65337 H.sapiens C
c 663	18	2.5	208983	9	AC021124	AC021124 Homo sapi	c 736	17	2.4	291	9	AF462657	AF462657 Homo sapi
c 664	18	2.5	209512	9	CNS018OV	AL109758 Human chr	c 737	17	2.4	300	9	HS3Q1026	Z56606 H.sapiens t
c 665	18	2.5	209693	2	AC113363	AC113363 Homo sapi	c 738	17	2.4	311	14	AF008009	AF008009 Hepatitis
c 666	18	2.5	210000	2	AC004599	AC004599 Homo sapi	c 739	17	2.4	350	6	AX246782	AX246782 Sequence
c 667	18	2.5	211201	9	AC009958	AC009958 Homo sapi	c 740	17	2.4	364	11	AU026036	AU026036 Rattus no
c 668	18	2.5	211463	2	AC016508	AC016508 Homo sapi	c 741	17	2.4	369	6	A40218	A40218 Sequence 1
c 669	18	2.5	211960	2	AC090288	AC090288 Mus muscu	c 742	17	2.4	369	8	CDAL13135	AJ131335 Cynodon d
c 670	18	2.5	212553	2	AC099581	AC099581 Mus muscu	c 743	17	2.4	369	8	DGL131334	AJ131334 Dactylis
c 671	18	2.5	212621	2	AL808013	AL808013 Mus muscu	c 744	17	2.4	369	8	HLA131336	AJ131336 Holium it
c 672	18	2.5	213053	2	AC114611	AC114611 Mus muscu	c 745	17	2.4	369	8	LIT131339	AJ131339 Lolium la
c 673	18	2.5	213946	2	AC102534	AC102534 Mus muscu	c 746	17	2.4	369	8	PPRI31337	AJ131337 Poa prate
c 674	18	2.5	214000	10	AC093317	AC093317 Mus muscu	c 747	17	2.4	369	8	TAE131338	AJ131338 Triticum
c 675	18	2.5	215524	10	AL603913	AL603913 Mouse DNA	c 748	17	2.4	378	9	S76053	S76053 LW opsin=lo
c 676	18	2.5	218074	9	HUAC002044	AC002044 Human Chr	c 749	17	2.4	420	6	AR025424	AR025424 Sequence
c 677	18	2.5	218093	2	AC114999	AC114999 Mus muscu	c 750	17	2.4	420	6	AR094234	AR094234 Sequence
c 678	18	2.5	218237	2	AL805924	AL805924 Mus muscu	c 751	17	2.4	421	11	G67698	G67698 MARC3086-30
c 679	18	2.5	218511	2	AC099420	AC099420 Rattus no	c 752	17	2.4	422	14	AF060831	AF060831 Hepatitis
c 680	18	2.5	218588	2	AC116317	AC116317 Homo sapi	c 753	17	2.4	432	11	G06957	G06957 human STS W
c 681	18	2.5	219381	2	AC125077	AC125077 Mus muscu	c 754	17	2.4	438	10	RATTCRAP	L37971 Rattus norv
c 682	18	2.5	219522	2	AC091324	AC091324 Mus muscu	c 755	17	2.4	525	8	PPPHLP11	X75925 P.pratense
c 683	18	2.5	219696	2	AC112960	AC112960 Mus muscu	c 756	17	2.4	539	4	AF163296	AF163296 Equus cab
c 684	18	2.5	220684	2	AC095514	AC095514 Rattus no	c 757	17	2.4	539	4	AF163297	AF163297 Equus cab
c 685	18	2.5	220727	2	AL672234	AL672234 Mus muscu	c 758	17	2.4	547	9	HUMPLAP2A	ML9891 Human germ
c 686	18	2.5	221003	2	AC103294	AC103294 Rattus no	c 759	17	2.4	617	6	AX011652	AX011652 Sequence
c 687	18	2.5	221986	9	AC010999	AC010999 Homo sapi	c 760	17	2.4	645	10	MMRAB17AA	X70804 M.musculus
c 688	18	2.5	222722	2	AC125348	AC125348 Mus muscu	c 761	17	2.4	715	9	HS3332076	AJ3332076 Homo sapi
c 689	18	2.5	223412	2	AC124500	AC124500 Mus muscu	c 762	17	2.4	724	3	AF519414	AF519414 Strongylo
c 690	18	2.5	224257	2	AC091248	AC091248 Mus muscu	c 763	17	2.4	724	11	PM6C8G	AL684926 Penicill
c 691	18	2.5	224790	2	AC127556	AC127556 Mus muscu	c 764	17	2.4	736	3	AF519413	AF519413 Strongylo
c 692	18	2.5	225016	2	AC105703	AC105703 Rattus no	c 765	17	2.4	745	11	G67670	G67670 MARC4001-40
c 693	18	2.5	226013	2	AC073680	AC073680 Mus muscu	c 766	17	2.4	757	8	PEQ131963	AJ131963 Doritis p
c 694	18	2.5	226220	10	AL603829	AL603829 Mouse DNA	c 767	17	2.4	763	9	HS3333930	AJ3333930 Homo sapi
c 695	18	2.5	226872	2	AC105471	AC105471 Rattus no	c 768	17	2.4	877	10	BC008256	BC008256 Mus muscu
c 696	18	2.5	228330	2	AC087417	AC087417 Mus muscu	c 769	17	2.4	905	9	HS3334267	AJ3334267 Homo sapi
c 697	18	2.5	229302	2	AC023534	AC023534 Homo sapi	c 770	17	2.4	942	3	AF159386	AF159386 Secale ce
c 698	18	2.5	232270	2	AC098445	AC098445 Rattus no	c 771	17	2.4	942	3	AF218885S3	AF218887 Drosophil
c 699	18	2.5	234133	2	AC105610	AC105610 Rattus no	c 772	17	2.4	962	9	HSB802047	AL137360 Homo sapi
c 700	18	2.5	235586	2	AC024173	AC024173 Mus muscu	c 773	17	2.4	984	9	AF211977	AF211977 Homo sapi
c 701	18	2.5	236165	6	A79351	A79351 Sequence 2	c 774	17	2.4	999	6	AX018072	AX018072 Sequence
c 702	18	2.5	236165	6	A93003	A93003 Sequence 2	c 775	17	2.4	1025	9	AF115252	AF115252 Homo sapi
c 703	18	2.5	239289	2	AC079818	AC079818 Mus muscu	c 776	17	2.4	1030	1	AF064522	AF064522 Moraxella
c 704	18	2.5	239995	2	AC073154	AC073154 Mus muscu	c 777	17	2.4	1041	5	AF185587	AF185587 Rana pipi
c 705	18	2.5	244254	9	HSAC001228	AC001228 244Kb Con	c 778	17	2.4	1118	8	AF305075	AF305075 Nicotiana
c 706	18	2.5	244382	2	AC125044	AC125044 Mus muscu	c 779	17	2.4	1165	9	AF060515	AF060515 Homo sapi
c 707	18	2.5	244978	9	AF241726	AF241726 Homo sapi	c 780	17	2.4	1201	4	AF091738	AF091738 Oryctolag
c 708	18	2.5	245207	2	AL732491	AL732491 Mus muscu	c 781	17	2.4	1307	9	HSPTK6S1	U61406 Homo sapien
c 709	18	2.5	249469	3	AE003653	AE003653 Drosophil	c 782	17	2.4	1368	9	BC006361	BC006361 Homo sapi
c 710	18	2.5	251202	2	AC091902	AC091902 Homo sapi	c 783	17	2.4	1383	1	AF373208	AF373208 Bacillus
c 711	18	2.5	253108	2	AC104517	AC104517 Mus muscu	c 784	17	2.4	1493	6	AR025393	AR025393 Sequence
c 712	18	2.5	259158	2	AL645478	AL645478 Mus muscu	c 785	17	2.4	1493	6	AR094203	AR094203 Sequence
c 713	18	2.5	259498	2	AC020876	AC020876 Mus muscu	c 786	17	2.4	1640	6	AX018177	AX018177 Sequence
c 714	18	2.5	260310	2	AL645852	AL645852 Mus muscu	c 787	17	2.4	1643	10	MUSEAR2TFA	L25674 Mus musculu
c 715	18	2.5	262432	2	AC127551	AC127551 Mus muscu	c 788	17	2.4	1653	10	BC013170	BC013170 Mus muscu
c 716	18	2.5	262951	2	AC124848	AC124848 Homo sapi	c 789	17	2.4	1657	3	AF172639	AF172639 Drosophil
c 717	18	2.5	264752	10	AL669856	AL669856 Mouse DNA	c 790	17	2.4	1734	6	AR068185	AR068185 Sequence
c 718	18	2.5	266552	2	AC091362	AC091362 Rattus no	c 791	17	2.4	1734	6	AR076937	AR076937 Sequence
c 719	18	2.5	271789	2	AC098259	AC098259 Rattus no	c 792	17	2.4	1734	6	AR078770	AR078770 Sequence
c 720	18	2.5	272047	2	AC123944	AC123944 Mus muscu	c 793	17	2.4	1734	6	ARI28037	ARI28037 Sequence
c 721	18	2.5	340000	9	AP001747	AP001747 Homo sapi	c 794	17	2.4	1734	14	NDU37187	U37187 Newcastle d
c 722	18	2.5	340000	9	HS21C003	AL163203 Homo sapi	c 795	17	2.4	1734	14	NDU37191	U37191 Newcastle d

796	17	2.4	1734	14	NDU37193	U37193 Newcastle d	869	17	2.4	3416	6	AR055725	Sequence
797	17	2.4	1737	14	AF222036	AF222036 Influenza	870	17	2.4	3416	6	AR058275	Sequence
798	17	2.4	1757	14	AF222035	AF222035 Influenza	871	17	2.4	3416	6	HSU33284	Human prote
799	17	2.4	1772	14	AF222027	AF222027 Influenza	c 872	17	2.4	3444	10	BC016891	Mus muscu
800	17	2.4	1773	14	AF222026	AF222026 Influenza	c 873	17	2.4	3504	6	AR085763	Sequence
801	17	2.4	1775	9	AK057638	AK057638 Homo sapi	c 874	17	2.4	3504	6	I73041	Sequence 3
802	17	2.4	1797	9	AF058317	AF058317 Homo sapi	c 875	17	2.4	3507	6	AX189651	Sequence
803	17	2.4	1797	9	HS269477	HS269477 Homo sapi	c 876	17	2.4	3594	9	HSU12472	Human gluta
804	17	2.4	1803	4	DOGBNPA	M31777 Dog brain n	877	17	2.4	3617	9	HSU12472	Human gluta
805	17	2.4	1803	6	AX050405	AX050405 Sequence	878	17	2.4	3620	9	HSU12472	Human gluta
806	17	2.4	1804	6	AR073103	AR073103 Sequence	c 879	17	2.4	3620	9	S80542	Homo sapien
807	17	2.4	1818	3	AF193812	AF193812 Sequence	c 880	17	2.4	3649	1	AF062350	Bacillus
808	17	2.4	1824	3	AF193812	AF193812 Sequence	c 881	17	2.4	3671	1	U01158	Rhodospirill
809	17	2.4	1838	3	AF181624	AF181624 Drosophil	c 882	17	2.4	3780	1	AB012288	Bacillus
810	17	2.4	1867	9	HS269477	HS269477 Homo sapi	c 883	17	2.4	3802	1	AFACOSYN	M97217 Alicaligenes
811	17	2.4	1907	6	AR034177	AR034177 Sequence	c 884	17	2.4	3905	9	HSU12472	Human gluta
812	17	2.4	1907	6	AR111525	AR111525 Sequence	c 885	17	2.4	3913	1	BTCTRYPTB	Sequence
813	17	2.4	1907	6	AR158151	AR158151 Sequence	c 886	17	2.4	3936	9	AF156539	Homo sapi
814	17	2.4	1925	9	BC015935	BC015935 Homo sapi	c 887	17	2.4	3956	10	AF366052	Mus muscu
815	17	2.4	1935	9	HUMPYPI	D13897 Human DNA f	c 888	17	2.4	3974	10	RUU77971	U77971 Rattus norv
816	17	2.4	1959	10	BC008138	BC008138 Mus muscu	c 889	17	2.4	4003	9	HSCU2NSO	Z29336 H.sapiens g
817	17	2.4	1962	14	M16573	M16573 Newcastle d	c 890	17	2.4	4041	9	AB046859	Homo sapi
818	17	2.4	1971	10	AF258602	AF258602 Mus muscu	c 891	17	2.4	4089	9	HUMPAK2R	L49207 Homo sapien
819	17	2.4	1986	10	AF041788	AF041788 Rattus no	c 892	17	2.4	4127	9	AK074158	Homo sapi
820	17	2.4	1989	10	AF031642	AF031642 Rattus no	c 893	17	2.4	4151	9	HSU43522	Human cell
821	17	2.4	1991	9	AK092558	AK092558 Homo sapi	c 894	17	2.4	4177	6	AR093362	Sequence
822	17	2.4	2000	9	HSFAP11	AF101267 Homo sapi	c 895	17	2.4	4177	6	AR135444	Sequence
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828	17	2.4	2142	1	AB072372	AB072372 Thermococ	c 901	17	2.4	4674	9	F261892508	Sequence
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ALIGNMENTS

RESULT 1

AF123659

LOCUS

AF123659

DEFINITION

AF123659

ACCESSION

AF123659.1

VERSION

AF123659.1

KEYWORDS

GI:4572475

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

5492 bp

mRNA

linear

PRI 07-APR-1999

complete cds.

REFERENCE	1 (bases 1 to 5492)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.	
TITLE	The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)	
MEDLINE	99199287	
PUBMED	10097140	
REFERENCE	2 (bases 1 to 5492)	
AUTHORS	Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.	
TITLE	Direct Submission	
JOURNAL	Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer Institute, 233S 10th street, Philadelphia, PA 19107, USA	
FEATURES	Location/Qualifiers	
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BASE COUNT	1137 a 1704 c 1565 g 1086 t	
ORIGIN		
Query Match	100.0%; Score 715; DB 9; Length 5492;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches	715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	4215 ACTGCCCCCAGGAGACAGAGAAAGGGCTGGCTCCCCCTCCCCAGGCTGGAGACCCCCCCC 4274	
Qy	61 CAATCCAGAAAGAGCAGTCAGAGTCAGTGTCTGCCTCAGACGTTGCTTGAGAGAA 120	
Db	4275 CAATCCAGAAAGAGCAGTCAGAGTCAGTGTCTGCCTCAGACGTTGCTTGAGAGAA 4334	
Qy	121 GTGGCTGCCACCCAGGAGAGCCCTGAGGGGAGGCTGTGCTCCGCCATGTGTCTCC 180	
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Qy	241 CCGGCCCAGATGTGTCTCCCCCAGGCCCTTGTCTTACGTCAAGTGGCAGATGTCTTCCC 300	
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DEFINITION Rattus norvegicus clone CH230-28C24, *** SEQUENCING IN PROGRESS
VERSION    AC107283
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SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 113331)
AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,P.R., Allen,C.,
            Albrooks,S.L., Amarantunga,H.C., Are,J.R., Ayelle,M., Banks,T.,
            Barbacia,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
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            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
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            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
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            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
            Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
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            Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
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            Umani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
            Direct Submission
            Unpublished
            2 (bases 1 to 113331)
            Worley,K.C.
            Direct Submission
            Submitted (18-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 113331)
            Worley,K.C.
            Direct Submission
            Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On Jul 12, 2002 this sequence version replaced gi:18702073.
            ----- Genome Center
            Center: Baylor College of Medicine
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            ----- Project Information
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Center project name: GPFI
Center clone name: CH230-28C24
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 62012 bases at least Q40
Consensus quality: 5120 bases at least Q30
Consensus quality: 68175 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 48 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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1787: gap of unknown length
3327: contig of 1540 bp in length
3427: gap of unknown length
4435: contig of 1008 bp in length
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6230: contig of 1695 bp in length
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7926: contig of 1596 bp in length
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37421: gap of unknown length
38858: contig of 1437 bp in length
38958: gap of unknown length
40805: contig of 1847 bp in length
40905: gap of unknown length
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* 58442 58941: gap of unknown length
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* 73256 73355: gap of unknown length
* 73356 77171: contig of 3816 bp in length
* 77172 77271: gap of unknown length
* 77272 80397: contig of 3126 bp in length
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* 80498 84201: contig of 3704 bp in length
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* 84302 87189: contig of 2888 bp in length
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* 92345 92444: gap of unknown length
* 92445 95257: contig of 2813 bp in length
* 95258 95357: gap of unknown length
* 95358 98362: contig of 3005 bp in length
* 98363 98462: gap of unknown length
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* 103125 103224: gap of unknown length
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BASE COUNT 32601 a 20688 c 21073 g 34187 t 4782 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GAGGAAGGGTGGCTCCCCCT 39
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Db 11232 GAGGAAGGGTGGCTCCCCCT 11211

RESULT 5
AC073991 AC073991 159838 bp DNA linear PRI 07-NOV-2001
LOCUS Homo sapiens BAC clone RP11-512120 from 4, complete sequence.
DEFINITION AC073991
ACCESSION AC073991
VERSION AC073991.2 GI:14209802
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 159838)
AUTHORS Sulston, J.E. and Waterston, R.
TITRE Toward a complete human genome sequence

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Genome Res. 8 (11), 1097-1108 (1998)

98063792

9847074

2 (bases 1 to 159838)

Harris, A. and Kozlowski, A.

The sequence of Homo sapiens BAC clone RP11-512120

Unpublished

3 (bases 1 to 159838)

Waterston, R.H.

Direct Submission

Submitted (08-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 159838)

Waterston, R.H.

Direct Submission

Submitted (03-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

5 (bases 1 to 159838)

Waterston, R.

Direct Submission

Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On May 26, 2001 this sequence version replaced gi:8980014.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0512120

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanese, J.J. and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-669F3; the clone sequenced to the right is AC006230. Actual start of this clone is at base position 1 of RP11-512120; actual end is at base position 159838 of RP11-512120.

Location/Qualifiers

1..159838

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/db_xref="taxon:9606"

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FEATURES

source


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Best Local Similarity 100.0%; Pred.No. 0.86;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 418 CCTCACTATCTTGGACCATG 439
Db 5217 CCTCACTATCTTGGACCATG 5238

RESULT 6
AC093682/c 251905 bp DNA linear HTG 07-SEP-2001
LOCUS Homo sapiens chromosome UL clone RP11-665024, *** SEQUENCING IN
DEFINITION PROGRESS ***, 87 unordered pieces.
AC093682
AC093682.1 GI:15487525
VERSION HTG; HTGS_PHASE1.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 251905)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 251905)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,

```

MO 63108, USA

COMMENT

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 ----- Project Information -----
 Center project name: H_NH065024
 ----- Summary Statistics -----
 Sequencing vector: M13, 0%
 Sequencing vector: plasmid, 100%
 Chemistry: Dye-primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 218076 bases at least Q40
 Consensus quality: 226311 bases at least Q30
 Consensus quality: 231845 bases at least Q20

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 87 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 1465: gap of unknown length
 * 1565: contig of 1744 bp in length
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 * 3309: contig of 1149 bp in length
 * 3409: 4557: contig of 1149 bp in length
 * 4558: gap of unknown length
 * 4657: gap of unknown length
 * 6013: contig of 1356 bp in length
 * 6014: 6113: gap of unknown length
 * 6114: 7388: contig of 1275 bp in length
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 * 8606: 8705: gap of unknown length
 * 8706: 10381: contig of 1676 bp in length
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 * 16488: 17735: contig of 1248 bp in length
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 * 17836: 19227: contig of 1392 bp in length
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 * 21640: 22913: contig of 1274 bp in length
 * 22914: 23013: gap of unknown length
 * 23014: 24337: contig of 1224 bp in length
 * 24338: 26153: contig of 1816 bp in length
 * 26154: 26253: gap of unknown length
 * 26254: 27657: contig of 1404 bp in length
 * 27658: 27757: gap of unknown length
 * 27758: 29223: contig of 1566 bp in length
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* 142603 142702: gap of unknown length
* 142703 149141: contig of 6439 bp in length
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* 149242 153550: contig of 4309 bp in length
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* 170675 170774: gap of unknown length
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* 177941 178040: gap of unknown length
* 178041 184340: contig of 6300 bp in length
* 184341 184440: gap of unknown length
* 184441 193683: contig of 9243 bp in length
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* 199762 199861: gap of unknown length
* 199862 206203: contig of 6342 bp in length
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* 206304 215044: contig of 8741 bp in length
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* 215145 226115: contig of 10971 bp in length
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Query Match      3.1%; Score 22; DB 2; Length 251905;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 418 CCTCATATCTTGGACCATG 439
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Db 229984 CCTCATATCTTGGACCATG 229963

RESULT 7
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LOCUS AE001783 11215 bp DNA linear BCT 02-JUN-1999
DEFINITION Thermotoga maritima section 95 of 136 of the complete genome.
ACCESSION AE001783 AE000512
VERSION AE001783.1 GI:4981832
KEYWORDS Thermotoga maritima.
SOURCE Thermotoga maritima.
ORGANISM Bacteria; Thermotogae; Thermotogae; Thermotogales; Thermotogaceae;
Thermotogae.
REFERENCE 1 (bases 1 to 11215)
AUTHORS Nelson,K.E., Clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J.,
Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A.,
McDonald,L., Uitterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M.,
Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A.,
Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D.,
Eisen,J.A., Fraser,C.M. et al.
EVIDENCE for lateral gene transfer between Archaea and bacteria
from genome sequence of Thermotoga maritima
JOURNAL Nature 399 (6734), 323-329 (1999)
MEDLINE 99287316
PUBMED 10360571
REFERENCE 2 (bases 1 to 11215)
AUTHORS Nelson,K.E., Clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J.,
Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A.,
McDonald,L., Uitterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M.,
Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A.,
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Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D.,
White,O., Salzberg,S.L., Smith,H.O., Venter,J.C. and Fraser,C.M.
Direct Submission
Submitted (01-JUN-1999) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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EGTVAYGMIPMAGDEITEAGKGLDLDFTABHVKRTVFSERVKVKNILDRIEILN
VREVSIAIKPVVDQITTEISTVVTVEGAPSVVMVVGCGKAPGFSVLRKLDLPL
DVSLSKVESTGLVEDITGVKGVSEYITPVGIAYSAMNRGVSFQVFNVPVKLMG
GVGRYSVMQVLIQAGRFSSLVGEMISFELNGKTLRPRRTSVKIFVNGEENLSS
RVXRGKIDIQTEEEETPLRIKOLKVPVKLPDGGVEEVFPPEIVKNGTVPVPPADVE
EGVDVSPKEIKISETKSKISYKGTIRVNGEEKWISLVNFDLKGVPVKDDEEVL
GEEDLVKGRKTEALEVPHITVSPNGELKKIPLKILHRIDEEVELKDFKPMVID
LLKDLGLDKYELLKNGRRAMFTELLEDGDVIEPIKK"
complement(3466..5739)
/gene="TM1278"
complement(3466..5739)
/gene="TM1278"
/notes="similar to GB:AL009126 percent identity: 60.26;
identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
/product="DNA mismatch repair protein, putative"
/protein_id="AAD36353.1"
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/db_xref="GI:4981836"
/translation="MDVLESLDPKVEIVKVKYALSDLGKRLDLDLTKPTVPMDELEL
VEELNENRGEPIKGLNDISOEVKSGSPLEWELLRVSVFLEGCDILKKEPE
KREYLRKSTPREFVEENRCIEQGEISDRASPLREIRTEKRLSEIKR
KADDFVTHQIQEQMYVYRDGYLFPVKASMNAGVGVHHLSSGATVFLPEDF
VLLNNRVLLLEERLEISRLIQLTWLLSLRNLDERNVELIARFDSLVARVKFAE
FNGTVKPSRRLVNARHPLIPKRVVPIINLEPPNKGFIITGPNMGKTVTKIV
GLFTALMMSGPPLPCDSETELKVPKIMADIGEOSJEQSLSTFSSHMKIVKVA
DSDSLVLDLGSCTDPEGNALAIILDLLEKGAIFVTHLTPVKVFAMHPLLL
NASMEFPELSPYRVLVGVGSHAFQAEKGLDKRIENARSLSREMELEGL
IRSLHEKISLSEERKLOKEREYMKLEEDYKJRMKTEEDFKELRELNDYI
RKTVELDQALHVAKTSQVDMREAVKTIKEKKDLQKKEIEATEEIEIKPGDHVME
GKTSVGVKEVSGTALVDFGLRLKVPVSKLRTKKEEKKESTFSGYKSPRTEID
IRGTVSEAEPPVKKFIDDLMMNGISKGVIHGGTGLASGWEILRKDKRVVSPF
GTPSEGGTGTVVEVK"
complement (5743..6120)
/gene="TM1279"
CDS
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/gene="TM1279"
/notes="similar to percent identity: 0.00; identified by
sequence similarity; putative"
/transl_table=1
/codon_start=1
/product="hypothetical protein"
/protein_id="AAD36354.1"
/db_xref="GI:4981837"
/translation="MKKIIALLIVSVQMGDVVFSYDFSEGETVSSVGMDTGEF
TAGVELMDFSSICFFGAVNRDLIDGFMTLETRVGFSSRPYLAVVFFWKKHGVKW
GFGYSITLKDSSIRPFLFVLGW"
6158..7126
/gene="TM1280"
6158..7126
/gene="TM1280"
/notes="similar to GP:2661703 percent identity: 48.00;
identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="conserved hypothetical protein"
/protein_id="AAD36355.1"
/db_xref="GI:4981838"
/translation="MKRLFLGVGVGTGKTLLAVLSDEQGNVLAIVKGGKANGVQVVGKE
NAVRLKDVIKEDIDRAGKREIDFAFGVAGADFDYEMKIVREILEKLGLEKDFD
NDGIALRGSDYDIDIGVSCGTSISVSDGRRVNRIGLSFSLGRSLGSHYIASIV
TSAMRAKGRDDMTLIDVEKEIGPVENLLRYDYGGYTAELVKKVNOALRCAEK
GDVSLRFPDVEIVVEVKLIIDARKALNFTPIKILLEGSPFKNAPSLLINWIESAIG
REYELVPEHPDVIGAVLFAMERVGLRVLTEDLYNLRVNYLREVK"
7123..8370
/gene="TM1281"
7123..8370
/gene="TM1281"
/notes="similar to SP:P46320 PID:895751 PID:1783269
GB:A009126 percent identity: 59.43; identified by
sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="6-phospho-beta-glucosidase"
/protein_id="AAD36356.1"
/db_xref="GI:4981839"
/translation="MRIAIVGGSSYTPELVKGLLDISEDVRIDEVIFYDIBEKQKI
VDFVKRLVKDFKVLISDETEGAVDAKYVIFQPGKLGRENDEGIPLYKGLIG
ETTVGGFSAALRAPPIVEYVDVTRKSNATVITNPSGHTEFTVRYNLYEYKFG
LCNPVPIRIAEAFSARLEDVFLKYGLNHLGFIEKVFKVKGEDVTEKVFENLKL
SNIDPEPTWYDSVRLVNPYLRYLMEKMKKISTHELRAEVMKIEKLEPKY
RAVEBELTWFYDSVRLVNPYLRYLMEKMKKISTHELRAEVMKIEKLEPKY
PCYVNSGRVHTLSQKGFALSFHVAVMYERLTIEAYLKRKKLALLKALLSHPLGP
DVEAKOLLEILEANREYVKLG"
8375..9458
/gene="TM1282"
/notes="This region contains an authentic frame shift and
is not the result of a sequencing artifact; similar to
GP:I340131 percent identity: 56.11; identified by sequence
similarity; putative; conserved hypothetical protein,
authentic frameshift"

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9479..10090
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9479..10090
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/transl_table=1
/product="conserved hypothetical protein"
/protein_id="AAD36357.1"
/db_xref="GI:4981840"
/translation="MLNFFLIITQFLSGAVMYGHIIAKIKGIDLRKIDRGNPGSSNLW
RAAGKATFGPALMDYFKGTFPIAFFWMNESFHVNRVYIAAALSGILGHAFSPFLKF
KGGKATATFGAMSVLTKEGPMVLGTVTFTFISILHLRGKNKTTPEDAFRVMIGFA
ALLIYTMKVFNGMPELAILYFGNFLVLFVFKHLELRRLYKGV"
10096..11091
/gene="TM1284"
10096..11091
/gene="TM1284"
/notes="similar to GP:2815311 percent identity: 53.47;
identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="oxidase-related protein"
/protein_id="AAD36358.1"
/db_xref="GI:4981841"
/translation="MIKNOHYVLSRELKKGILGVTRFGEKLAFRDSNGKVHCIS
DICHRGASISHGKVLNNGERVMPCHFGFYDSQGRVTTIPANGRNTVPENFRVKS
Y"
Query Match 2.9%; Score 21; DB 1; Length 11215;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 394 TCITTCCTGCGCTGTCACAAA 414
| | | | | | | | | | | | | | | | | | | | |
Db 6347 TCTTTCCTGCGCTGTCACAAA 6327

RESULT 8
AL353695
LOCUS Human DNA sequence from clone RP11-17L7 on chromosome 9, complete
DEFINITION AL353695
ACCESSION AL353695
VERSION AL353695.7 GI:14787448
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 84661)
AUTHORS Laird,G.
TITLE Direct Submission
JOURNAL Submitted (13-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 17, 2001 this sequence version replaced gi:14267775.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP

```

database can be found at

http://www.sanger.ac.uk/projects/c_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9> RP11-17L7 is from the library RP11-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-17L7 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-57C19 is at 84562 in this sequence. The true right end of clone RP11-618A20 is at 100 in this sequence.

FEATURES

source

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1..84661
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="9"
    /clone="RP11-17L7"
    /clone_lib="RP11-11.1"
    444..747
        /note="AluY repeat: matches 1..304 of consensus"
    908..1002
        /note="MERSA repeat: matches 97..187 of consensus"
    923..1013
        /note="MERSA repeat: matches 8..91 of consensus"
    1301..1443
        /note="MIR repeat: matches 100..250 of consensus"
    1495..1833
        /note="THEIC repeat: matches 2..371 of consensus"
    2114..2346
        /note="AluDb repeat: matches 1..231 of consensus"
    2680..2774
        /note="L2 repeat: matches 2651..2746 of consensus"
    2822..2917
        /note="L2 repeat: matches 2362..2450 of consensus"
    3940..4131
        /note="MIR repeat: matches 16..218 of consensus"
    4255..4278
        /note="AluDb repeat: matches 114..137 of consensus"
    4279..4603
        /note="AluSx repeat: matches 1..304 of consensus"
    4604..4762
        /note="AluDb repeat: matches 137..294 of consensus"
    4773..4846
        /note="L1MB3 repeat: matches 6104..6180 of consensus"
    4992..5290
        /note="AluSx repeat: matches 1..302 of consensus"
    5871..5927
        /note="MIR repeat: matches 33..91 of consensus"
    7528..7582
        /note="MERSA repeat: matches 47..99 of consensus"
    7839..7973
        /note="L2 repeat: matches 2637..2747 of consensus"
    7974..8089
        /note="MERS3 repeat: matches 1..102 of consensus"
    8090..8365
        /note="AluDb repeat: matches 1..288 of consensus"
    8366..8538
        /note="MERS33 repeat: matches 102..324 of consensus"
    8539..8579
        /note="L2 repeat: matches 2593..2637 of consensus"
    8708..8911
        /note="AluDb repeat: matches 6..210 of consensus"
    9015..9117
        /note="MLTIE repeat: matches 418..521 of consensus"
    9226..9358
        /note="MLTIE repeat: matches 283..426 of consensus"
    9440..9743
        /note="AluSx repeat: matches 3..307 of consensus"
    9943..10069
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repeat_region
    /note="FLAM A repeat: matches 1..126 of consensus"
    1204..10511
        /note="AluSx repeat: matches 1..309 of consensus"
    10618..10843
        /note="L1MB3 repeat: matches 7497..7728 of consensus"
    10850..10988
        /note="FLAM C repeat: matches 3..142 of consensus"
    11380..11688
        /note="AluSp repeat: matches 3..311 of consensus"
    11692..12000
        /note="AluSx repeat: matches 1..312 of consensus"
    12132..12348
        /note="L2 repeat: matches 2079..2302 of consensus"
    12399..12460
        /note="L2 repeat: matches 1881..1945 of consensus"
    13093..13284
        /note="AluSx repeat: matches 114..293 of consensus"
    13285..13595
        /note="AluSc repeat: matches 1..306 of consensus"
    13596..13698
        /note="AluSx repeat: matches 9..114 of consensus"
    14000..14083
        /note="L2 repeat: matches 2626..2708 of consensus"
    14312..14374
        /note="MERS7B repeat: matches 295..376 of consensus"
    14414..14724
        /note="AluSx repeat: matches 1..312 of consensus"
    16091..16187
        /note="MIR repeat: matches 47..163 of consensus"
    16306..16547
        /note="L2 repeat: matches 2182..2461 of consensus"
    17845..18096
        /note="AluDb repeat: matches 2..249 of consensus"
    18104..18146
        /note="L2 repeat: matches 2704..2745 of consensus"
    18235..18307
        /note="L2 repeat: matches 2580..2660 of consensus"
    18367..18575
        /note="MIR repeat: matches 12..231 of consensus"
    18700..19006
        /note="AluSx repeat: matches 1..307 of consensus"
    19351..19783
        /note="AluSg/x repeat: matches 69..303 of consensus"
    19784..19867
        /note="42 copies 2 mer ag 65% conserved"
    20041..20525
        /note="L2 repeat: matches 2123..2652 of consensus"
    20526..20834
        /note="AluSg repeat: matches 1..310 of consensus"
    20835..20847
        /note="L2 repeat: matches 2113..2123 of consensus"
    20875..21010
        /note="FLAM C repeat: matches 1..133 of consensus"
    21020..21234
        /note="MIR repeat: matches 13..228 of consensus"
    21213..21347
        /note="L2 repeat: matches 2605..2708 of consensus"
    21486..21628
        /note="MIR repeat: matches 7..148 of consensus"
    21778..21815
        /note="L2 repeat: matches 2709..2747 of consensus"
    21970..22101
        /note="AluJo/FRAM repeat: matches 158..289 of consensus"
    22321..22360
        /note="20 copies 2 mer ga 95% conserved"
    23203..23248
        /note="23 copies 2 mer gt 100% conserved"
    23336..23369
        /note="17 copies 2 mer ag 82% conserved"
    24137..24260
        /note="FLAM C repeat: matches 1..124 of consensus"
    24305..24452
        /note="L2 repeat: matches 2562..2707 of consensus"
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repeat_region 24557. 24862
/note="AluSq repeat: matches 1. .306 of consensus"
repeat_region 24865. 25075
/note="MSTC repeat: matches 1. .271 of consensus"
repeat_region 25076. 25238
/note="AluJb repeat: matches 136. .298 of consensus"
repeat_region 25243. 25423
/note="FLAM A repeat: matches 20. .99 of consensus"
repeat_region 25427. 25556
/note="MLR1A1 repeat: matches 226. .365 of consensus"
repeat_region 25606. 25789
/note="AluSg/x repeat: matches 110. .291 of consensus"
repeat_region 25804. 26097
/note="MLR1C repeat: matches 182. .466 of consensus"
repeat_region 26252. 26560
/note="AluSg repeat: matches 1. .306 of consensus"
repeat_region 26976. 27291
/note="AluSx repeat: matches 1. .312 of consensus"
repeat_region 27494. 27556
/note="LTR2 repeat: matches 387. .449 of consensus"
repeat_region 27749. 27953

Query Match 2.9%; Score 21; DB 9; Length 84661;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 CCCCCCACTCCAGGAAGAG 76
Db 5568 CCCCCCACTCCAGGAAGAG 5588
|||||

RESULT 9
AC114256/c AC114256 147968 bp DNA linear HTG 13-JUL-2002
LOCUS Rattus norvegicus clone CH230-246M19, *** SEQUENCING IN PROGRESS
DEFINITION *** 34 unordered pieces.
ACCESSION AC114256
VERSION AC114256.2 GI:21738399
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 147968)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbaxia,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleaveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsone,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtonson,J., Newtonson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,

```

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Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umami,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 147968)
Worley,K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 147968)
Worley,K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:19224583.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GQZM
Center clone name: CH230-246M19
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124266 bases at least Q40
Consensus quality: 127938 bases at least Q30
Consensus quality: 130857 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1691: contig of 1691 bp in length
1791: gap of unknown length
2943: contig of 1152 bp in length
3043: gap of unknown length
4200: contig of 1157 bp in length
4300: gap of unknown length
6408: contig of 2108 bp in length
6508: gap of unknown length
7794: contig of 1286 bp in length
7894: gap of unknown length
9561: contig of 1667 bp in length
9661: gap of unknown length
11448: contig of 1787 bp in length
11549: gap of unknown length
14400: contig of 2852 bp in length
14500: gap of unknown length
16918: contig of 2418 bp in length
17018: gap of unknown length
19566: contig of 2548 bp in length
19567: gap of unknown length

```



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* 17894 21718: contig of 3835 bp in length
* 21719 21816: gap of 100 bp
* 21819 26832: contig of 5014 bp in length
* 26833 26932: gap of 100 bp
* 26933 31533: contig of 4601 bp in length
* 31534 31633: gap of 100 bp
* 31634 35717: contig of 4084 bp in length
* 35718 35817: gap of 100 bp
* 35818 40501: contig of 4684 bp in length
* 40502 40601: gap of 100 bp
* 40602 44757: contig of 4156 bp in length
* 44758 44857: gap of 100 bp
* 44858 53242: contig of 8385 bp in length
* 53243 53342: gap of 100 bp
* 53343 62709: contig of 9367 bp in length
* 62710 62809: gap of 100 bp
* 62810 73051: contig of 10242 bp in length
* 73052 73151: gap of 100 bp
* 73152 83723: contig of 10572 bp in length
* 83724 83823: gap of 100 bp
* 83824 94188: contig of 10365 bp in length
* 94189 94288: gap of 100 bp
* 94289 105339: contig of 11051 bp in length
* 105340 105439: gap of 100 bp
* 105440 126812: contig of 21373 bp in length
* 126813 126912: gap of 100 bp
* 126913 155334: contig of 28422 bp in length.

```

FEATURES

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. source
1. 155334
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-7M2"
/clone_lib="RPC1-11 Human Male BAC"
1. 1514
/note="assembly_fragment"
1615. 3445
/note="assembly_fragment"
3546. 5810
/note="assembly_fragment"
5911. 7766
/note="assembly_fragment"
7867. 9524
/note="assembly_fragment"
9625. 12146
/note="assembly_fragment"
12247. 14992
/note="assembly_fragment"
15093. 17783
/note="assembly_fragment"
17884. 21718
/note="assembly_fragment"
21819. 26832
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26933. 31533
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31634. 35717
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35818. 40501
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40602. 44757
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44858. 53242
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53343. 62709
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62810. 73051
/note="assembly_fragment"
73152. 83723
/note="assembly_fragment"
83824. 94188
/note="assembly_fragment"
94289. 105339
/note="assembly_fragment"

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vector_side:left"
misc_feature
105440..126812
/note="assembly_fragment"
misc_feature
126913..155334
/note="assembly_fragment"
BASE COUNT 38380 a 38857 c 38853 g 37140 t 2104 others
ORIGIN

Query Match 2.9%; Score 21; DB 2; Length 155334;
Best Local Similarity 100.0%; Pred. NO. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CCCCCCAACTCCAGGAAGAG 76
|||||
Db 154464 CCCCCCAACTCCAGGAAGAG 154444

RESULT 11
AC122029/c
LOCUS AC122029 163315 bp DNA linear HTG 27-MAY-2002
DEFINITION Mus musculus chromosome UNK clone RP24-400A11, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
AC122029
AC122029.2 GI:21217607
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT
On May 27, 2002 this sequence version replaced gi:21040157.

```

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0400A11
----- Summary Statistics -----
Sequencing vector: M13, 0%
Sequencing vector: plasmid, 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 158150 bases at least Q40
Consensus quality: 159182 bases at least Q30
Consensus quality: 159759 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 161735; sum-of-contigs
Quality coverage: 9.80 in Q20 bases; agarose-fp
Quality coverage: 8.16 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

```


* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1454: contig of 1454 bp in length
 * 1455 gap of unknown length
 * 1555 3760: contig of 2206 bp in length
 * 3761 3860: gap of unknown length
 * 3861 5218: contig of 1358 bp in length
 * 5219 7855: contig of 2537 bp in length
 * 7856 gap of unknown length
 * 7956 17927: contig of 9972 bp in length
 * 17928 18027: gap of unknown length
 * 18028 35513: contig of 17486 bp in length
 * 35514 35613: gap of unknown length
 * 35614 56404: contig of 20791 bp in length
 * 56405 56504: gap of unknown length
 * 56505 99102: contig of 42598 bp in length
 * 99103 99202: gap of unknown length
 * 99203 161202: contig of 62000 bp in length
 * 161203 161302: gap of unknown length
 * 161303 161955: contig of 653 bp in length
 * 161956 162056: gap of unknown length
 * 162056 163315: contig of 1260 bp in length.

FEATURES

source
 1. .163315
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 /db_xref="taxon:10090"
 /chromosome="UNK"
 /clone="RP24-400A11"
 1. .1454
 /note="assembly_name:Contig13"
 1555. .3760
 /note="assembly_name:Contig14"
 3861. .5218
 /note="assembly_name:Contig15"
 5319. .7855
 /note="assembly_name:Contig16"
 7956. .17927
 /note="assembly_name:Contig17"
 18028. .35513
 /note="assembly_name:Contig18"
 35614. .56404
 /note="assembly_name:Contig19"
 56505. .99102
 /note="assembly_name:Contig20"
 99203. .161202
 /note="assembly_name:Contig21"
 161303. .161955
 /note="assembly_name:Contig12"
 162056. .163315
 /note="assembly_name:Contig11"
 46606 a 37885 c 36992 g 40818 t 1014 others

BASE COUNT 46606 a 37885 c 36992 g 40818 t 1014 others
 ORIGIN

Query Match 2.9%; Score 21; DB 2; Length 163315;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 497 CCTGCCCCAGGCCAGACA 517
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 Db 64493 CCTGCCCCAGGCCAGACA 64473

RESULT 12

AC098966 AC098966 164924 bp DNA linear PRI 06-FEB-2002
 DEFINITION Homo sapiens chromosome 16 clone RP11-465H19, complete sequence.
 ACCESSION AC098966
 VERSION AC098966.2 GI:18542981
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE

AUTHORS DOE Joint Genome Institute.

TITLE Sequencing of Human Chromosome 16

JOURNAL

REFERENCE 2 (bases 1 to 164924)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL

REFERENCE 3 (bases 1 to 164924)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL

Submitted (06-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Feb 6, 2002 this sequence version replaced gi:16756239.

COMMENT

Sequence Quality Assessment:
 This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

FEATURES

Location/Qualifiers
 source
 1. .164924
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-465H19"

BASE COUNT 47132 a 40504 c 37718 g 39570 t
 ORIGIN

Query Match 2.9%; Score 21; DB 9; Length 164924;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 488 AGCACAGAGCTGGCCCCAGG 508
 |||||

Db 47187 AGCACAGAGCTGGCCCCAGG 47207

RESULT 13

AC068091/c

LOCUS

DEFINITION Homo sapiens chromosome 8 clone RP11-387M9 map 8, WORKING DRAFT
 SEQUENCE, 3 unordered pieces.

ACCESSION AC068091

VERSION AC068091.5 GI:14029903

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 184835)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 8, clone RP11-387M9

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 184835)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 164924)

AUTHORS DOE Joint Genome Institute.

TITLE Sequencing of Human Chromosome 16

JOURNAL

REFERENCE 2 (bases 1 to 164924)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL

Submitted (07-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 164924)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL

Submitted (06-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Feb 6, 2002 this sequence version replaced gi:16756239.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Location/Qualifiers

source
 1. .164924
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-465H19"

BASE COUNT 47132 a 40504 c 37718 g 39570 t

ORIGIN

Query Match 2.9%; Score 21; DB 9; Length 164924;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 488 AGCACAGAGCTGGCCCCAGG 508
 |||||

Db 47187 AGCACAGAGCTGGCCCCAGG 47207

RESULT 13

AC068091/c

LOCUS

DEFINITION Homo sapiens chromosome 8 clone RP11-387M9 map 8, WORKING DRAFT
 SEQUENCE, 3 unordered pieces.

ACCESSION AC068091

VERSION AC068091.5 GI:14029903

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 184835)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 8, clone RP11-387M9

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 184835)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,


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               complement(7991..8748)
               /evidence=not_experimental
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repeat_region /rpt_family="L2"
               9881..9915
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               21328..21634
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repeat_region 34890..34916
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repeat_region complement(34954..35023)
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repeat_region 41600..41706
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repeat_region 46113..46158
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               /rpt_family="G-rich"
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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 457 GGAAGAGGCTCTGGACAGCA 477
      |||||
Db 168969 GGAAGAGGCTCTGGACAGCA 168949

RESULT 15
AF139185 LOCUS 6975 bp mRNA linear ROD 02-APR-2001
DEFINITION Rattus norvegicus myomegalin mRNA, complete cds.
ACCESSION AF139185
VERSION AF139185.1 GI:4761643
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 6975)
AUTHORS Verde, I., Pahlke, G., Salanova, M., Zhang, G., Wang, S., Coletti, D.,
Onuffer, J., Jin, S. L. and Conti, M.
TITLE Myomegalin is a novel protein of the golgi/centrosome that
interacts with a cyclic nucleotide phosphodiesterase
J. Biol. Chem. 276 (14), 11189-11198 (2001)
JOURNAL 21179171
MEDLINE 11334006
PUBMED
REFERENCE 2 (bases 1 to 6975)
AUTHORS Pahlke, G., Verde, I., Salanova, M., Jin, S.-L.C., Zhang, G., Onuffer, J.
and Conti, M.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-1999) Gynecology & Obstetrics, Stanford
University Medical Center, 300 Pasteur Drive, Room A344, Stanford,
CA 94305-5317, USA
FEATURES
source
Location/Qualifiers
1..6975
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue type="skeletal muscle; heart; testis"
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/product="myomegalin"
/protein_id="AAD29427.1"
/db_xref="GI:4761644"
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LDQYSALAAQRDRIEELRQLAAQGLVEQLSEKQQLHLLPEPGMEVQPMKGL
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OKQDTTOSLKMELKRESSETELYQVTEGQNTMAKPEMLHQSOLQOLQSSRGIA
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QELQLQYRDTDTKTLDTNEVLEFKQRIODRAVALDERVIDEFKSALEKQKELRQ
LRLAVDRDLRLRCLVSNCAETMQSMESLLRARGLEVEQLIATQNLQWKEELE
TKFHWQKEQESIIOQLQTLSDRNKEVEDLSATLLHKLPGQSEVEELCQRLQKE
RVQLDLSDRNKQAMEHEMVQGLQSGMTRQERQAVAEKQVAFERNSELQALRQ
YLGKELDAWQAQAFISNOPAGATSVGPHHGQTOGQSTQMPSRDDSTSLTAREASIP
RSTLGDSTVAGLEKELSNAXEELMAKKERESQIELSALQSMVAQVEELQVQAD
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RRQULLLLEGLVDRSLRNEALQAEQYLSLVKFAQPTTFEDRTIQLVLEGQAV
LRSLEELVGLSRLETLTAAGTAGTDEDTSTQFTDSTIEEAHNSHQQLI
KVSLEKSLTTWETONTQLOPPSPVCGDNHLOEMLHRAEIHQPLEKKAKAEAK
ELKAGIEAGFSSVSHIENTWLSLCLENAELKEOMGEAMSDGWEEDKEKEGVNVT
VYAKGLEDSELSQAEFRKQGLKSAYNIIINLLKQVLVRSSEGNKEMPFLVRLAR
EVDNWMGLPSEKRGHQEQENWTAPRPGRLKIGTALSVDGQLGNKSCAQDSGH
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KSEKEAGLEPLALRUSRELOKEKEKIEVLEQAKLDTRFSFPSSHAASDSHRGASSTS
FLSDDIEACSDMDVASEYTHYEKKEPSGNSAASASQGLKEPRSSISLPTQNPVK
EASQAQPGHFNSIPKPAISLQAPMHTVPSFMPFGSPGPPHGCCCTPVVSLAEAAQ
ELQMLQKOLGRSVSIAPPTSTSLNHNTEASSPYSNPAQPHSPARGTIELGRILEP
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ICVNDRIEQLQHRLSSTARENGSTSHFYSGLESMPLYNENRALRENOQLQTRLS
HASRHSQEVHDHUREALLSSSQLEKEKEQKAEERQLLEDLQKQKQEI VHFRE
RLSLQNNRSLQHKLALLQOCEKQOLSLQSELOIYESLYENPKKGLSKAFSLDSC
YQVPEGLSCLVAEIRALRYLEQSIQVNNRRLQLEQMDHGAGKAGLSKCPVNSDES
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EGNLMKELLDLRAQVQQQLQSTAVRLKNTANQRKKSMEQFIVSHLTRHVDVKKK
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BASE COUNT 1971 a 1820 c 1947 g 1237 t
ORIGIN

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Query Match      2.8%; Score 20; DB 10; Length 6975;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 GCCTGGCCCCCAGGCCCCAGCA 515
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Db 3516 GCCTGGCCCCCAGGCCCCAGCA 3535
      |||||

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Search completed: June 17, 2003, 04:00:26
Job time : 1371.49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 126.225 Seconds
(without alignments)
12756.396 Million cell updates/sec

Title: US-09-513-888c-1_COPY_7806_8520

Perfect score: 715

Sequence: 1 actgcccacagagacag.....ttccctctctagctctccag 715

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq 101002.*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
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- 23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715	100.0	5492	21	AAA64508
2	715	100.0	9048	21	AAA64507
3	486	68.0	1855	22	AA181887
4	63	8.8	591	21	AAA64516
5	49	6.9	393	16	AAT23583
6	20	2.8	9679	21	AAD00768
7	20	2.8	10437	22	AAS41709
8	20	2.8	12620	22	ABA16691
9	19	2.7	531	24	ABN79134

					cDNA sequence of t
					Nucleotide sequenc
					Human polynucleoti
					F37 probe used to
					Human gene signatu
					Rat phosphodiester
					Genomic sequence #
					Human nervous syst
					Human ORF4081 cDNA

Human phosphatidyl	10	19	2.7	2472	24	ABL59550
Human protein enco	11	19	2.7	2730	22	AAH99704
Human protein enco	12	19	2.7	2735	22	AAH99710
Human polynucleoti	13	19	2.7	2735	22	AA159663
Human polynucleoti	14	19	2.7	2735	22	AA159664
Human polynucleoti	15	19	2.7	2739	22	AA157877
Human polynucleoti	16	19	2.7	2916	22	AA157878
Human immune/haema	17	19	2.7	27082	22	AAK70447
Human immune/haema	18	18	2.5	485	22	AA109721
Human breast cance	19	18	2.5	583	24	ABN65898
Human breast cance	20	18	2.5	628	22	AA118393
Human immune/haema	21	18	2.5	860	22	AAK70648
Human immune/haema	22	18	2.5	860	22	AAK70649
Human immune/haema	23	18	2.5	860	22	AAK70650
Scenedemus D1 pro	24	18	2.5	1680	19	AAV39818
cDNA encoding scen	25	18	2.5	1680	24	ABK48203
cDNA sequence #8 e	26	18	2.5	2144	24	AAK62221
Human cancer asoc	27	18	2.5	2662	21	AAK77608
Human nervous syst	28	18	2.5	3031	22	ABA18518
Novel human coding	29	18	2.5	4919	24	ABN59815
Human polynucleoti	30	18	2.5	5643	22	AAK51612
Human nervous syst	31	18	2.5	6643	22	ABA16216
Human cDNA differe	32	18	2.5	6704	24	ABK84002
DNA encoding novel	33	18	2.5	11336	22	AAK27780
Human wolfram in ge	34	18	2.5	26379	21	AAZ88922
WFS1 variant genom	35	18	2.5	67212	21	AAA08954
Human DNA sequence	36	18	2.5	123219	23	AAH88703
Rhizobium species	37	18	2.5	534720	19	AAV30458
Rhizobium species	38	18	2.5	536165	19	AAV30459
Human SNP oligonuc	39	17	2.4	50	22	AA133953
Human SNP oligonuc	40	17	2.4	51	22	AA132942
Human polymerase-1	41	17	2.4	232	24	ABN76645
Human gene express	42	17	2.4	300	20	AAZ14903
Human immune/haema	43	17	2.4	311	22	AAK85122
Novel human diseno	44	17	2.4	350	22	AAK38654
Human immune/haema	45	17	2.4	362	22	AAK68500
Human prostate exp	46	17	2.4	365	23	ABV08368
Human immune/haema	47	17	2.4	367	22	AAK56639
EST clone BJ87. H	48	17	2.4	368	20	AAV87083
Human prostate exp	49	17	2.4	382	23	ABV38275
Human immune/haema	50	17	2.4	416	22	AAK60046
Human secreted pro	51	17	2.4	418	21	AAK06586
Sequence of the sp	52	17	2.4	420	19	AAV09982
Human polynucleoti	53	17	2.4	456	22	AA189467
Human prostate exp	54	17	2.4	457	23	ABV05112
Human cardiovascular	55	17	2.4	467	22	AAK35563
Human immune/haema	56	17	2.4	490	22	AAK82396
Recombinant timoth	57	17	2.4	525	15	AAQ77731
Human brain expres	58	17	2.4	543	22	AAK11774
Human immune/haema	59	17	2.4	563	22	AAK78328
Human immune/haema	60	17	2.4	563	22	AAK78329
Human immune/haema	61	17	2.4	563	22	AAK78330
Human immune/haema	62	17	2.4	563	22	AAK78723
Human immune/haema	63	17	2.4	563	22	AAK78724
Human immune/haema	64	17	2.4	563	22	AAK78725
Human prostate tum	65	17	2.4	617	20	AAZ52905
DNA encoding novel	66	17	2.4	660	23	AAK76917
Human breast cance	67	17	2.4	690	22	AAK22819
Human ovarian anti	68	17	2.4	691	24	ABQ54423
DNA encoding novel	69	17	2.4	882	23	AAK82232
DNA encoding novel	70	17	2.4	960	23	AAK78328
Human colon cancer	71	17	2.4	967	21	AAK98223
Human breast cance	72	17	2.4	993	22	AAK25098
Human prostate can	73	17	2.4	999	20	AAZ33442
Human signal pepti	74	17	2.4	1066	21	AAZ38135
DNA encoding novel	75	17	2.4	1107	23	AAK80914
Human polynucleoti	76	17	2.4	1128	22	AAI82348
Human polynucleoti	77	17	2.4	1225	24	ABL90131
Human polynucleoti	78	17	2.4	1238	21	AAA09482
Human Zeig24 codin	79	17	2.4	1254	21	AAA40579
Murine adult bone	80	17	2.4	1264	20	AAZ06243
Human secreted pro	81	17	2.4	1275	20	AAZ06258
Human secreted pro	82	17	2.4	1298	21	AAK74927

83	17	2.4	1345	24	ABN86910	Human NOV1 encodin	156	17	2.4	5454	24	AAD38865	Human kinase (PKIN
84	17	2.4	1380	22	ABA09465	Human membrane-ass	c 157	17	2.4	6075	22	AAK79246	Human immune/haema
85	17	2.4	1409	21	AAZ97090	Human secreted pro	158	17	2.4	6100	15	AAQ79728	Human L5/3 tumour
86	17	2.4	1452	23	ABL27531	Drosophila melanog	159	17	2.4	6100	18	AAK62440	Human L5/3 growth
87	17	2.4	1493	19	AAZ09951	cDNA encoding a no	c 160	17	2.4	6232	24	AAK42134	Human Kruppel-like
88	17	2.4	1558	21	AAZ65254	Human secreted pro	c 161	17	2.4	6232	24	AAK42135	Human Kruppel-like
89	17	2.4	1635	13	AAQ24010	Mutant thermotabl	162	17	2.4	6239	24	ABK93553	Human breast speci
90	17	2.4	1734	17	AAAT18205	Newcastle disease	163	17	2.4	6866	22	AAK70762	Human immune/haema
91	17	2.4	1752	23	AAK72292	DNA encoding novel	164	17	2.4	6866	22	AAK71754	Human immune/haema
92	17	2.4	1803	22	AAK82675	Canine BNP fragmen	165	17	2.4	7487	23	AAK92457	DNA encoding novel
93	17	2.4	1804	11	AAQ02851	cDNA encoding a ca	166	17	2.4	7574	22	AAK74485	Human immune/haema
94	17	2.4	1840	23	ABL02133	Drosophila melanog	167	17	2.4	7574	22	AAK74613	Human immune/haema
95	17	2.4	1867	24	ABA99929	NDV HN DNA fragmen	168	17	2.4	7928	22	AAK62287	cDNA encoding a sp
96	17	2.4	1898	22	AAK91896	Human secreted pro	169	17	2.4	8543	23	ABV22726	Human prostate exp
97	17	2.4	1899	13	AAQ24009	Mutant thermotabl	170	17	2.4	8543	23	ABV227551	Human prostate exp
98	17	2.4	1907	14	AAQ46678	NDV Haemagglutinin	c 171	17	2.4	8628	24	ABK64727	Human benign proct
99	17	2.4	1907	16	AAQ99633	Newcastle's diseas	c 172	17	2.4	8791	17	AAK737090	Human T cell inosi
100	17	2.4	2037	21	AAK66421	Human secreted pro	c 173	17	2.4	9110	24	ABK47941	Human Jun B Proto-
101	17	2.4	2043	13	AAQ24008	Mutant thermotabl	c 174	17	2.4	9517	24	ABL61755	Colon adenocarcino
102	17	2.4	2070	22	AAK59630	Human cell cycle a	c 175	17	2.4	9517	24	ABL65220	Lung cancer relate
103	17	2.4	2085	20	AAK01362	Nucleobase permeas	c 176	17	2.4	9517	24	ABL66638	Lung cancer relate
104	17	2.4	2112	22	AAK74448	Human PRO17 nucleo	c 177	17	2.4	9664	22	ABA16496	Human cardiovascular
105	17	2.4	2203	22	AAK89786	Nucleotide sequenc	c 178	17	2.4	9664	22	AAK36626	Human nervous syst
106	17	2.4	2277	13	AAQ24007	Mutant thermotabl	c 179	17	2.4	9848	21	AAK98272	Mouse IP3 receptor
107	17	2.4	2295	22	AAH23380	Human transferase	c 180	17	2.4	9871	12	AAQ13593	Inositol-3-phospha
108	17	2.4	2367	13	AAQ24006	Mutant thermotabl	181	17	2.4	9980	24	ABN96855	Gene #3353 used to
109	17	2.4	2379	23	AAK89880	DNA encoding novel	182	17	2.4	9980	24	ABN96855	Kidney cancer rela
110	17	2.4	2437	22	AAK89785	Nucleotide sequenc	183	17	2.4	10053	22	AAK73765	Human immune/haema
111	17	2.4	2493	13	AAQ24005	Mutant thermotabl	184	17	2.4	10659	23	ABL02132	Drosophila melanog
112	17	2.4	2507	16	AAQ81189	Breast tumour kina	185	17	2.4	10828	24	ABK12302	Human tyrosine hyd
113	17	2.4	2512	16	AAQ92369	TfII DNA-polymeras	186	17	2.4	12290	22	ABK19042	Human nervous syst
114	17	2.4	2519	22	AAH35022	Human colon cancer	187	17	2.4	13329	24	ABK12301	Human tyrosine hyd
115	17	2.4	2520	21	AAK35035	Human colon cancer	188	17	2.4	13875	13	AAQ02040	Human centromeric
116	17	2.4	2528	22	AAK83503	Human PRO848 nucle	c 189	17	2.4	15987	22	AAK83592	Human immune/haema
117	17	2.4	2528	21	AAZ65079	Membrane-bound pro	c 190	17	2.4	15987	22	ABK42414	Genomic sequence #
118	17	2.4	2528	22	AAK21474	Human cDNA sequenc	c 191	17	2.4	16038	22	AAK89507	Human digestive sy
119	17	2.4	2528	22	AAK44225	Human PRO848 (UNQ5	c 192	17	2.4	16831	22	AAK73455	Human immune/haema
120	17	2.4	2556	23	AAK80084	DNA encoding novel	193	17	2.4	17084	22	AAK70764	Human immune/haema
121	17	2.4	2567	20	AAK52889	Human prostate tum	194	17	2.4	17084	22	AAK71755	Human immune/haema
122	17	2.4	2644	22	AAK89784	Nucleotide sequenc	c 195	17	2.4	17904	22	ABA07913	Human ovarian and
123	17	2.4	3129	22	ABA16690	Human nervous syst	c 196	17	2.4	17904	22	AAK03730	Human reproductive
124	17	2.4	3133	20	AAK57463	Rat U3 gene trap d	c 197	17	2.4	19199	22	AAK70995	Human immune/haema
125	17	2.4	3225	24	AAK26467	Human kinase PKIN-	c 198	17	2.4	19659	22	AAK64731	Human immune/haema
126	17	2.4	3416	17	AAK30373	Protein tyrosine ki	c 199	17	2.4	19659	22	AAK75600	Human immune/haema
127	17	2.4	3416	17	AAK40859	Human PK-2 protei	c 200	17	2.4	19659	22	AAK91504	Human digestive sy
128	17	2.4	3416	24	ABK84297	Human cDNA differe	c 201	17	2.4	23452	22	AAK42122	Genomic sequence #
129	17	2.4	3504	17	AAK16553	CryIF class toxin	c 202	17	2.4	23457	22	AAK42121	Genomic sequence #
130	17	2.4	3507	22	AAH28241	Nucleotide sequenc	c 203	17	2.4	23458	22	AAK42120	Genomic sequence #
131	17	2.4	3527	23	AAK66986	DNA encoding novel	c 204	17	2.4	26657	24	AAI72317	Human transporter
132	17	2.4	3594	24	ABK84227	Human cDNA differe	c 205	17	2.4	32192	22	ABA17963	Human nervous syst
133	17	2.4	3621	19	AAK17800	Human related adhe	c 206	17	2.4	32192	22	AAK17929	Human musculoskele
134	17	2.4	3628	23	ABL27530	Drosophila melanog	c 207	17	2.4	32192	22	AAK07103	Human reproductive
135	17	2.4	3834	21	AAZ51204	Rat hypoxia regula	c 208	17	2.4	32195	22	AAK36105	Human cardiovascular
136	17	2.4	3957	22	ABA06411	Human cDNA SEQ ID	c 209	17	2.4	32195	22	AAK31532	Human DNA for a no
137	17	2.4	4089	21	AAK36693	Nucleotide sequenc	c 210	17	2.4	32195	22	AAK31538	Human DNA for a no
138	17	2.4	4151	24	ABK84331	Human cDNA differe	c 211	17	2.4	32195	23	ABK44045	Genomic DNA encodi
139	17	2.4	4175	22	AAK62285	cDNA encoding a hu	c 212	17	2.4	32195	24	ABQ66856	Human polynucleoti
140	17	2.4	4177	15	AAK68943	Sfil fragment cont	c 213	17	2.4	32195	24	ABQ66852	Human polynucleoti
141	17	2.4	4177	15	AAQ70570	Sfil fragment cont	c 214	17	2.4	37925	22	AAK72372	Human immune/haema
142	17	2.4	4177	18	AAK48510	Sfil fragment enco	c 215	17	2.4	42519	22	AAK81318	Human immune/haema
143	17	2.4	4177	20	AAK81147	Seq ID No: 12 of U	c 216	17	2.4	62944	24	ABL66947	Lung cancer relate
144	17	2.4	4177	21	AAK67862	Sfil fragment comp	c 217	17	2.4	62944	24	ABL68262	Kidney cancer rela
145	17	2.4	4177	21	AAZ49295	cDNA encoding NDV	c 218	17	2.4	92638	24	ABQ88096	Human osteoblast d
146	17	2.4	4339	23	ABV25367	Human prostate exp	c 219	17	2.4	100301	24	ABQ88176	Human osteoblast d
147	17	2.4	4420	22	AAK90043	Human resistin gen	c 220	17	2.4	183999	22	AAK92831	Human ABC1 genom
148	17	2.4	4936	22	AAH46904	cDNA encoding huma	c 221	17	2.4	201143	24	ABK83568	Human DNA differen
149	17	2.4	5007	16	AAK69927	Tps17 polymerase	c 222	16	2.2	20	21	AAA07650	HERG gene intron 1
150	17	2.4	5047	22	AAK62286	cDNA encoding a fu	c 223	16	2.2	116	22	AAK76951	Human genome fragm
151	17	2.4	5190	24	AAK62911	Breast cancer rela	c 224	16	2.2	124	15	AAQ76402	Human genome fragm
152	17	2.4	5207	24	AAK43908	Human kinase prote	c 225	16	2.2	148	22	AAI61577	Soybean 318013 reg
153	17	2.4	5207	24	AAK43909	Human kinase prote	c 226	16	2.2	164	24	ABL61761	Human ovarian can
154	17	2.4	5312	22	AAK40665	DNA encoding huma	c 227	16	2.2	193	22	ABA41047	Probe #19513 for g
155	17	2.4	5312	22	AAK06553	Human reproductive	c 228	16	2.2	193	22	AAK25176	Human brain expres

C 229	16	2.2	193	22	AAK51182	Human bone marrow	302	16	2.2	551	22	AAK80387	Human immune/haema
C 230	16	2.2	193	22	AAI28191	Probe #18124 for g	C 303	16	2.2	551	22	AAK80388	Human immune/haema
C 231	16	2.2	193	22	AAI57234	Probe #25920 used	C 304	16	2.2	568	21	AAFO9733	Fusarium venenatum
C 232	16	2.2	193	22	ABS24712	Human genome-deriv	C 305	16	2.2	569	22	ABA310954	Probe #9420 for ge
C 233	16	2.2	212	24	ABL74686	Corn tassell-derive	C 306	16	2.2	569	22	AAK12277	Human brain expres
C 234	16	2.2	235	22	AA506580	Mouse microglia an	C 307	16	2.2	569	22	AAK37998	Human bone marrow
C 235	16	2.2	244	22	AAH08137	Human breast cance	C 308	16	2.2	569	22	AAI18768	Probe #8701 for ge
C 236	16	2.2	266	22	AAH45500	Human REIC related	C 309	16	2.2	569	22	AAI43881	Probe #12567 used
C 237	16	2.2	284	22	AAK75717	Human immune/haema	C 310	16	2.2	569	24	ABS12001	Human genome-deriv
C 238	16	2.2	297	21	AAK05431	Human secreted pro	C 311	16	2.2	573	24	AAI47594	Metridia longa luc
C 239	16	2.2	305	24	ABN18832	Human ORFX polynuc	C 312	16	2.2	573	24	AAI46656	Metridia longa luc
C 240	16	2.2	314	23	AA872213	DNA encoding novel	C 313	16	2.2	578	24	ABU83163	Human ovarian can
C 241	16	2.2	349	24	ABN78962	Human ORF3909 cDNA	C 314	16	2.2	579	22	AAH65994	C Glutamicum codin
C 242	16	2.2	353	22	AAK64358	Human immune/haema	C 315	16	2.2	587	15	AAQ55685	Rabbit CAP18 gene.
C 243	16	2.2	356	24	ABN15855	Human ORFX polynuc	C 316	16	2.2	587	20	AAI19928	Lilly male gamete-s
C 244	16	2.2	364	24	ABN27002	Human ORFX polynuc	C 317	16	2.2	590	22	ABA62140	Human foetal liver
C 245	16	2.2	366	22	AAK59221	Human immune/haema	C 318	16	2.2	590	22	ABA29548	Probe #8014 for ge
C 246	16	2.2	366	22	AAH34263	Human colon cancer	C 319	16	2.2	590	22	AAK10459	Human brain expres
C 247	16	2.2	368	21	AAK02351	Human secreted pro	C 320	16	2.2	590	22	AAK36360	Human bone marrow
C 248	16	2.2	371	24	ABL83929	Human ovarian can	C 321	16	2.2	590	22	AAI17285	Probe #7218 for ge
C 249	16	2.2	379	22	AAI86621	Human polynucleoti	C 322	16	2.2	590	22	AAI42088	Probe #10774 used
C 250	16	2.2	381	21	AAH30648	Human colon cancer	C 323	16	2.2	590	24	ABS10414	Human genome-deriv
C 251	16	2.2	383	22	AAI84957	Human polynucleoti	C 324	16	2.2	594	22	AAI44533	Probe #13219 used
C 252	16	2.2	386	14	AAQ50267	Human brain Expres	C 325	16	2.2	617	21	AAFI8363	Lung cancer associ
C 253	16	2.2	386	21	AAK27717	Human secreted pro	C 326	16	2.2	623	22	AAK69166	Human immune/haema
C 254	16	2.2	388	22	AAI81643	Human polynucleoti	C 327	16	2.2	623	22	AAK69167	Human immune/haema
C 255	16	2.2	393	22	ABA44353	Human breast cell	C 328	16	2.2	624	24	ABO88907	Human prostate exp
C 256	16	2.2	393	22	ABA54807	Human foetal liver	C 329	16	2.2	634	24	ABK73913	Bacillus lichenifo
C 257	16	2.2	393	22	ABA24572	Probe #3038 for ge	C 330	16	2.2	635	20	AAK39813	Gastric cancer ass
C 258	16	2.2	393	22	AAK03083	Human brain expres	C 331	16	2.2	637	22	AAK56951	Human immune/haema
C 259	16	2.2	393	22	AAK28535	Human bone marrow	C 332	16	2.2	647	22	AAK91659	Human CDNA 5'-end
C 260	16	2.2	393	22	AAI13109	Probe #3042 for ge	C 333	16	2.2	647	22	AAK93640	Human CDNA clone r
C 261	16	2.2	393	22	AAI34459	Probe #3145 used t	C 334	16	2.2	661	22	AAH04792	Human CDNA for nov
C 262	16	2.2	393	22	AAI03011	Probe #3002 used t	C 335	16	2.2	668	24	ABK34390	Human polynucleoti
C 263	16	2.2	393	24	ABN94576	Gene #1074 used to	C 336	16	2.2	676	22	AAI81744	Human polynucleoti
C 264	16	2.2	393	24	ABS03047	Human genome-deriv	C 337	16	2.2	700	22	AAH92940	Human inflammatory
C 265	16	2.2	393	24	ABN23152	Human ORFX polynuc	C 338	16	2.2	738	18	AAH95234	Macaque islet cell
C 266	16	2.2	409	21	AAK03640	Human secreted pro	C 339	16	2.2	767	20	AAK39815	Gastric cancer ass
C 267	16	2.2	409	22	AAK89184	Human digestive sy	C 340	16	2.2	771	22	AAI67176	Nucleotide sequenc
C 268	16	2.2	409	22	AAK89185	Human digestive sy	C 341	16	2.2	778	22	AAI96364	Human neuroblastom
C 269	16	2.2	425	22	AAK21960	Human collagen gen	C 342	16	2.2	784	22	AAK51974	Human polynucleoti
C 270	16	2.2	427	22	ABA69666	Human pancreatic c	C 343	16	2.2	791	22	AAI91505	Human polynucleoti
C 271	16	2.2	427	22	AAK88165	Human digestive sy	C 344	16	2.2	793	22	AAK26203	Human CDNA encodin
C 272	16	2.2	433	22	AAK62405	Human immune/haema	C 345	16	2.2	816	22	AAH65897	C Glutamicum codin
C 273	16	2.2	436	24	ABL81139	Human ovarian can	C 346	16	2.2	818	24	ABA94145	Human ATP dependen
C 274	16	2.2	438	22	AAK90128	Human prostate can	C 347	16	2.2	821	21	AAK98850	Human pancreatic c
C 275	16	2.2	440	21	AAK27881	Human secreted pro	C 348	16	2.2	827	22	AAK52958	Human polynucleoti
C 276	16	2.2	440	22	AAK90121	Human prostate can	C 349	16	2.2	830	22	AAK90127	Human prostate can
C 277	16	2.2	447	14	AAQ59652	Human brain Expres	C 350	16	2.2	834	22	AAK90120	Human prostate can
C 278	16	2.2	455	22	AAK90129	Human prostate can	C 351	16	2.2	907	22	AAI58762	Human polynucleoti
C 279	16	2.2	457	22	AAK545193	CDNA encoding nove	C 352	16	2.2	912	22	AAK06492	Arabidopsis thalia
C 280	16	2.2	457	22	AAK90122	Human prostate can	C 353	16	2.2	932	18	AAH95235	Macaque islet cell
C 281	16	2.2	481	22	AAK55262	Human immune/haema	C 354	16	2.2	936	10	AAH92189	TA13 CDNA. Nicoti
C 282	16	2.2	481	22	AAK74761	Human immune/haema	C 355	16	2.2	955	21	AAH92189	Arachidonic acid m
C 283	16	2.2	481	23	ABV52441	Human prostate exp	C 356	16	2.2	982	24	ABA93657	Human chicken wing
C 284	16	2.2	482	22	ABA08881	Human secreted pro	C 357	16	2.2	999	18	AAH95236	Macaque islet cell
C 285	16	2.2	499	21	AAK99146	Human pancreatic c	C 358	16	2.2	1011	18	AAH95237	Macaque islet cell
C 286	16	2.2	505	23	AAK84768	DNA encoding novel	C 359	16	2.2	1047	24	ABQ86183	Novel human gene.
C 287	16	2.2	511	23	AAK80311	DNA encoding novel	C 360	16	2.2	1049	21	AAZ48763	Human CIDE-A codin
C 288	16	2.2	513	24	ABQ58536	Human colon cancer	C 361	16	2.2	1050	24	ABQ88238	Human osteoblast d
C 289	16	2.2	514	23	ABK58429	Human prostate exp	C 362	16	2.2	1050	24	ABL63683	Breast cancer rela
C 290	16	2.2	516	24	ABK09679	Human ovarian tumo	C 363	16	2.2	1086	23	AAK84767	DNA encoding novel
C 291	16	2.2	524	22	ABA62321	Human foetal liver	C 364	16	2.2	1096	20	AAK22275	Human secreted pro
C 292	16	2.2	524	22	ABA29664	Probe #8130 for ge	C 365	16	2.2	1100	21	AAK93460	Human secreted pro
C 293	16	2.2	524	22	AAK10657	Human brain expres	C 366	16	2.2	1100	21	AAK75819	Human ORFX ORF1374
C 294	16	2.2	524	22	AAK36542	Human bone marrow	C 367	16	2.2	1129	24	ABU90679	Human polynucleoti
C 295	16	2.2	524	22	AAI17400	Probe #7333 for ge	C 368	16	2.2	1145	22	AAK87328	Human immune/haema
C 296	16	2.2	524	22	AAI42300	Probe #10986 used	C 369	16	2.2	1145	22	AAK87329	Human immune/haema
C 297	16	2.2	524	24	ABN83559	Human acyl-CoA deh	C 370	16	2.2	1225	21	AAK98090	Human colon cancer
C 298	16	2.2	524	24	ABN10538	Human genome-deriv	C 371	16	2.2	1230	22	AAH68436	C Glutamicum codin
C 299	16	2.2	545	21	AAH31082	Human colon cancer	C 372	16	2.2	1247	23	AAH59706	Propionibacterium
C 300	16	2.2	551	22	AAK61554	Human immune/haema	C 373	16	2.2	1289	21	AAK41140	Arabidopsis thalia
C 301	16	2.2	551	22	AAK69681	Human immune/haema	C 374	16	2.2	1290	23	AAH71002	DNA encoding novel

C 375	16	2.2	1292	22	AAH15754	Human cDNA sequenc	C 448	16	2.2	2535	24	ABA90342	Human polynucleoti
C 376	16	2.2	1308	22	AAS42067	Genomic sequence #	C 449	16	2.2	2538	22	AAI58106	Human polynucleoti
C 377	16	2.2	1330	22	AAH64762	Human secreted pro	C 450	16	2.2	2562	22	AAH16160	Human cDNA sequenc
C 378	16	2.2	1347	22	AAKS1783	Human polynucleoti	C 451	16	2.2	2586	20	AAH52255	Protein PRO295 CDN
C 379	16	2.2	1353	22	AAF1965	Corynebacterium gl	C 452	16	2.2	2586	22	AAF92061	Human PRO295 CDNA
C 380	16	2.2	1354	22	ABA09093	Human preproenkeph	C 453	16	2.2	2586	22	AAF72413	Human PRO295 CDNA
C 381	16	2.2	1383	22	AAI06178	Human reproductive	C 454	16	2.2	2586	24	ABL95585	Human angiogenesis
C 382	16	2.2	1383	23	ABL98743	Human testicular a	C 455	16	2.2	2586	24	ABL88096	Human PRO295 CDNA
C 383	16	2.2	1435	24	ABQ73781	Human colon specif	C 456	16	2.2	2589	22	AAI19616	Human cDNA polymera
C 384	16	2.2	1495	21	AAKS5201	Human secreted pro	C 457	16	2.2	2608	22	ABL92089	Human Tumour Endot
C 385	16	2.2	1511	24	ABK35819	cDNA sequence #210	C 458	16	2.2	2632	22	AAH45491	Human reduced expr
C 386	16	2.2	1537	21	AACT7967	Human secreted pro	C 459	16	2.2	2660	22	AAH45490	Human reduced expr
C 387	16	2.2	1567	21	AAF16305	Human prostate can	C 460	16	2.2	2694	23	ABV22598	Human prostate exp
C 388	16	2.2	1583	21	AAZ65262	Human secreted pro	C 461	16	2.2	2694	23	ABV28419	Human prostate exp
C 389	16	2.2	1659	20	AAAT39816	Gastric cancer ass	C 462	16	2.2	2715	22	AAI59452	Human polynucleoti
C 390	16	2.2	1734	18	AAAT1745	Paramyxovirus haem	C 463	16	2.2	2785	22	AAI05110	Human reproductive
C 391	16	2.2	1743	21	AAD286927	Netrin coding sequ	C 464	16	2.2	2785	22	AAK75530	Human immune/haema
C 392	16	2.2	1819	22	AAD07351	Human DNA encoding	C 465	16	2.2	2785	23	ABL98002	Human testicular a
C 393	16	2.2	1819	24	ABK84637	Human cDNA differe	C 466	16	2.2	2807	23	AAK84436	DNA encoding novel
C 394	16	2.2	1833	23	AAK67931	DNA encoding novel	C 467	16	2.2	2840	18	AAK67295	Type I diabetes-as
C 395	16	2.2	1852	22	AAK94173	Human full-length	C 468	16	2.2	2888	24	ABK35818	cDNA sequence #209
C 396	16	2.2	1855	24	ABK35190	Human cDNA encodin	C 469	16	2.2	2935	23	ABL13221	Drosophila melanog
C 397	16	2.2	1882	22	AAH18358	Human cDNA sequenc	C 470	16	2.2	2943	18	AAK88478	Human insulinoma-a
C 398	16	2.2	1897	24	AAD27276	Human transporter	C 471	16	2.2	2943	23	AAK84770	DNA encoding novel
C 399	16	2.2	1898	21	AAF22376	Human secreted pro	C 472	16	2.2	2985	22	ABA06555	Human cDNA SEQ ID
C 400	16	2.2	1906	24	ABL39786	Human NS cDNA sequ	C 473	16	2.2	2990	22	AAI61237	Human polynucleoti
C 401	16	2.2	1916	24	ABL92366	Human secreted pro	C 474	16	2.2	2990	22	AAI61238	Human polynucleoti
C 402	16	2.2	1923	23	AAK77428	DNA encoding novel	C 475	16	2.2	2994	18	AAK788479	Human insulinoma-a
C 403	16	2.2	1928	23	ABL26971	Drosophila melanog	C 476	16	2.2	3001	24	ABN80332	Human chemically m
C 404	16	2.2	1976	22	ABA46129	Human breast cell	C 477	16	2.2	3032	24	ABL88369	Pain regulated CDN
C 405	16	2.2	1976	22	ABA56675	Human foetal liver	C 478	16	2.2	3046	22	AAK89786	Human digestive sy
C 406	16	2.2	1976	22	ABA62820	Probe #476 for ge	C 479	16	2.2	3090	22	AAI59451	Human polynucleoti
C 407	16	2.2	1976	22	AAK30334	Human bone marrow	C 480	16	2.2	3102	24	ABK31759	DNA encoding novel
C 408	16	2.2	1976	22	AAI14938	Probe #481 for ge	C 481	16	2.2	3219	23	AAK77606	DNA encoding novel
C 409	16	2.2	1976	22	AAI04715	Probe #4706 used t	C 482	16	2.2	3253	22	AAH17470	Human cDNA sequenc
C 410	16	2.2	1976	24	ABS04921	Human genome-deriv	C 483	16	2.2	3279	14	AAO49397	TMF gene. Homo sa
C 411	16	2.2	1999	22	AAK69415	Human immune/haema	C 484	16	2.2	3282	24	ABK09761	Human ovarian tumo
C 412	16	2.2	2000	19	AAV49651	Human SRCR protein	C 485	16	2.2	3287	18	AAK95220	Macaque islet cell
C 413	16	2.2	2002	24	AAK62701	cDNA sequence #488	C 486	16	2.2	3310	18	AAK67296	Type I diabetes-as
C 414	16	2.2	2006	20	AAK20417	Human secreted pro	C 487	16	2.2	3358	20	AAK87773	Human mucin gene M
C 415	16	2.2	2013	24	ABL89702	Human polynucleoti	C 488	16	2.2	3389	23	AAK86290	DNA encoding novel
C 416	16	2.2	2025	22	AAK52767	Human polynucleoti	C 489	16	2.2	3510	23	AAK666874	DNA encoding novel
C 417	16	2.2	2064	21	AAK65424	Porcine BAC-PIGF2-	C 490	16	2.2	3563	22	AAH18525	Human cDNA sequenc
C 418	16	2.2	2064	21	AAK45648	Human cancer cell	C 491	16	2.2	3628	22	AAH17549	Human cDNA sequenc
C 419	16	2.2	2064	24	AAK45649	Human cancer cell	C 492	16	2.2	3634	22	AAK81730	Human protease and
C 420	16	2.2	2088	24	AAK33852	Human secreted pro	C 493	16	2.2	3698	19	AAK62170	HSV-2 strain SB5 C
C 421	16	2.2	2101	22	AAH24245	Human oxidoreducta	C 494	16	2.2	3711	22	AAH34925	Human colon cancer
C 422	16	2.2	2102	24	AAK52284	cDNA sequence #71	C 495	16	2.2	3825	8	AAK70261	Sequence of Newcas
C 423	16	2.2	2113	22	AAK91328	Human polynucleoti	C 496	16	2.2	3856	23	AAK887632	DNA encoding novel
C 424	16	2.2	2124	22	AAK81745	Human membrane ass	C 497	16	2.2	4039	19	AAV05886	Human Tbc-1 gene.
C 425	16	2.2	2142	20	AAK22230	Human secreted pro	C 498	16	2.2	4068	22	AAK86707	Human polynucleoti
C 426	16	2.2	2155	24	ABL90322	Human polynucleoti	C 499	16	2.2	4136	18	AAK95368	Human protein tyro
C 427	16	2.2	2236	23	ABL05697	Drosophila melanog	C 500	16	2.2	4144	22	AAH18648	Human cDNA sequenc
C 428	16	2.2	2238	23	AAK76384	DNA encoding novel	C 501	16	2.2	4203	22	AAI05112	Human reproductive
C 429	16	2.2	2293	6	AAK50491	Sequence of herpes	C 502	16	2.2	4203	22	AAI05113	Human reproductive
C 430	16	2.2	2297	10	AAK90526	Herpes simplex vir	C 503	16	2.2	4203	22	AAK75531	Human immune/haema
C 431	16	2.2	2301	24	ABA96102	Human membrane tra	C 504	16	2.2	4203	22	AAK75532	Human immune/haema
C 432	16	2.2	2323	23	AAK91161	DNA encoding novel	C 505	16	2.2	4203	23	ABL98004	Human testicular a
C 433	16	2.2	2339	24	AAK33824	Human secreted pro	C 506	16	2.2	4203	23	ABL98005	Human testicular a
C 434	16	2.2	2349	24	ABA90343	Human polynucleoti	C 507	16	2.2	4294	22	AAK86072	Human immune/haema
C 435	16	2.2	2351	23	ABL25332	Drosophila melanog	C 508	16	2.2	4465	20	AAK35142	LTC4 synthase gene
C 436	16	2.2	2370	23	AAK72793	DNA encoding novel	C 509	16	2.2	4465	21	AAK21010	Human low adenosin
C 437	16	2.2	2408	23	ABL27512	Drosophila melanog	C 510	16	2.2	4465	21	AAK34888	Human adenosine re
C 438	16	2.2	2446	22	AAK16281	Human ubiquitin ca	C 511	16	2.2	4465	24	ABL67233	Thyroid cancer rel
C 439	16	2.2	2452	22	AAK84753	Nucleotide sequenc	C 512	16	2.2	4465	24	AAK624654	Human leukotriene
C 440	16	2.2	2469	22	AAK51822	Human polynucleoti	C 513	16	2.2	4546	23	ABL09809	Drosophila melanog
C 441	16	2.2	2479	19	AAV07906	Human cysteine-ric	C 514	16	2.2	4698	13	AAQ32370	PIA genomic DNA.
C 442	16	2.2	2479	21	AAK75128	cDNA encoding a hu	C 515	16	2.2	4698	15	AAQ32375	Entire PIA genomic
C 443	16	2.2	2479	22	AAK69309	Human DRK-3 DNA.	C 516	16	2.2	4698	16	AAQ72475	P815A antigen prec
C 444	16	2.2	2490	19	AAK38798	Homo sapiens cereb	C 517	16	2.2	4698	17	AAI01176	MAGE genomic DNA.
C 445	16	2.2	2495	21	AAK77555	Human ORFX ORF3110	C 518	16	2.2	4698	20	AAK84111	PIA genomic sequen
C 446	16	2.2	2495	22	AAK94900	Human full-length	C 519	16	2.2	4740	21	AAK95896	Human KLK-L1 gene.
C 447	16	2.2	2522	23	ABL28102	Drosophila melanog	C 520	16	2.2	4844	23	ABL26970	Drosophila melanog

521	16	2.2	4856	23	AAS97633	DNA encoding novel
522	16	2.2	4888	24	ABQ88240	Human osteoblast d
523	16	2.2	4897	23	ABL05696	Drosophila melanog
524	16	2.2	5034	22	ABA07244	Human pancreatic c
525	16	2.2	5034	22	AAK89885	Human digestive sy
526	16	2.2	5036	22	ABA07245	Human pancreatic c
527	16	2.2	5036	22	AAK99886	Human digestive sy
528	16	2.2	5087	21	AAA39482	Human NNT-1 DNA
529	16	2.2	5087	24	AAK11648	Human novel neurot
530	16	2.2	5088	19	AAV47511	Human neurotrophic
531	16	2.2	5088	19	AAV22653	Human genomic DNA
532	16	2.2	5130	21	AAK21011	Human low adenosin
533	16	2.2	5130	21	AAK34889	Human adenosine re
534	16	2.2	5306	22	AAS30054	Human lung antigen
535	16	2.2	5333	22	AAK80368	Human immune/haema
536	16	2.2	5521	22	AAH17603	Human G-protein co
537	16	2.2	5538	22	AAH18660	Human cDNA sequenc
538	16	2.2	5581	18	AAK48737	Human leucocyte sp
539	16	2.2	5581	18	AAK45451	Human LST-1 (leuko
540	16	2.2	5631	20	AAK98274	Human tumour suppr
541	16	2.2	5652	23	ABL13220	Drosophila melanog
542	16	2.2	5788	22	ABAL15481	Human nervous syst
543	16	2.2	5788	22	ABAL15482	Human nervous syst
544	16	2.2	5802	19	AAV49652	Human SRCR protein
545	16	2.2	6095	22	AAS29815	Human cytoskeletal
546	16	2.2	6120	24	ABN60303	Human chemically m
547	16	2.2	6120	24	ABK28440	DNA transcription
548	16	2.2	6193	24	ABN95699	Gene #2197 used to
549	16	2.2	6249	23	AAS79371	DNA encoding novel
550	16	2.2	6459	22	AAK88336	S. spinosa DNA fra
551	16	2.2	6545	23	ABL14373	Drosophila melanog
552	16	2.2	6850	22	AAK81486	Human immune/haema
553	16	2.2	6850	22	AAK81489	Human immune/haema
554	16	2.2	7175	22	ABA07728	Human ovarian and
555	16	2.2	7175	22	AAK02954	Human reproductive
556	16	2.2	7213	22	AAK85121	Human immune/haema
557	16	2.2	7452	16	AAQ85594	Human glycoprotein
558	16	2.2	7452	21	AAZ61217	DNA encoding human
559	16	2.2	7452	22	AAK90646	Human secreted pro
560	16	2.2	7452	24	ABK48275	DNA encoding human
561	16	2.2	7702	21	AAK88739	Human protein tyro
562	16	2.2	7702	21	AAK91908	Human protein tyro
563	16	2.2	7702	21	AAK59133	LAR tyrosine phosph
564	16	2.2	7705	22	AAH98405	Human EST-derived
565	16	2.2	7705	22	AAS22684	Human cDNA encodin
566	16	2.2	7741	22	AAS22448	Human cDNA encodin
567	16	2.2	7945	23	ABV27897	Human prostate exp
568	16	2.2	9457	23	ABU18290	Drosophila melanog
569	16	2.2	9618	24	AAK25946	Human protease inh
570	16	2.2	9618	24	AAK26033	Human protease inh
571	16	2.2	10210	24	AAS18100	Human angiotensin
572	16	2.2	10211	19	AAV62152	HSV-2 strain SB5 C
573	16	2.2	10438	23	ABL14372	Drosophila melanog
574	16	2.2	10552	22	ABAL19272	Human nervous syst
575	16	2.2	10552	22	ABAL19272	Human nervous syst
576	16	2.2	10557	24	AAS18240	Reference sequence
577	16	2.2	11853	22	AAS32785	Human genomic DNA
578	16	2.2	13102	22	ABAL19342	Human nervous syst
579	16	2.2	13206	11	AAQ05243	Rat acyl peptide h
580	16	2.2	13634	23	ABLO2686	Drosophila melanog
581	16	2.2	14212	22	AAK79692	Human immune/haema
582	16	2.2	14212	22	AAK80024	Human immune/haema
583	16	2.2	14212	22	AAK85921	Human immune/haema
584	16	2.2	14637	22	AAS32620	Human genomic DNA
585	16	2.2	15186	21	AAZ44617	Newcastle disease
586	16	2.2	17679	22	AAI67271	Human FK506-bindin
587	16	2.2	17679	22	AAI67272	Human FK506-bindin
588	16	2.2	18544	22	AAK80364	Human immune/haema
589	16	2.2	20084	22	AAS21773	Human gene for col
590	16	2.2	20084	22	AAK83656	Nucleotide sequenc
591	16	2.2	20693	23	ABU16740	Drosophila melanog
592	16	2.2	21535	22	AAS29834	Human cytoskeletal
593	16	2.2	21535	22	AAS35081	DNA #31 encoding h
594	16	2.2	23580	22	AAS28556	DNA encoding novel
595	16	2.2	23580	22	AAK87248	Human immune/haema
596	16	2.2	24221	23	ABK09808	Drosophila melanog
597	16	2.2	24843	24	AAS17764	Human Genomic DNA
598	16	2.2	24843	24	AAS17764	Human Genomic DNA
599	16	2.2	26767	23	ABL08654	Drosophila melanog
600	16	2.2	26960	23	ABL08712	Drosophila melanog
601	16	2.2	29222	24	ABL39412	Human electron-tra
602	16	2.2	29973	22	AAS29814	Human cytoskeletal
603	16	2.2	31168	22	ABA07295	Human pancreatic c
604	16	2.2	31168	22	AAS42115	Genomic sequence #
605	16	2.2	31168	22	AAS27804	DNA encoding novel
606	16	2.2	31168	22	AAK64760	Human immune/haema
607	16	2.2	31168	22	AAK89940	Human digestive sy
608	16	2.2	31348	22	AAS35759	Human cardiovascular
609	16	2.2	31348	22	AAK79227	Human immune/haema
610	16	2.2	32192	22	ABAL15328	Human nervous syst
611	16	2.2	32192	22	AAK05357	Human reproductive
612	16	2.2	32192	22	AAK05352	Human reproductive
613	16	2.2	32192	22	AAK05631	Human testicular a
614	16	2.2	32192	23	ABL98141	Genomic sequence #
615	16	2.2	32192	23	ABK42529	Human cardiovascular
616	16	2.2	32195	22	AAS36105	Human DNA for a no
617	16	2.2	32195	22	AAS31532	Human DNA for a no
618	16	2.2	32195	22	AAS31538	Genomic DNA encodi
619	16	2.2	32195	23	ABK44045	Human polynucleoti
620	16	2.2	32195	24	ABO66856	Human polynucleoti
621	16	2.2	32195	24	ABO66862	Human polynucleoti
622	16	2.2	32249	22	ABAL17555	Human nervous syst
623	16	2.2	33023	24	ABN96853	Gene #3351 used to
624	16	2.2	36140	22	AAA91326	Partial sequence o
625	16	2.2	43069	21	AAS236335	Genomic sequence o
626	16	2.2	50000	22	AAK88313	S. spinosa DNA fra
627	16	2.2	50000	22	AAK88316	S. spinosa DNA fra
628	16	2.2	51751	22	AAA91327	Genomic sequence o
629	16	2.2	65140	22	ABD17184	Streptomyces nous
630	16	2.2	65608	24	ABL62910	Breast cancer rela
631	16	2.2	65608	24	ABL64414	Stomach cancer rel
632	16	2.2	65608	24	ABL67668	Oesophagus cancer
633	16	2.2	66685	22	AAS07380	Human genomic DNA
634	16	2.2	80161	20	AAZ21501	DNA fragment of Sa
635	16	2.2	81800	24	ABK84756	Human cDNA differe
636	16	2.2	86080	24	ABQ88164	Human osteoblast d
637	16	2.2	86080	24	ABK83561	Human cDNA differe
638	16	2.2	110096	24	ABN95044	Gene #1542 used to
639	16	2.2	117213	19	AAV62176	HSV-2 strain SB5 C
640	16	2.2	125401	22	ABD17186	Streptomyces nous
641	16	2.2	143899	24	ABK38336	Genomic sequence e
642	16	2.2	148834	24	AAK83570	Human cDNA differe
643	16	2.2	154746	24	AAD25519	Human herpesvirus
644	16	2.2	155074	24	ABN85735	Human genomic regi
645	16	2.2	220895	24	ABK84798	Human cDNA differe
646	16	2.2	249487	24	ABN85733	Mouse genomic regi
647	16	2.2	349980	22	AAH41224	Pyrococcus abyssi
648	16	2.2	349980	22	AAH68526	C glutamicum codin
649	16	2.2	349980	22	AAH68527	C glutamicum codin
650	16	2.2	349980	22	AAH68529	C glutamicum codin
651	16	2.2	513445	22	AAI61373	Soybean 318013 reg
652	16	2.2	4403765	22	AAI99683	Mycobacterium tube
653	16	2.2	4403765	22	AAI99683	Mycobacterium tube
654	16	2.2	4411529	22	AAI99682	Mycobacterium tube
655	16	2.2	4411529	22	AAI99682	Primer P53-5XAMP f
656	15	2.1	24	17	AAT08649	Primer for exon 4
657	15	2.1	24	18	AAT99830	Primer for exon 4
658	15	2.1	24	18	AAT99860	MBV-specific PCR p
659	15	2.1	24	22	AAD18707	Mammalian ZAP-70 P
660	15	2.1	25	20	AAV73863	Human MUC1 derivat
661	15	2.1	27	22	AAS00594	Human MUC1 derivat
662	15	2.1	30	20	AAK32237	Primer for amplifi
663	15	2.1	30	20	AAK18653	Human p53 gene PCR
664	15	2.1	33	20	AAZ29926	PCR primer CBPI us
665	15	2.1	34	15	AAQ77966	Primer for amplifi
666	15	2.1	51	22	AAK31757	Human SNP oligonuc

c 667	15	2.1	60	24	ABN37991	Human spliced tran	c 740	15	2.1	285	21	AA00387	Human Mucin 1 (MUC
c 668	15	2.1	60	24	ABN49231	Human spliced tran	c 741	15	2.1	285	24	ABN76494	Human ORF1441 cDNA
c 669	15	2.1	90	20	AAH87016	Human single nucle	c 742	15	2.1	284	21	ABN01582	Human prostate exp
c 670	15	2.1	92	23	ABL51695	Human GFRA1pha4 ex	c 743	15	2.1	285	23	ABV60596	Human ovarian can
c 671	15	2.1	96	22	ABA35288	Probe #13754 for g	c 744	15	2.1	299	20	ABL80579	Human gene express
c 672	15	2.1	96	22	AAK42422	Human bone marrow	c 745	15	2.1	300	20	AA214894	Human gene express
c 673	15	2.1	112	18	AAV77186	Staphylococcus aur	c 746	15	2.1	300	20	AA213648	Human secreted pro
c 674	15	2.1	116	21	AAK31372	Human secreted pro	c 747	15	2.1	300	21	AA09756	Human colon cancer
c 675	15	2.1	133	22	AAH36493	Human colon cancer	c 748	15	2.1	300	21	AAA00497	Human colon cancer
c 676	15	2.1	139	24	ABL69210	Prostate cancer re	c 749	15	2.1	300	21	AAA00975	Human bone marrow
c 677	15	2.1	139	24	ABL69863	Prostate cancer re	c 750	15	2.1	303	22	AAK40168	Human bone marrow
c 678	15	2.1	147	24	ABK30456	Human G-protein-co	c 751	15	2.1	303	22	AAI46185	Probe #14871 used
c 679	15	2.1	156	22	ABA69904	Human foetal liver	c 752	15	2.1	306	24	ABO91342	M. capsulatus gene
c 680	15	2.1	156	22	ABA36757	Probe #15223 for g	c 753	15	2.1	311	21	AA251940	Human sperm anti
c 681	15	2.1	156	22	AAK18105	Human brain expres	c 754	15	2.1	311	21	AA251940	Human ovarian can
c 682	15	2.1	156	22	AAK33994	Human bone marrow	c 755	15	2.1	315	21	AAC00964	Human secreted pro
c 683	15	2.1	156	22	AAI24679	Human bone marrow	c 756	15	2.1	315	24	ABN75463	Human ORF410 cDNA,
c 684	15	2.1	156	22	AAI50004	Probe #14612 for g	c 757	15	2.1	316	22	AAK86654	Human immune/haema
c 685	15	2.1	156	24	ABN18227	Human genome-deriv	c 758	15	2.1	317	22	AAK74571	Human immune/haema
c 686	15	2.1	160	16	ABT24242	Human gene signatu	c 759	15	2.1	321	24	AAI46139	Human ALADIN gene
c 687	15	2.1	167	22	ABA41172	Probe #19638 for g	c 760	15	2.1	321	24	AAK62566	CDNA sequence #353
c 688	15	2.1	167	22	AAK25300	Human brain expres	c 761	15	2.1	325	22	AAK58397	Human immune/haema
c 689	15	2.1	167	22	AAK51307	Human bone marrow	c 762	15	2.1	325	24	AAI46140	Human ALADIN gene
c 690	15	2.1	167	22	AAI28318	Probe #18251 for g	c 763	15	2.1	327	24	AAK59128	Human immune/haema
c 691	15	2.1	167	22	ABN24850	Human genome-deriv	c 764	15	2.1	327	24	ABL80486	Human ovarian can
c 692	15	2.1	183	21	AAK10175	Human secreted pro	c 765	15	2.1	331	22	AAK72671	Human immune/haema
c 693	15	2.1	184	21	AAK14003	Human secreted pro	c 766	15	2.1	331	22	AAK72672	Human immune/haema
c 694	15	2.1	203	22	AAK57755	Human immune/haema	c 767	15	2.1	331	22	AAK72672	Human immune/haema
c 695	15	2.1	207	24	ABN22940	Human ORFX polynuc	c 768	15	2.1	331	24	ABK11573	Rat obesity relate
c 696	15	2.1	209	20	AAK40902	Human secreted pro	c 769	15	2.1	332	24	ABO57656	Human colon cancer
c 697	15	2.1	211	21	AAK13886	Human secreted pro	c 770	15	2.1	333	21	AAK02284	Human secreted pro
c 698	15	2.1	213	21	AAK10404	Human secreted pro	c 771	15	2.1	333	23	AAK84796	DNA encoding novel
c 699	15	2.1	216	24	ABK38903	CDNA encoding lung	c 772	15	2.1	334	22	AAH23043	Stem cell growth f
c 700	15	2.1	216	24	ABK39172	CDNA encoding lung	c 773	15	2.1	338	24	ABN78870	Human ORF3817 cDNA
c 701	15	2.1	219	24	ABK80415	Bacillus clausii g	c 774	15	2.1	338	24	ABN24031	Human ORFX polynuc
c 702	15	2.1	223	22	AAK56926	Human breast cance	c 775	15	2.1	339	22	AAH24345	Human breast cance
c 703	15	2.1	225	22	AAI12822	Human ovarian can	c 776	15	2.1	340	22	AAH83877	Human ovarian tumo
c 704	15	2.1	226	22	AAK52530	Human ovarian PCR-	c 777	15	2.1	340	24	ABL50494	Human nPCR-Seq107
c 705	15	2.1	227	22	AAK525413	Human ovarian PCR-	c 778	15	2.1	340	24	ABL50494	Human cancer relat
c 706	15	2.1	227	22	AAA57515	Trabecular meshwor	c 779	15	2.1	341	22	ABN61007	Human reproductive
c 707	15	2.1	229	22	ABN75649	Human foetal liver	c 780	15	2.1	341	23	ABL97193	Human testicular a
c 708	15	2.1	229	22	AAK24257	Human brain expres	c 781	15	2.1	342	20	AAH87233	Human single nucle
c 709	15	2.1	229	22	AAI56251	Probe #24937 used	c 782	15	2.1	342	22	AAK06443	Mouse microglia an
c 710	15	2.1	231	14	AAK09059	Human brain expres	c 783	15	2.1	343	21	ABO62971	Mycobacterium tube
c 711	15	2.1	231	24	ABN25707	Human ORFX polynuc	c 784	15	2.1	343	22	AAI14150	Human breast cance
c 712	15	2.1	234	24	ABN18013	Human ORFX polynuc	c 785	15	2.1	343	22	AAI14150	Human breast cance
c 713	15	2.1	247	22	AAH36651	Human colon cancer	c 786	15	2.1	344	24	ABL70735	Novel human polynu
c 714	15	2.1	251	19	AAK11282	Human biallelic po	c 787	15	2.1	349	22	AAK64995	Novel human polynu
c 715	15	2.1	251	19	AAK11281	Human biallelic po	c 788	15	2.1	351	22	AAK60364	Human immune/haema
c 716	15	2.1	255	22	AAH82197	Rat differential t	c 789	15	2.1	355	20	AAV87068	EST clone BH316
c 717	15	2.1	260	22	ABN49402	Human breast cell	c 790	15	2.1	356	22	AAK06577	Mouse microglia an
c 718	15	2.1	260	22	ABN67312	Human foetal liver	c 791	15	2.1	359	22	AAI80858	Human polynucleoti
c 719	15	2.1	260	22	ABA34404	Probe #12870 for g	c 792	15	2.1	361	22	AAH02307	Human lipoprotein
c 720	15	2.1	260	22	AAK15748	Human brain expres	c 793	15	2.1	362	22	AAK75795	Human immune/haema
c 721	15	2.1	260	22	AAK14186	Human bone marrow	c 794	15	2.1	363	21	AAC02356	Human secreted pro
c 722	15	2.1	260	22	AAI22233	Probe #12166 for g	c 795	15	2.1	363	22	AAK64313	Novel human polynu
c 723	15	2.1	260	22	AAI47528	Probe #16214 used	c 796	15	2.1	365	20	AAK20819	Polynucleotide seq
c 724	15	2.1	260	22	AAI07932	Probe #7923 used t	c 797	15	2.1	366	22	AAI85545	Human polynucleoti
c 725	15	2.1	260	24	ABN15491	Human genome-deriv	c 798	15	2.1	366	22	AAH23042	Stem cell growth f
c 726	15	2.1	261	22	AAK64088	Human immune/haema	c 799	15	2.1	367	22	AAI23012	Human breast cance
c 727	15	2.1	261	22	ABL53208	Nucleotide sequenc	c 800	15	2.1	371	21	AAK31351	Human secreted pro
c 728	15	2.1	269	21	AAK28262	Human secreted pro	c 801	15	2.1	371	22	ABN51966	Human foetal liver
c 729	15	2.1	270	22	AAK28024	Novel cDNA encodin	c 802	15	2.1	371	22	ABA21784	Probe #250 for gen
c 730	15	2.1	270	22	AAH33015	Human colon cancer	c 803	15	2.1	371	22	AAK00252	Human brain expres
c 731	15	2.1	273	22	AAK28484	Genomic sequence #	c 804	15	2.1	371	22	AAK25693	Human bone marrow
c 732	15	2.1	273	22	AAK28485	Genomic sequence #	c 805	15	2.1	371	22	AAI10321	Probe #254 for gen
c 733	15	2.1	277	24	ABN19823	Human ORFX polynuc	c 806	15	2.1	371	22	AAI31574	Probe #248 used to
c 734	15	2.1	278	22	AAH97915	Murine 7-transemb	c 807	15	2.1	371	22	AAI00257	Probe #248 used to
c 735	15	2.1	279	24	ABN77037	Human ORF1984 cDNA	c 808	15	2.1	371	24	ABS00272	Human genome-deriv
c 736	15	2.1	283	21	AAK57514	Trabecular meshwor	c 809	15	2.1	379	22	ABA44248	Human foetal liver
c 737	15	2.1	284	20	AAH89382	EST clone CL399	c 810	15	2.1	379	22	ABA54696	Human foetal liver
c 738	15	2.1	284	22	AAK75717	Human immune/haema	c 811	15	2.1	379	22	ABA24477	Probe #2943 for ge
c 739	15	2.1	284	24	ABN23278	Human ORFX polynuc	c 812	15	2.1	379	22	AAK02982	Human brain expres

813	15	2.1	379	22	AAK28428	Human bone marrow	c 886	15	2.1	442	22	AAI04656	Probe #4647 used t
814	15	2.1	379	22	AAI12995	Probe #2928 for ge	c 887	15	2.1	442	24	ABL04852	Human genome-deriv
815	15	2.1	379	22	AAI13452	Probe #3038 used t	c 888	15	2.1	442	24	ABL04852	Colon adenocarcino
816	15	2.1	379	22	AAI02913	Probe #2904 used t	c 889	15	2.1	443	24	AAI15353	Human breast cance
817	15	2.1	379	24	ABS02936	Human genome-deriv	c 890	15	2.1	443	24	ABN96087	Gene #2585 used to
818	15	2.1	381	21	AAH30934	Human colon cancer	c 891	15	2.1	445	24	ABK64586	Human benign prost
819	15	2.1	381	22	AAI87309	Human polynucleoti	c 892	15	2.1	447	15	AAQ62530	Allinase clone pAI
820	15	2.1	382	22	AAF65213	Novel human polynu	c 893	15	2.1	447	22	ABA52420	Human foetal liver
821	15	2.1	385	21	AAK57701	Arachidonic acid m	c 894	15	2.1	447	22	ABA22215	Probe #681 for gen
822	15	2.1	385	22	AAK57020	Human immune/haema	c 895	15	2.1	447	22	AAK00689	Human brain expres
823	15	2.1	385	24	ABN25901	Human ORFX polynuc	c 896	15	2.1	447	22	AAK26140	Human bone marrow
824	15	2.1	385	24	ABN26541	Human ORFX polynuc	c 897	15	2.1	447	22	AAI10770	Probe #703 for gen
825	15	2.1	388	22	AAI82264	Human polynucleoti	c 898	15	2.1	447	22	AAI32028	Probe #714 used to
826	15	2.1	393	22	AAI91201	Human polynucleoti	c 899	15	2.1	447	22	AAI00696	Probe #687 used to
827	15	2.1	395	22	AAK79670	Human immune/haema	c 900	15	2.1	447	24	ABS00725	Human genome-deriv
828	15	2.1	395	22	AAK931764	Human immune/haema	c 901	15	2.1	449	22	ABA59098	Human foetal liver
829	15	2.1	395	22	AAK95310	Human immune/haema	c 902	15	2.1	449	22	AAK07276	Human brain expres
830	15	2.1	396	22	AAI91264	Human polynucleoti	c 903	15	2.1	449	22	AAK33035	Human bone marrow
831	15	2.1	397	22	ABA09379	Human p53 homologu	c 904	15	2.1	449	22	AAI38838	Probe #7524 used t
832	15	2.1	397	22	AAK293367	CDNA encoding nove	c 905	15	2.1	449	24	ABS07849	Human genome-deriv
833	15	2.1	397	24	ABN17460	Human ORFX polynuc	c 906	15	2.1	449	24	ABQ60783	Human defensin 5 D
834	15	2.1	400	22	AAK23267	DNA encoding novel	c 907	15	2.1	450	22	AAK65088	Human immune/haema
835	15	2.1	400	23	AAK64408	DNA encoding novel	c 908	15	2.1	450	22	AAK65089	Human immune/haema
836	15	2.1	400	23	AAK76908	DNA encoding novel	c 909	15	2.1	450	23	AAK69759	DNA encoding novel
837	15	2.1	400	23	AAK91226	DNA encoding novel	c 910	15	2.1	450	23	AAK76455	DNA encoding novel
838	15	2.1	400	23	AAK92406	DNA encoding novel	c 911	15	2.1	450	23	AAK83763	DNA encoding novel
839	15	2.1	401	22	AAK96118	Human neuregulin g	c 912	15	2.1	451	22	AAI81766	Human polynucleoti
840	15	2.1	401	22	AAK97611	Human neuregulin g	c 913	15	2.1	451	24	ABK15916	Human lung tumour
841	15	2.1	401	22	AAK67113	Novel human polynu	c 914	15	2.1	452	16	AAK20964	Human gene signatu
842	15	2.1	402	22	AAK66385	C glutamicum codin	c 915	15	2.1	453	21	ABQ63054	Mycobacterium tube
843	15	2.1	402	22	AAK66246	Novel human polynu	c 916	15	2.1	453	21	AAZ42758	Human 5' EST isola
844	15	2.1	402	23	ABV05128	Human prostate exp	c 917	15	2.1	453	22	AAZ42758	Human musculoskele
845	15	2.1	405	21	AAI88744	Human polynucleoti	c 918	15	2.1	453	23	AAI35025	Drosophila melanog
846	15	2.1	407	21	AAK17911	Human secreted pro	c 919	15	2.1	455	22	ABK24873	Human foetal liver
847	15	2.1	409	22	AAI89479	Human polynucleoti	c 920	15	2.1	455	22	ABA57465	Probe #5426 for ge
848	15	2.1	409	24	ABL78169	Human ovarian canc	c 921	15	2.1	455	22	ABA26960	Human brain expres
849	15	2.1	410	22	AAK75147	Human immune/haema	c 922	15	2.1	455	22	AAK05504	Human bone marrow
850	15	2.1	410	22	ABL02338	Human ovarian canc	c 923	15	2.1	455	22	AAK31105	Probe #5481 for ge
851	15	2.1	411	22	AAK09623	Human breast cance	c 924	15	2.1	455	22	AAI15548	Probe #1721 used t
852	15	2.1	411	24	ABQ60009	Human colon cancer	c 925	15	2.1	455	22	AAI33035	Probe #5700 used t
853	15	2.1	412	22	AAK15501	Human breast cance	c 926	15	2.1	455	22	AAI37014	Human genome-deriv
854	15	2.1	412	24	ABK39009	CDNA encoding lung	c 927	15	2.1	455	24	ABS05856	Human foetal liver
855	15	2.1	416	22	AAH35488	Human colon cancer	c 928	15	2.1	458	22	ABA52086	Human foetal liver
856	15	2.1	419	20	AAK51878	Human secreted pro	c 929	15	2.1	458	22	ABA21898	Probe #364 for gen
857	15	2.1	424	14	AAQ53216	Sequence encoding	c 930	15	2.1	458	22	AAK00368	Human brain expres
858	15	2.1	426	22	AAK537960	Novel CDNA encoding	c 931	15	2.1	458	22	AAK25811	Human bone marrow
859	15	2.1	426	24	ABK62372	Rat sequence diffe	c 932	15	2.1	458	22	AAI10440	Probe #373 for gen
860	15	2.1	427	22	ABA57273	Human foetal liver	c 933	15	2.1	458	22	AAI31693	Probe #379 used to
861	15	2.1	427	22	ABA26836	Probe #5302 for ge	c 934	15	2.1	458	22	AAI00376	Probe #367 used to
862	15	2.1	427	22	AAK05300	Human brain expres	c 935	15	2.1	458	22	ABS00392	Human genome-deriv
863	15	2.1	427	22	AAK30892	Human bone marrow	c 936	15	2.1	461	20	AAK39539	Human secreted pro
864	15	2.1	427	22	AAI15450	Probe #5383 for ge	c 937	15	2.1	461	24	ABN60707	Human cancer relat
865	15	2.1	427	22	AAI36805	Probe #4911 used t	c 938	15	2.1	463	22	AAH72149	Human cervical can
866	15	2.1	427	24	ABS05640	Human genome-deriv	c 939	15	2.1	463	24	ABS08205	Human genome-deriv
867	15	2.1	430	21	AAK48145	Zea mays DNA fragm	c 940	15	2.1	466	21	AAK01377	Human secreted pro
868	15	2.1	432	22	AAH23056	Stem cell growth f	c 941	15	2.1	467	24	ABN73004	CDNA sequence 1043
869	15	2.1	431	24	ABN21098	Human ORFX polynuc	c 942	15	2.1	468	21	AAK79292	Pinus radiata cell
870	15	2.1	432	22	AAI56352	Probe #25038 used	c 943	15	2.1	468	24	ABN73035	CDNA sequence PB r
871	15	2.1	433	22	AAK24618	Human ovarian PCR-	c 944	15	2.1	470	20	AAK40578	Human secreted pro
872	15	2.1	433	22	AAH83241	Human ovarian tumo	c 945	15	2.1	470	22	ABA58932	Human foetal liver
873	15	2.1	437	22	AAK59365	Human immune/haema	c 946	15	2.1	470	22	ABA59267	Human foetal liver
874	15	2.1	439	22	AAH11434	Human CDNA clone (c 947	15	2.1	470	22	ABA27798	Probe #6264 for ge
875	15	2.1	439	23	AAK58724	CDNA #1400 encodin	c 948	15	2.1	470	22	ABA28002	Probe #6468 for ge
876	15	2.1	440	24	ABL89689	Human polynucleoti	c 949	15	2.1	470	22	AAK07095	Human brain expres
877	15	2.1	441	21	AAK69703	Human ovarian carc	c 950	15	2.1	470	22	AAK07479	Human brain expres
878	15	2.1	441	22	AAK64882	Human immune/haema	c 951	15	2.1	470	22	AAK32835	Human bone marrow
879	15	2.1	441	24	ABN72597	Ovarian carcinoma	c 952	15	2.1	470	22	AAK33264	Human bone marrow
880	15	2.1	442	22	ABA46064	Human breast cell	c 953	15	2.1	470	22	AAI16226	Probe #6159 for ge
881	15	2.1	442	22	ABA56602	Human foetal liver	c 954	15	2.1	470	22	AAI16389	Probe #6322 for ge
882	15	2.1	442	22	ABA26215	Probe #4681 for ge	c 955	15	2.1	470	22	AAI38650	Probe #7336 used t
883	15	2.1	442	22	AAK30274	Human bone marrow	c 956	15	2.1	470	22	AAI39058	Probe #7744 used t
884	15	2.1	442	22	AAI14868	Probe #4801 for ge	c 957	15	2.1	470	24	ABS07639	Human genome-deriv
885	15	2.1	442	22	AAI36225	Probe #4911 used t	c 958	15	2.1	470	24	ABS08096	Human genome-deriv

959 15 2.1 470 24 ABN73003
960 15 2.1 475 21 AAX79633
961 15 2.1 476 24 ABA96249
962 15 2.1 477 22 ABA52332
963 15 2.1 477 22 ABA22127
964 15 2.1 477 22 AAK00604
965 15 2.1 477 22 AAK26054
966 15 2.1 477 22 AAI10682
967 15 2.1 477 22 AAI13198
968 15 2.1 477 22 ABS00637
969 15 2.1 477 22 ABA52184
970 15 2.1 478 22 ABA21990
971 15 2.1 478 22 AAK00460
972 15 2.1 478 22 AAK25907
973 15 2.1 478 22 AAI10537
974 15 2.1 478 22 AAI131790
975 15 2.1 478 22 AAI00470
976 15 2.1 478 24 ABS00490
977 15 2.1 480 23 ABV12653
978 15 2.1 481 20 AAX1874
979 15 2.1 482 22 AAD10355
980 15 2.1 484 22 AAS29085
981 15 2.1 484 22 AAS29956
982 15 2.1 484 22 AAS29958
983 15 2.1 484 22 AAI99995
984 15 2.1 485 24 ABN73022
985 15 2.1 487 22 ABA44799
986 15 2.1 487 22 ABA52554
987 15 2.1 487 22 ABA24999
988 15 2.1 487 22 AAK03509
989 15 2.1 487 22 AAI13550
990 15 2.1 487 22 AAI34913
991 15 2.1 487 22 AAI03439
992 15 2.1 487 24 ABS03498
993 15 2.1 489 24 ABA54931
994 15 2.1 491 24 ABA94901
995 15 2.1 493 20 AAV88064
996 15 2.1 494 22 AAH71087
997 15 2.1 496 24 ABL80151
998 15 2.1 498 22 AAH35626
999 15 2.1 498 22 AAF90635
1000 15 2.1 498 22 AAF90668

ALIGNMENTS

RESULT 1
ID AAA64508 standard; cDNA; 5492 BP.
XX
AC AAA64508;
XX
DT 02-JAN-2001 (first entry)
XX
DE .cDNA sequence of the wild type human FEZ1 gene.
XX
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
KW tumour proliferation; tubulin; microtubule; protein BFI-gamma;
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
KW tumorigenesis; tumour survival; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200050565-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US04950.
XX
PR 25-FEB-1999; 99US-0121537.
XX

PA (UVJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Ishii H;
XX WPI; 2000-558396/51.
DR
XX
PT New polynucleotide homologous with a portion of one strand of the human
FEZ1 gene, useful for alleviating abnormal cell proliferation such as
cancer -
XX
XX Example 2; Fig 5B; 255pp; English.
XX
XX The present sequence represents the cDNA sequence of the human FEZ1 gene.
FEZ1 is a tumour suppressor gene, located at chromosome location 8p22.
Decreased or no expression of FEZ1 is detected in a variety of cancer
cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
also interacts with tubulin, with microtubules, and with protein
BFI-gamma. Post-translational phosphorylation and dephosphorylation
modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
expression are useful for inducing cells to proliferate. Compounds
which modulate FEZ1 association with tubulin are useful for alleviating
tubulin hyper- or hypo- polymerisation disorders, such as those
associated with aberrant initiation of mitosis, modulation of the
initiation and rate of cell proliferation and cell growth, modulation of
cell shape, cell rigidity, cell motility, rate and stage of cellular
DNA replication, intracellular distribution of organelles, metastatic
potential of cell and cellular transformation from a non-cancerous to
cancerous phenotype. Compounds which modulate FEZ1 binding and
phosphorylation are also useful for alleviating a disorder, such as
tumorigenesis, tumour survival, growth and metastasis.
XX
SQ Sequence 5492 BP; 1137 A; 1704 C; 1565 G; 1086 T; 0 other;
Query Match 100.0%; Score 715; DB 21; Length 5492;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTGCCCCCAGGACAGAGAGAGGCTGGCTCCCTCCCGAGGTGGAGACCCCCCC 60
Db 4215 ACTGCCCCCAGGACAGAGAGAGGCTGGCTCCCTCCCGAGGTGGAGACCCCCCC 4274
Qy 61 CAATCCAGGAAAGAGCAGTCCAGTGTCTGCCTCAGACGTTGGCTGAGAAGAA 120
Db 4275 CAATCCAGGAAAGAGCAGTCCAGTGTCTGCCTCAGACGTTGGCTGAGAAGAA 4334
Qy 121 GTGCTGCCACACCCAGGGGAAGCCCTGAGGGGAGGCTGTGCTCCGCATGTGTCTCC 180
Db 4335 GTGCTGCCACACCCAGGGGAAGCCCTGAGGGGAGGCTGTGCTCCGCATGTGTCTCC 4394
Qy 181 GGTACCTTCCATACACAGAGAGTGCAGCCTTCTCCATATCTCCATGCGCTGTCCAGG 240
Db 4395 GGTACCTTCCATACACAGAGAGTGCAGCCTTCTCCATATCTCCATGCGCTGTCCAGG 4454
Qy 241 CCGGCCCCAGATGTGTCCCCCCCCCAGGCTTGTCTACGTCCAAAGGTGGCAGATGCTTCCC 300
Db 4455 CCGGCCCCAGATGTGTCCCCCCCCCAGGCTTGTCTACGTCCAAAGGTGGCAGATGCTTCCC 4514
Qy 301 TGGGCTGCCACAGCCCGCCCGCCAGAGTGCCACCGTGGCAGTGAATCAAGTATCC 360
Db 4515 TGGGCTGCCACAGCCCGCCCGCCAGAGTGCCACCGTGGCAGTGAATCAAGTATCC 4574
Qy 361 TGGGACCTTGCACCTCACCTTCTGCTGGGTGTCTTCTCTGCGCTGTCCAAAAGCGGCC 420
Db 4575 TGGGACCTTGCACCTCACCTTCTGCTGGGTGTCTTCTCTGCGCTGTCCAAAAGCGGCC 4634
Qy 421 TCACTATTCTTGGACCATGCCAGATTCTGCCTCTCTCGAAAGAGGCTCTGGACAGAGAA 480
Db 4635 TCACTATTCTTGGACCATGCCAGATTCTGCCTCTCTCGAAAGAGGCTCTGGACAGAGAA 4694
Qy 481 GCCTCCAGACAGAGCCTGGCCCCCAGGCCCCCAGAGGGTGGGCTTCTGCGCTTCCCT 540
Db 4695 GCCTCCAGACAGAGCCTGGCCCCCAGGCCCCCAGAGGGTGGGCTTCTGCGCTTCCCT 4754

PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR P-PSDB; AAO01956.
XX
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 1; SEQ ID NO 1947; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910), that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1855 BP; 423 A; 480 C; 588 G; 364 T; 0 other;

Query Match 68.0%; Score 486; DB 22; Length 1855;
Best Local Similarity 100.0%; Pred. No. 3.7e-23; Indels 0; Gaps 0;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 CCGTGTCCAGCGCGCCAGAGTGTGTCCCGCCAGCGCTTGTCTTACCTCAAGGTGCA 289
DB 1025 CCGTGTCCAGCGCGCCAGAGTGTGTCCCGCCAGCGCTTGTCTTACCTCAAGGTGCA 966
QY 290 GATGTCTTCCCTGGGCTGCCACAGCCCGCCCGCCAGAGTGTGTCTTACCTCAAGGTGCA 349
DB 965 GATGTCTTCCCTGGGCTGCCACAGCCCGCCCGCCAGAGTGTGTCTTACCTCAAGGTGCA 906
QY 350 TGCAAGTATCTCGGACCTTGCAACTTCTGTGGGTGTCTTCTTCTGCGCTCTC 409
DB 905 TGCAAGTATCTCGGACCTTGCAACTTCTGTGGGTGTCTTCTTCTGCGCTCTC 846
QY 410 CAAAAGCGCCCTCACTATTCTTGGACCATGCGAGATTTGCTCTCTGTGAAGAGGCTCT 469
DB 845 CAAAAGCGCCCTCACTATTCTTGGACCATGCGAGATTTGCTCTCTGTGAAGAGGCTCT 786
QY 470 GACACGACAGCTTCCAGACAGAGCTGTGCCCCAGCCCGCCAGAGGTGGGCTTCC 529
DB 785 GGACACGACAGCTTCCAGACAGAGCTGTGCCCCAGCCCGCCAGAGGTGGGCTTCC 726
QY 530 TGCCCTTCTCTTGGGCGCGCTGTGCGCCGACCCCACTGACCCACTTGGATGGACCAACC 589
DB 725 TGCCCTTCTCTTGGGCGCGCTGTGCGCCGACCCCACTGACCCACTTGGATGGACCAACC 666
QY 590 TGCTCTGTGCCCCAAGGACGCTTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 649
DB 665 TGCTCTGTGCCCCAAGGACGCTTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
QY 650 ATCGGACTTGCCCTTGGACCTGGGACGAGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 709
DB 605 ATCGGACTTGCCCTTGGACCTGGGACGAGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 712
QY 710 TCCAG 715
|||||

Db 545 TCCAG 540

RESULT 4

AAA64516
ID AAA64516 standard; DNA; 591 BP.

XX AC AAA64516;

XX DT 02-JAN-2001 (first entry)

XX DE F37 probe used to isolate a human FEZ1 gene.

XX KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
XX KW tumulin polymerisation disorder; mitosis initiation; protein EFL-gamma;
XX KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
XX KW tumorigenesis; tumour survival; metastasis; probe; ss.

XX OS Homo sapiens.

XX PN WO2000050565-A2.

XX PD 31-AUG-2000.

XX PF 25-FEB-2000; 2000WO-US04950.

XX PR 25-FEB-1999; 99US-0121537.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Croce CM, Ishii H;

XX DR WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
PT cancer -

XX Example 1; Fig 5Q; 255pp; English.

XX The present sequence represents a probe which is used for isolating a
CC human FEZ1 gene. The encoding mRNA is transcribed by tumour cells. FEZ1
CC is a tumour suppressor gene, located at chromosome location 8p22.
CC Decreased or no expression of FEZ1 is detected in a variety of cancer
CC cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
CC also interacts with tubulin, with microtubules, and with protein
CC EFL-gamma. Post-translational phosphorylation and dephosphorylation
CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
CC expression are useful for inducing cells to proliferate. Compounds
CC which modulate FEZ1 association with tubulin are useful for alleviating
CC tubulin hyper- or hypo- polymerisation disorders, such as those
CC associated with aberrant initiation of mitosis, modulation of the
CC initiation and rate of cell proliferation and cell growth, modulation of
CC cell shape, cell rigidity, cell motility, rate and stage of cellular
CC DNA replication, intracellular distribution of organelles, metastatic
CC potential of cell and cellular transformation from a non-cancerous to
CC cancerous phenotype. Compounds which modulate FEZ1 binding and
CC phosphorylation are also useful for alleviating a disorder, such as
CC tumorigenesis, tumour survival, growth and metastasis.

XX Sequence 591 BP; 111 A; 160 C; 163 G; 157 T; 0 other;

Query Match 8.8%; Score 63; DB 21; Length 591;

Best Local Similarity 100.0%; Pred. No. 3.3e-20;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 653 GGACTCTCCCTGGACCTGGACGACTGTGTACGGGGTTCCTCTAGCTCTCC 712

DB 1 GGACTCTCCCTGGACCTGGACGACTGTGTACGGGGTTCCTCTAGCTCTCC 60

QY 713 CAG 715
|||||

Db 61 CAG 63

RESULT 5
AAT23583
ID AAT23583 standard; cDNA to mRNA; 393 BP.
XX AC AAT23583;
XX DT 02-SEP-1996 (first entry)
XX DE Human gene signature HUMGS05436.
XX KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX OS Homo sapiens.
XX PN W09514772-A1.
XX PD 01-JUN-1995.
XX PF 11-NOV-1994; 94WO-JP01916.
XX PR 12-NOV-1993; 93JP-0355504.
XX PA (MATS//) MATSUBARA K.
XX PA (OKUB//) OKUBO K.
XX PI Matsubara K, Okubo K;
XX DR WPI; 1995-206931/27.
XX PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX PS Claim 1; Page 1404; 2245pp; Japanese.
XX CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX SQ Sequence 393 BP; 73 A; 117 C; 121 G; 78 T; 4 other;

Query Match 6.9%; Score 49; DB 16; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 649 GATCGACTGTGCCCTGGACCTGGGAACGACTGTGACTGTACCGGGTT 697
|||||
DB 1 GATCGACTGTGCCCTGGACCTGGGAACGACTGTGACTGTACCGGGTT 49
|||||

RESULT 6
AAD00768
ID AAD00768 standard; cDNA; 9679 BP.
XX AC AAD00768;

XX DT 08-SEP-2000 (first entry)
XX DE Rat phosphodiesterase interacting protein, myomegalin cDNA.
XX KW Rat; phosphodiesterase interacting protein; myomegalin; PDE; CAMP-PDE;
KW cyclic adenosine monophosphate phosphodiesterase; antiasthmatic; asthma;
KW antiinflammatory; antipruritic; dermatological; antibacterial; shock;
KW analgesic; immunosuppressive; antitumor; vasotropic; antiarthritic;
KW antidiabetic; urticaria; antiallergic; antiarteriosclerotic; diagnosis;
KW antirheumatic; treatment; inflammatory disease; psoriasis; arthritis;
KW atherosclerosis; Crohn's disease; cystic fibrosis; chronic bronchitis;
KW eosinophilic granuloma; proliferative skin disease; ulcerative colitis;
KW reperfusion injury; atopic dermatitis; diabetes insipidus;
KW conjunctivitis; adult respiratory distress syndrome; allergic rhinitis;
KW arterial restenosis; ankylosing spondylitis; transplant rejection;
KW graft versus host disease; ss.
XX OS Rattus sp.
XX PN W0200027861-A1.
XX PD 18-MAY-2000.
XX PF 12-NOV-1999; 99WO-US26860.
XX PR 12-NOV-1998; 98US-0108255.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PI Conti M, Pahlke G;
XX DR WPI; 2000-376479/32.
XX DR P-PSDB; AAY71158.
XX PT Polynucleotide encoding a phosphodiesterase (PDE) interacting
PT polypeptide, useful for diagnosis and treatment of asthma, cystic
PT fibrosis, Crohn's disease, and rheumatoid arthritis -
XX PS Disclosure; Fig 2; 77pp; English.
XX CC The present sequence is a cDNA encoding a phosphodiesterase (PDE)
CC interacting protein, myomegalin from rat skeletal muscle cDNA library.
CC The protein modulates the functions and properties of PDEs, specifically
CC CAMP-PDEs, and also targets them to specific subcellular compartments.
CC Rat myomegalin has at least four differently sized transcripts, two of
CC which are expressed in heart (7.5 and 5.9 kb), two in skeletal muscle
CC (7.5 and 4.3 kb) and one in testis (2.5 kb). The present sequence
CC can be used in the diagnosis and treatment of disease conditions
CC associated with PDE activity. The diseases include asthma, cystic
CC fibrosis, inflammatory airway disease, chronic bronchitis, eosinophilic
CC granuloma, psoriasis, proliferative skin diseases, endotoxin shock,
CC septic shock, ulcerative colitis, Crohn's disease, reperfusion injury,
CC inflammatory arthritis, atopic dermatitis, urticaria, adult respiratory
CC distress syndrome, diabetes insipidus, allergic rhinitis, allergic
CC conjunctivitis, vernal conjunctivitis, arterial restenosis,
CC atherosclerosis, inflammatory diseases associated with irritation and
CC pain, rheumatoid arthritis, ankylosing spondylitis, transplant
CC rejection and graft versus host disease, disease conditions associated
CC with hypersecretion of gastric acid, and disease conditions in which
CC cytokines are mediators.
XX SQ Sequence 9679 BP; 2549 A; 2626 C; 2636 G; 1867 T; 1 other;

Query Match 2.8%; Score 20; DB 21; Length 9679;
Best Local Similarity 100.0%; Pred. No. 13;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 496 GCCTGGCCCCAGGCCCGAGA 515
Db 5267 GCCTGGCCCCAGGCCCGAGA 5286
RESULT 7
AAS41709
ID AAS41709 standard; DNA; 10437 BP.
XX
AC AAS41709;
XX
DT 17-DEC-2001 (first entry)
XX
DE Genomic sequence #25 encoding novel human enzyme polypeptide.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246533.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465566/50.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
XX preventing, treating neural, immune system, muscular, reproductive,
XX pulmonary, cardiovascular, renal, proliferative disorders and cancerous
XX diseases -
XX
XX Disclosure; SEQ ID No 1835; 1180pp; English.
XX
XX The present invention relates to the isolation of novel human enzyme
XX polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
XX encoding them. The enzyme polypeptides of the invention may comprise the
XX functional classes of oxidoreductases, transferases, hydrolases, lyases,
XX isomerases or ligases. The sequences of the invention are useful in the
XX diagnosis, treatment, prevention and/or prognosis of a wide range of
XX disorders including hyperproliferative disorders (e.g. cancer),
XX immunodeficiency disorders (e.g. AIDS) autoimmune disorders
XX (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
XX metabolic disorders (e.g. phenylketonuria), inflammatory disorders
XX (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
XX blood-related disorders (e.g. haemophilia), reproductive disorders
XX (e.g. infertility) and infectious disorders (e.g. Influenza). The
XX polynucleotides of the invention can also be used in gene therapy.
XX AA541685-AAS42192 represent DNA sequences encoding for the novel human
XX enzyme polypeptides of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences..
XX
XX Sequence 10437 BP; 2265 A; 3267 C; 2795 G; 2110 T; 0 other;
XX
XX Query Match 2.8%; Score 20; DB 22; Length 10437;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 223 CCATGGCCCTGTCCAGGCC 242
XX |||||||||
XX Db 2240 CCATGGCCCTGTCCAGGCC 2259
XX
XX RESULT 8
XX ABA16691/c
XX ID ABA16691 standard; DNA; 13620 BP.
XX
XX AC ABA16691;
XX
XX DT 23-JAN-2002 (first entry)
XX XX Human nervous system related polynucleotide SEQ ID NO 9022.
XX
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
XX antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
XX antirheumatic; hepatotropic; cerebrotective; antiinflammatory;
XX antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
XX OS Homo sapiens.
XX
XX WO200159063-A2.
XX
XX 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184684.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.

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PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244611.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 03-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
XX Disclosure; SEQ ID NO 9022; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 12620 BP; 2244 A; 3902 C; 3765 G; 2709 T; 0 other;

Query Match 2.8%; Score 20; DB 22; Length 12620;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 CCATGGCCCTGTCCAGGCC 242
Db 4030 CCATGGCCCTGTCCAGGCC 4011
|||||
|||||

RESULT 9
ABN79134
ID ABN79134 standard; cDNA; 531 BP.
XX
XX AC ABN79134;
XX
XX DT 08-JUL-2002 (first entry)
XX
XX DE Human ORF4081 cDNA, SEQ ID NO:8161.
XX
XX Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibitor; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotrophic; antipsoriatic; antidiabetic; cytostatic; nootropic;
```

KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiatic; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
XX Homo sapiens.
XX WO200190366-A2.
XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17076.
XX 24-MAY-2000; 2000US-206690P.
XX (CURA-) CURAGEN CORP.
XX Leach MD, Shimkets RA;
XX WPI; 2002-106200/14.
XX P-PSDB; ABP35108.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and disorders related to organ
XX transplantation -
XX Claim 1; Page 2286; 2508pp; English.

XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins
XX designated ORF (open reading frame) 1-4534, and sequences ABN75054-
XX ABN79587 represent cDNAs encoding them. The invention also encompasses
XX polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
XX referred to as ORFX) proteins, polynucleotides at least 85% identical to
XX the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
XX polynucleotides, the recombinant production of ORFX proteins, antibodies
XX specific for ORFX proteins, methods of detecting ORFX polynucleotides and
XX polypeptides, methods of screening for modulators of ORFX expression or
XX activity, and methods of screening individuals for a predisposition to an
XX ORFX-associated disorder. The ORFX proteins of the invention have a wide
XX range of biological activities, such as cytokine, cell proliferation,
XX cell differentiation, immune modulation, haematopoiesis regulation,
XX tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
XX chemokinetic activity, haemostatic activity, thrombolytic activity,
XX receptor/ligand, antiinflammatory activity, tumour inhibition activity,
XX and antiinfective activity, and may also be involved in the determination
XX of bodily characteristics, fertility and behaviour. ORFX proteins,
XX nucleic acids and antibodies may be used in the treatment of cancers,
XX other proliferative disorders such as psoriasis and benign tumours,
XX neurological disorders such as epilepsy and Alzheimer's disease,
XX cardiovascular diseases, immune system disorders, disorders related to
XX organ transplantation, disorders of tissue growth and regeneration,
XX diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
XX storage disease, and infectious diseases caused by viral, bacterial,
XX fungal and other pathogens. ORFX nucleic acids may also be used as a
XX source of primers and probes, in the detection of ORFX genomic sequences
XX or transcripts, in the identification and cloning of homologous
XX sequences, in genetic diagnosis, and in forensic biology. The ORFX
XX nucleic acids may additionally be used to produce transgenic animals
XX which may be useful for studying the function and/or activity of ORFX
XX protein, and in drug screening. The ORFX proteins may also be used as
XX immunogens to generate specific antibodies, which are useful in the
XX diagnosis, treatment and monitoring of ORFX-associated diseases.

XX SQ Sequence 531 BP; 169 A; 138 C; 140 G; 84 T; 0 other;
Query Match 2.7%; Score 19; DB 24; Length 531;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 473 CAGCAGAGCCTCCACGA 491
|||||
Db 382 CAGCAGAGCCTCCACGA 400

RESULT 10

ABL59550
ID ABL59550 standard; cDNA; 2472 BP.

XX ABL59550;
AC ABL59550;
XX 16-JUL-2002 (first entry)

XX Human phosphatidylserine decarboxylase cDNA SEQ ID NO:50.
DE Human phosphatidylserine decarboxylase; tumour; lipid associated gene;
XX Human; phosphatidylserine decarboxylase; enzyme; ss.
KW Lipid metabolism; lipid synthesis; gene; ss.
XX Homo sapiens.
XX WO200227028-A1.
XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-US30366.
XX 28-SEP-2000; 2000US-0676052.
XX (ATAI-) ATAIRGIN TECHNOLOGIES INC.

XX Skinner MK, Patton JL, Chaudhary J;
XX WPI; 2002-402054/43.

XX Identifying tumor characteristics in a tissue sample taken from a
XX patient, involves determining the copy number or expression level of
XX genes associated with lipid metabolism, synthesis or action -
XX Example 1; Page 107-108; 113pp; English.

XX The present invention describes a method for identifying tumour
XX characteristics, comprising measuring a copy number or expression level
XX of at least two genes associated with lipid metabolism, synthesis, or
XX action in cells from a patient tissue sample, and comparing the results
XX with a copy number or expression level of the genes in a normal cell.
XX Also described is an array of nucleic acid polymers immobilised on a
XX solid support, comprising a solid support, at least two different nucleic
XX acid polymers which are each specific for a different gene associated
XX with lipid metabolism, synthesis or action, where each nucleic acid
XX polymer is located at a predetermined position on the solid support, and
XX the array comprises nucleic acid polymers which are specific for less
XX than 100 genes other than the selected genes. The method is useful for
XX determining tumour characteristics in a tissue sample taken from a
XX patient. The present sequence represents a human lipid-associated gene
XX related cDNA sequence, which is used in the exemplification of the
XX present invention.

XX SQ Sequence 2472 BP; 537 A; 711 C; 684 G; 540 T; 0 other;
Query Match 2.7%; Score 19; DB 24; Length 2472;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 GGCCCTGAGCGGAGGCTG 161
|||||
Db 295 GGCCCTGAGCGGAGGCTG 313

RESULT 11

AAH99704/c
ID AAH99704 standard; cDNA; 2730 BP.

XX AAH99704;
AC AAH99704;
XX 16-OCT-2001 (first entry)

XX Human protein encoding cDNA sequence SEQ ID NO:539.
DE Human protein encoding cDNA sequence SEQ ID NO:539.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder; ss.
 XX Homo sapiens.
 XX WO200153455-A2.
 XX 26-JUL-2001.
 XX 22-DEC-2000; 2000WO-US35017.
 XX 23-DEC-1999; 99US-0471275.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-457603/49.
 XX P-PSDB; AAM25763.
 XX Isolated human polynucleotides encoding polypeptides, useful for the
 XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 XX Claim 1; Page 592; 1217pp; English.
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 XX AAM25963. The proteins can have activities based on the tissues and
 XX cells they are expressed in, such as: antiinflammatory; antirheumatic;
 XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 XX cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;
 XX antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
 XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 XX encoding them can be used in gene therapy, antisense therapy and vaccine
 XX production. The proteins and polynucleotides are useful for screening for
 XX agonists or antagonists of a protein and for the treatment and diagnosis
 XX of disorders associated with the activity of a protein e.g. inflammation,
 XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 XX osteoporosis, severe combined immunodeficiency, eczema, allergic
 XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 XX Alzheimer's disease, Parkinson's disease, neurodegenerative and
 XX neurological disorders.
 XX Sequence 2730 BP; 589 A; 764 C; 795 G; 582 T; 0 other;
 XX Query Match 2.7%; Score 19; DB 22; Length 2730;
 XX Best Local Similarity 100.0%; Pred. No. 40;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 143 GCCTCTAGCGGAGGCTG 161
 DB 2204 GCCTCTAGCGGAGGCTG 2186

RESULT 12
 AAH99710/c
 ID AAH99710 standard; CDNA; 2735 BP.
 XX AC AAH99710;
 XX DT 16-OCT-2001 (first entry)
 XX DE Human protein encoding cDNA sequence SEQ ID NO:545.
 XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder; ss.
 XX Homo sapiens.
 XX WO200153455-A2.
 XX 26-JUL-2001.
 XX 22-DEC-2000; 2000WO-US35017.
 XX 23-DEC-1999; 99US-0471275.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-457603/49.
 XX P-PSDB; AAM25763.
 XX Isolated human polynucleotides encoding polypeptides, useful for the
 XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 XX Claim 1; Page 597-598; 1217pp; English.
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 XX AAM25963. The proteins can have activities based on the tissues and
 XX cells they are expressed in, such as: antiinflammatory; antirheumatic;
 XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 XX cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;
 XX antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
 XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 XX encoding them can be used in gene therapy, antisense therapy and vaccine
 XX production. The proteins and polynucleotides are useful for screening for
 XX agonists or antagonists of a protein and for the treatment and diagnosis
 XX of disorders associated with the activity of a protein e.g. inflammation,
 XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 XX osteoporosis, severe combined immunodeficiency, eczema, allergic
 XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 XX Alzheimer's disease, Parkinson's disease, neurodegenerative and
 XX neurological disorders.

SQ Sequence 2735 BP; 592 A; 767 C; 794 G; 582 T; 0 other;
Query Match 2.7%; Score 19; DB 22; Length 2735;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 143 GGCCCTGAGCGGAGGCTG 161
Db 2209 GGCCCTGAGCGGAGGCTG 2191

RESULT 13
AAI59663/c
ID AAI59663 standard; cDNA; 2735 BP.
XX
XX
XX AAI59663;
DT 22-OCT-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 3652.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX P-PSDB; AAM40507.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 3652; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
CC specification.
SQ Sequence 2735 BP; 592 A; 767 C; 794 G; 582 T; 0 other;
Query Match 2.7%; Score 19; DB 22; Length 2735;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 143 GGCCCTGAGCGGAGGCTG 161
Db 2209 GGCCCTGAGCGGAGGCTG 2191

RESULT 14
AAI59664/c
ID AAI59664 standard; cDNA; 2735 BP.
XX
XX
XX AAI59664;
DT 22-OCT-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 3653.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX P-PSDB; AAM40508.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 3653; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

SQ Sequence 2735 BP; 592 A; 767 C; 794 G; 582 T; 0 other;

Query Match 2.7%; Score 19; DB 22; Length 2735;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 GGCCCTGAGCGGAGGCTG 161

Db 2209 GGCCCTGAGCGGAGGCTG 2191

RESULT 15

AAI57877

ID AAI57877 standard; cDNA; 2739 BP.

XX AC AAI57877;

XX DT 22-OCT-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 80.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.

XX OS Homo sapiens.

XX OS WO200153312-A1.

XX PN 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US34263.

XX PR 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX PR 09-JUL-2000; 2000US-0598042.

XX PR 19-JUL-2000; 2000US-0620312.

XX PR 03-AUG-2000; 2000US-0653450.

XX PR 14-SEP-2000; 2000US-0662191.

XX PR 19-OCT-2000; 2000US-0691036.

XX PR 29-NOV-2000; 2000US-0727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX DR WPI; 2001-442253/47.

XX DR P-PSDB; AAM38721.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders

XX PT such as central nervous system injuries -

XX PS Claim 1; SEQ ID NO 80; 10078pp; English.

XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX SQ Sequence 2739 BP; 574 A; 801 C; 772 G; 592 T; 0 other;

Query Match 2.7%; Score 19; DB 22; Length 2739;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 GGCCCTGAGCGGAGGCTG 161

Db 554 GGCCCTGAGCGGAGGCTG 572

Search completed: June 16, 2003, 20:04:39

Job time : 153.225 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 27.9887 Seconds
(without alignments)
7834.381 Million cell updates/sec

Title: US-09-513-888C-1_COPY_7806_8520

Perfect score: 715

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 1533381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	18	2.5	1680	4	US-09-173-281-3
C 4	17	2.4	420	1	US-08-650-275-35
C 5	17	2.4	420	3	US-09-181-318-35
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C 7	17	2.4	1493	3	US-09-181-318-1
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C 9	17	2.4	1734	2	US-08-023-610-10
C 10	17	2.4	1734	2	US-08-288-065A-10
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c 109	15	2.1	422	4	US-08-486-841C-18	Sequence 18, Appl	c 182	15	2.1	2148	1	US-08-583-799-69	Sequence 69, Appl
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c 113	15	2.1	453	4	US-09-060-756-553	Sequence 553, App	c 186	15	2.1	2153	4	US-08-984-709A-19	Sequence 19, Appl
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c 172	15	2.1	2094	4	US-09-381-488-1	Sequence 1, Appl	c 245	15	2.1	4780	2	US-08-365-486A-20	Sequence 20, Appl
c 173	15	2.1	2094	4	US-09-381-488-3	Sequence 3, Appl	c 246	15	2.1	4780	3	US-09-123-708-3	Sequence 3, Appl

247	15	2.1	4780	3	US-09-123-624-3	Sequence 3, Appli	320	14	2.0	38	4	US-09-306-998-35	Sequence 35, Appl
248	15	2.1	4780	4	US-08-880-342-20	Sequence 20, Appl	321	14	2.0	42	1	US-08-233-009-53	Sequence 53, Appl
249	15	2.1	4877	2	US-08-404-531B-7	Sequence 7, Appli	C 322	14	2.0	42	1	US-08-233-009-54	Sequence 54, Appl
250	15	2.1	4877	3	US-08-404-531B-8	Sequence 8, Appli	C 323	14	2.0	44	3	US-08-660-645A-35	Sequence 35, Appl
251	15	2.1	4877	3	US-08-476-900A-7	Sequence 7, Appli	C 324	14	2.0	44	3	US-09-298-718-35	Sequence 35, Appl
252	15	2.1	4877	3	US-08-476-900A-8	Sequence 8, Appli	C 325	14	2.0	44	4	US-09-546-969-35	Sequence 35, Appl
253	15	2.1	4877	3	US-08-488-546A-7	Sequence 7, Appli	C 326	14	2.0	44	4	US-08-980-832-14	Sequence 14, Appl
254	15	2.1	4877	3	US-08-488-546A-8	Sequence 8, Appli	C 327	14	2.0	45	2	US-08-353-476-26	Sequence 26, Appl
255	15	2.1	5197	2	US-08-131-365B-53	Sequence 53, Appl	C 328	14	2.0	47	4	US-09-641-638-874	Sequence 874, App
256	15	2.1	5197	2	US-08-668-123-53	Sequence 53, Appl	C 329	14	2.0	50	1	US-08-171-389-331	Sequence 331, App
257	15	2.1	5300	4	US-08-938-669A-1	Sequence 1, Appli	C 330	14	2.0	50	1	US-08-123-936-331	Sequence 331, App
258	15	2.1	5304	4	US-08-938-669A-2	Sequence 2, Appli	C 331	14	2.0	50	2	US-08-475-228A-331	Sequence 331, App
259	15	2.1	5408	1	US-08-471-058-20	Sequence 20, Appl	C 332	14	2.0	50	3	US-08-482-080A-331	Sequence 331, App
260	15	2.1	5408	3	US-08-471-057-20	Sequence 20, Appl	C 333	14	2.0	50	4	US-09-354-947-331	Sequence 331, App
261	15	2.1	5538	2	US-08-231-193A-55	Sequence 55, Appl	C 334	14	2.0	50	5	PCT-US93-12388-331	Sequence 331, App
262	15	2.1	5538	2	US-08-486-273A-55	Sequence 55, Appl	C 335	14	2.0	54	2	US-08-585-684B-2473	Sequence 2473, Ap
263	15	2.1	5538	3	US-08-940-086A-55	Sequence 55, Appl	C 336	14	2.0	54	4	US-09-038-073-2473	Sequence 2473, Ap
264	15	2.1	5538	4	US-08-940-035A-55	Sequence 55, Appl	C 337	14	2.0	63	3	US-08-660-645A-33	Sequence 33, Appl
265	15	2.1	5538	4	US-08-935-105A-55	Sequence 55, Appl	C 338	14	2.0	63	3	US-09-298-718-33	Sequence 33, Appl
266	15	2.1	5538	4	US-08-648-797-55	Sequence 55, Appl	C 339	14	2.0	63	4	US-09-546-969-33	Sequence 33, Appl
267	15	2.1	5983	4	US-08-264-578-1	Sequence 1, Appli	C 340	14	2.0	63	4	US-08-980-832-12	Sequence 12, Appl
268	15	2.1	6169	4	US-08-938-669A-3	Sequence 3, Appli	C 341	14	2.0	99	1	US-08-472-255A-27	Sequence 27, Appl
269	15	2.1	6192	2	US-08-479-537A-1	Sequence 1, Appli	C 342	14	2.0	99	1	US-08-479-724A-27	Sequence 27, Appl
270	15	2.1	6192	4	US-08-083-116-1	Sequence 1, Appli	C 343	14	2.0	99	3	US-08-472-256B-27	Sequence 27, Appl
C 271	15	2.1	6192	4	US-08-134-916A-1	Sequence 1, Appli	C 344	14	2.0	99	4	US-08-952-793-27	Sequence 27, Appl
272	15	2.1	6524	4	US-08-669-656A-1	Sequence 1, Appli	C 345	14	2.0	99	5	PCT-US96-09455A-27	Sequence 27, Appl
273	15	2.1	6550	4	US-09-097-319A-1	Sequence 1, Appli	C 346	14	2.0	103	3	US-08-952-664-12	Sequence 12, Appl
274	15	2.1	7286	5	PCT-US95-11684-1	Sequence 1, Appli	C 347	14	2.0	103	4	US-09-487-874-12	Sequence 12, Appl
275	15	2.1	7785	2	US-08-276-967-1	Sequence 1, Appli	C 348	14	2.0	106	4	US-09-506-729-63	Sequence 63, Appl
276	15	2.1	7812	4	US-08-368-590-1	Sequence 1, Appli	C 349	14	2.0	141	4	US-08-943-731-8	Sequence 8, Appli
C 277	15	2.1	8625	4	US-08-980-832-1	Sequence 1, Appli	C 350	14	2.0	149	4	US-09-511-625B-30	Sequence 30, Appl
278	15	2.1	9299	4	US-08-097-319A-15	Sequence 15, Appl	C 351	14	2.0	192	6	5508199-6	Patent No. 5508199
279	15	2.1	9335	4	US-08-097-319A-19	Sequence 19, Appl	C 352	14	2.0	218	4	US-09-506-729-61	Sequence 61, Appl
280	15	2.1	9408	4	US-09-097-319A-16	Sequence 16, Appl	C 353	14	2.0	228	3	US-08-946-914-32	Sequence 32, Appl
C 281	15	2.1	10627	1	US-08-060-925A-12	Sequence 12, Appl	C 354	14	2.0	228	4	US-09-122-171D-2	Sequence 2, Appli
C 282	15	2.1	11233	1	US-08-980-832-27	Sequence 27, Appl	C 355	14	2.0	228	4	US-09-656-450-32	Sequence 32, Appl
C 283	15	2.1	11613	1	US-08-484-044-10	Sequence 10, Appl	C 356	14	2.0	231	4	US-08-930-285-20	Sequence 20, Appl
284	15	2.1	11673	4	US-09-334-220-3	Sequence 3, Appli	C 357	14	2.0	231	4	US-08-697-826A-18	Sequence 18, Appl
285	15	2.1	11784	4	US-09-097-319A-9	Sequence 9, Appli	C 358	14	2.0	285	4	US-09-812-484-5	Sequence 5, Appli
286	15	2.1	11991	4	US-09-097-319A-10	Sequence 10, Appl	C 359	14	2.0	301	4	US-09-643-597-304	Sequence 304, App
C 287	15	2.1	13011	2	US-08-791-849A-14	Sequence 14, Appl	C 360	14	2.0	322	2	US-08-691-814B-112	Sequence 112, App
288	15	2.1	16595	4	US-08-146-053-7	Sequence 7, Appli	C 361	14	2.0	326	1	US-08-700-575-3	Sequence 3, Appli
289	15	2.1	16836	4	US-09-147-236-1	Sequence 1, Appli	C 362	14	2.0	330	4	US-09-199-637A-24	Sequence 24, Appl
290	15	2.1	16836	4	US-09-147-236-10	Sequence 10, Appl	C 363	14	2.0	330	4	US-09-712-016-75	Sequence 75, Appl
291	15	2.1	19932	2	US-08-477-451-25	Sequence 25, Appl	C 364	14	2.0	336	6	5494663-13	Patent No. 5494663
292	15	2.1	29598	4	US-09-341-587-6	Sequence 6, Appli	C 365	14	2.0	339	2	US-08-619-542B-30	Sequence 30, Appl
C 293	15	2.1	35828	4	US-09-449-218D-17	Sequence 17, Appl	C 366	14	2.0	348	1	US-08-466-390-6	Sequence 6, Appli
294	15	2.1	37948	4	US-08-251-645-11	Sequence 11, Appl	C 367	14	2.0	348	1	US-08-470-950-6	Sequence 6, Appli
295	15	2.1	44453	4	US-08-146-053-5	Sequence 5, Appli	C 368	14	2.0	348	1	US-08-467-781-6	Sequence 6, Appli
296	15	2.1	45716	4	US-08-965-048-5	Sequence 5, Appli	C 369	14	2.0	348	1	US-08-195-487-6	Sequence 6, Appli
297	15	2.1	45989	4	US-08-965-048-6	Sequence 6, Appli	C 370	14	2.0	348	2	US-08-483-924-6	Sequence 6, Appli
C 298	15	2.1	70000	4	US-09-851-896-3	Sequence 3, Appli	C 371	14	2.0	348	5	PCT-US93-06160-6	Sequence 6, Appli
299	15	2.1	90050	4	US-08-245-041-5	Sequence 5, Appli	C 372	14	2.0	370	3	US-09-188-930-103	Sequence 103, App
C 300	15	2.1	111282	4	US-08-784-250-3	Sequence 3, Appli	C 373	14	2.0	373	1	US-08-592-126-131	Sequence 131, App
C 301	14	2.0	18	4	US-09-723-535-40	Sequence 40, Appl	C 374	14	2.0	388	4	US-09-325-932A-108	Sequence 108, App
302	14	2.0	21	4	US-09-338-907-175	Sequence 175, App	C 375	14	2.0	405	2	US-08-116-778B-4	Sequence 4, Appli
303	14	2.0	21	4	US-08-218-207-175	Sequence 175, App	C 376	14	2.0	405	2	US-08-438-562-4	Sequence 4, Appli
C 304	14	2.0	24	2	US-08-521-053-4	Sequence 4, Appli	C 377	14	2.0	405	2	US-08-483-528B-4	Sequence 4, Appli
305	14	2.0	24	2	US-08-521-053-5	Sequence 5, Appli	C 378	14	2.0	405	3	US-08-673-799C-4	Sequence 4, Appli
C 306	14	2.0	26	1	US-08-429-121B-42	Sequence 42, Appl	C 379	14	2.0	405	4	US-09-393-385B-4	Sequence 4, Appli
C 307	14	2.0	26	2	US-08-353-476-13	Sequence 13, Appl	C 380	14	2.0	411	4	US-08-651-155B-206	Sequence 206, App
C 308	14	2.0	26	2	US-09-003-067-42	Sequence 42, Appl	C 381	14	2.0	412	1	US-07-872-644-22	Sequence 22, Appl
309	14	2.0	26	4	US-09-309-317-10	Sequence 10, Appl	C 382	14	2.0	412	1	US-08-297-494-22	Sequence 22, Appl
C 310	14	2.0	29	1	US-08-436-464-3	Sequence 3, Appli	C 383	14	2.0	412	1	US-08-297-510-22	Sequence 22, Appl
311	14	2.0	31	1	US-08-530-492-87	Sequence 87, Appl	C 384	14	2.0	412	1	US-08-479-532-22	Sequence 22, Appl
312	14	2.0	31	4	US-08-906-517-87	Sequence 87, Appl	C 385	14	2.0	412	1	US-08-455-526-22	Sequence 22, Appl
C 313	14	2.0	32	1	US-08-436-464-5	Sequence 5, Appli	C 386	14	2.0	412	1	US-08-455-525-22	Sequence 22, Appl
314	14	2.0	36	3	US-08-957-302A-4	Sequence 4, Appli	C 387	14	2.0	412	3	US-09-139-491-22	Sequence 22, Appl
C 315	14	2.0	36	3	US-08-957-302A-14	Sequence 14, Appl	C 388	14	2.0	418	5	PCT-US92-03222-22	Sequence 22, Appl
316	14	2.0	36	3	US-08-957-302A-15	Sequence 15, Appl	C 389	14	2.0	418	2	US-08-927-307-7	Sequence 7, Appli
317	14	2.0	36	4	US-09-542-403-4	Sequence 4, Appli	C 390	14	2.0	418	3	US-09-385-947-7	Sequence 7, Appli
C 318	14	2.0	36	4	US-09-542-403-14	Sequence 14, Appl	C 391	14	2.0	423	1	US-08-470-179-109	Sequence 109, App
319	14	2.0	36	4	US-09-542-403-15	Sequence 15, Appl	C 392	14	2.0	441	1	US-07-998-003A-90	Sequence 90, Appl

C 393	14	2.0	441	1	US-08-453-274B-90	Sequence 90, Appl	466	14	2.0	1022	4	US-09-222-575-67	Sequence 67, Appl
C 394	14	2.0	441	1	US-08-453-695A-90	Sequence 90, Appl	467	14	2.0	1061	3	US-09-286-805-3	Sequence 3, Appl
C 395	14	2.0	441	1	US-08-288-619A-90	Sequence 90, Appl	C 468	14	2.0	1068	4	US-09-403-768-5	Sequence 5, Appl
C 396	14	2.0	441	2	US-08-453-702A-90	Sequence 90, Appl	C 469	14	2.0	1100	4	US-09-372-422A-47	Sequence 47, Appl
C 397	14	2.0	441	4	US-09-099-639-90	Sequence 90, Appl	C 470	14	2.0	1100	4	US-09-222-938A-32	Sequence 32, Appl
C 398	14	2.0	441	5	PCT-US93-12588-90	Sequence 90, Appl	471	14	2.0	1110	2	US-08-693-174-4	Sequence 4, Appl
C 399	14	2.0	441	5	PCT-US95-08071-90	Sequence 90, Appl	C 472	14	2.0	1110	4	US-09-253-738-4	Sequence 4, Appl
C 400	14	2.0	445	2	US-08-691-814B-124	Sequence 124, App	C 473	14	2.0	1110	4	US-09-336-536-27	Sequence 27, Appl
C 401	14	2.0	461	4	US-08-812-484-26	Sequence 26, Appl	474	14	2.0	1120	4	US-09-214-631-1	Sequence 1, Appl
C 402	14	2.0	471	4	US-09-643-597-328	Sequence 328, App	475	14	2.0	1129	1	US-08-470-261-1	Sequence 1, Appl
C 403	14	2.0	512	4	US-09-221-298-88	Sequence 88, Appl	476	14	2.0	1129	3	US-08-916-989B-1	Sequence 1, Appl
C 404	14	2.0	540	4	US-09-280-116-13	Sequence 13, Appl	477	14	2.0	1129	4	US-09-432-253-1	Sequence 1, Appl
C 405	14	2.0	569	3	US-09-109-204-15	Sequence 15, Appl	478	14	2.0	1129	5	PCT-US94-13187-1	Sequence 1, Appl
C 406	14	2.0	587	4	US-09-385-982-497	Sequence 9, Appl	C 479	14	2.0	1131	1	US-07-648-796A-14	Sequence 14, Appl
C 407	14	2.0	592	4	US-09-328-111-139	Sequence 139, App	480	14	2.0	1166	2	US-09-149-476-209	Sequence 209, App
C 408	14	2.0	596	4	US-09-328-111-153	Sequence 153, App	C 481	14	2.0	1168	2	US-08-530-569B-11	Sequence 11, Appl
C 409	14	2.0	597	4	US-09-134-001C-2771	Sequence 2771, App	C 482	14	2.0	1182	4	US-09-469-242-1	Sequence 1, Appl
C 410	14	2.0	607	4	US-09-385-982-412	Sequence 412, App	C 483	14	2.0	1215	2	US-08-370-156-26	Sequence 26, Appl
C 411	14	2.0	612	2	US-08-308-952-9	Sequence 9, Appl	484	14	2.0	1222	1	US-08-328-322-1	Sequence 1, Appl
C 412	14	2.0	612	4	US-08-124-141-12	Sequence 12, Appl	C 485	14	2.0	1222	4	US-09-484-970B-3	Sequence 3, Appl
C 413	14	2.0	642	2	US-08-480-753-5	Sequence 5, Appl	C 486	14	2.0	1225	1	US-08-494-577-11	Sequence 11, Appl
C 414	14	2.0	642	3	US-09-041-889-10	Sequence 10, Appl	487	14	2.0	1235	1	US-08-696-770-1	Sequence 1, Appl
C 415	14	2.0	642	3	US-08-837-058-10	Sequence 10, Appl	488	14	2.0	1235	2	US-09-015-557-1	Sequence 1, Appl
C 416	14	2.0	642	4	US-09-139-637A-26	Sequence 26, Appl	C 489	14	2.0	1235	2	US-08-530-569B-12	Sequence 12, Appl
C 417	14	2.0	642	4	US-09-328-111-816	Sequence 816, App	C 490	14	2.0	1238	2	US-08-795-868-11	Sequence 11, Appl
C 418	14	2.0	658	4	US-09-328-111-816	Sequence 816, App	C 491	14	2.0	1238	4	US-09-313-300-10	Sequence 10, Appl
C 419	14	2.0	670	4	US-09-335-948-3	Sequence 3, Appl	C 492	14	2.0	1238	4	US-09-303-069-11	Sequence 11, Appl
C 420	14	2.0	683	4	US-07-806-932B-4	Sequence 4, Appl	C 493	14	2.0	1238	4	US-09-134-250-11	Sequence 11, Appl
C 421	14	2.0	687	3	US-09-149-476-25	Sequence 25, Appl	C 494	14	2.0	1243	4	US-09-191-136-15	Sequence 15, Appl
C 422	14	2.0	696	4	US-08-998-416-954	Sequence 954, App	C 495	14	2.0	1248	4	US-09-545-944-1	Sequence 1, Appl
C 423	14	2.0	696	4	US-09-740-235-16	Sequence 16, Appl	C 496	14	2.0	1253	4	US-08-978-289-9	Sequence 9, Appl
C 424	14	2.0	720	4	US-09-274-825-1	Sequence 1, Appl	497	14	2.0	1255	4	US-09-149-476-75	Sequence 75, Appl
C 425	14	2.0	720	4	US-09-627-769-1	Sequence 1, Appl	498	14	2.0	1260	1	US-08-385-186-1	Sequence 1, Appl
C 426	14	2.0	736	1	US-08-846-012A-1	Sequence 1, Appl	C 499	14	2.0	1272	4	US-09-191-136-13	Sequence 13, Appl
C 427	14	2.0	736	2	US-09-100-297-1	Sequence 1, Appl	500	14	2.0	1272	4	US-09-227-357-46	Sequence 46, Appl
C 428	14	2.0	744	1	US-07-648-796A-10	Sequence 10, Appl	C 501	14	2.0	1281	4	US-09-327-487A-3	Sequence 3, Appl
C 429	14	2.0	792	1	US-08-578-709-10	Sequence 10, Appl	C 502	14	2.0	1284	4	US-09-327-487A-4	Sequence 4, Appl
C 430	14	2.0	806	5	5494663-4	Patent No. 5494663	503	14	2.0	1298	3	US-08-911-894-73	Sequence 73, Appl
C 431	14	2.0	810	4	US-09-221-017B-732	Sequence 732, App	504	14	2.0	1300	2	US-09-166-203-41	Sequence 41, Appl
C 432	14	2.0	814	4	US-08-858-207A-238	Sequence 238, App	505	14	2.0	1300	4	US-09-377-309-41	Sequence 41, Appl
C 433	14	2.0	822	1	US-07-936-267A-8	Sequence 8, Appl	C 506	14	2.0	1311	2	US-08-530-569B-1	Sequence 1, Appl
C 434	14	2.0	829	2	US-08-294-143-3	Sequence 3, Appl	507	14	2.0	1317	1	US-08-370-975B-2	Sequence 2, Appl
C 435	14	2.0	829	3	US-09-256-331-3	Sequence 3, Appl	C 508	14	2.0	1341	3	US-09-032-372-9	Sequence 9, Appl
C 436	14	2.0	829	4	US-09-593-483-3	Sequence 3, Appl	C 509	14	2.0	1379	2	US-08-437-607A-1	Sequence 1, Appl
C 437	14	2.0	833	2	US-08-837-029-1	Sequence 1, Appl	C 510	14	2.0	1380	2	US-08-437-607A-4	Sequence 4, Appl
C 438	14	2.0	835	3	US-08-957-302A-9	Sequence 9, Appl	511	14	2.0	1384	1	US-07-607-538C-1	Sequence 1, Appl
C 439	14	2.0	835	4	US-09-542-403-9	Sequence 9, Appl	512	14	2.0	1384	2	US-08-162-402B-1	Sequence 1, Appl
C 440	14	2.0	840	4	US-08-998-416-341	Sequence 341, App	C 513	14	2.0	1387	2	US-08-979-424-2	Sequence 2, Appl
C 441	14	2.0	842	4	US-08-998-416-517	Sequence 517, App	C 514	14	2.0	1394	1	US-07-730-953-1	Sequence 1, Appl
C 442	14	2.0	844	4	US-09-812-484-6	Sequence 6, Appl	515	14	2.0	1395	3	US-08-957-302A-3	Sequence 3, Appl
C 443	14	2.0	851	3	US-09-126-646-3	Sequence 3, Appl	516	14	2.0	1395	4	US-09-542-403-3	Sequence 3, Appl
C 444	14	2.0	851	4	US-09-421-491-3	Sequence 3, Appl	517	14	2.0	1419	2	US-08-619-542B-29	Sequence 29, Appl
C 445	14	2.0	861	3	US-09-187-050-4	Sequence 4, Appl	C 518	14	2.0	1449	3	US-08-103-170-5	Sequence 5, Appl
C 446	14	2.0	900	4	US-09-149-476-161	Sequence 161, App	C 519	14	2.0	1449	3	US-08-988-876-4	Sequence 4, Appl
C 447	14	2.0	903	4	US-09-934-551-1	Sequence 1, Appl	C 520	14	2.0	1452	2	US-08-807-044-4	Sequence 4, Appl
C 448	14	2.0	918	1	US-08-328-322-3	Sequence 3, Appl	C 521	14	2.0	1452	5	PCT-US91-04986-1	Sequence 1, Appl
C 449	14	2.0	941	2	US-08-203-532F-3	Sequence 3, Appl	C 522	14	2.0	1461	3	US-08-722-126A-4	Sequence 4, Appl
C 450	14	2.0	941	4	US-09-078-465-3	Sequence 3, Appl	523	14	2.0	1461	5	PCT-US95-04258-4	Sequence 4, Appl
C 451	14	2.0	941	5	PCT-US95-01882A-3	Sequence 3, Appl	524	14	2.0	1467	1	US-08-176-620A-3	Sequence 3, Appl
C 452	14	2.0	949	1	US-08-702-344-1	Sequence 1, Appl	525	14	2.0	1467	2	US-08-461-985-3	Sequence 3, Appl
C 453	14	2.0	957	4	US-09-199-637A-22	Sequence 22, Appl	526	14	2.0	1467	2	US-08-458-887-3	Sequence 3, Appl
C 454	14	2.0	958	2	US-08-633-514C-9	Sequence 9, Appl	527	14	2.0	1467	2	US-08-912-787B-3	Sequence 3, Appl
C 455	14	2.0	958	3	US-09-188-177-9	Sequence 9, Appl	528	14	2.0	1467	4	US-08-932-012C-3	Sequence 3, Appl
C 456	14	2.0	1001	4	US-09-641-638-220	Sequence 220, App	529	14	2.0	1467	4	US-08-820-170A-41	Sequence 41, Appl
C 457	14	2.0	1001	4	US-09-641-638-221	Sequence 221, App	530	14	2.0	1467	4	US-08-888-818C-3	Sequence 3, Appl
C 458	14	2.0	1001	4	US-09-641-638-285	Sequence 285, App	531	14	2.0	1497	2	US-09-055-699-41	Sequence 41, Appl
C 459	14	2.0	1001	4	US-09-641-638-555	Sequence 555, App	532	14	2.0	1497	3	US-09-273-565-41	Sequence 41, Appl
C 460	14	2.0	1001	4	US-09-641-638-563	Sequence 563, App	533	14	2.0	1497	4	US-09-565-538-41	Sequence 41, Appl
C 461	14	2.0	1001	4	US-09-641-638-564	Sequence 564, App	534	14	2.0	1497	4	US-09-661-468-41	Sequence 41, Appl
C 462	14	2.0	1006	1	US-08-076-091C-11	Sequence 11, Appl	535	14	2.0	1498	2	US-08-818-024-2	Sequence 2, Appl
C 463	14	2.0	1006	1	US-08-285-641-11	Sequence 11, Appl	536	14	2.0	1498	2	US-09-334-775A-2	Sequence 2, Appl
C 464	14	2.0	1017	4	US-08-849-751-1	Sequence 1, Appl	537	14	2.0	1498	4	US-09-039-046-1	Sequence 1, Appl
C 465	14	2.0	1017	4	US-09-478-816-1	Sequence 1, Appl	C 538	14	2.0	1508	4		

c 539	14	2.0	1517	4	US-09-149-476-295	Sequence 295, App	612	14	2.0	1758	3	US-09-191-171-6	Sequence 6, Appli
c 540	14	2.0	1537	4	US-09-556-877-57	Sequence 57, Appl	c 614	14	2.0	1758	4	US-09-385-707-6	Sequence 6, Appli
c 541	14	2.0	1537	4	US-09-620-412C-57	Sequence 57, Appl	c 614	14	2.0	1767	1	US-07-668-648-1	Sequence 1, Appli
542	14	2.0	1540	1	US-07-932-915-1	Sequence 1, Appli	c 615	14	2.0	1767	1	US-07-668-648-5	Sequence 5, Appli
543	14	2.0	1540	5	PCT-US91-05826-1	Sequence 1, Appli	c 616	14	2.0	1767	2	US-08-429-998-1	Sequence 1, Appli
c 544	14	2.0	1544	4	US-09-149-476-103	Sequence 103, App	c 617	14	2.0	1767	2	US-08-429-998-5	Sequence 5, Appli
545	14	2.0	1546	4	US-09-383-318A-1	Sequence 1, Appli	c 618	14	2.0	1767	2	US-08-431-333-1	Sequence 1, Appli
546	14	2.0	1547	2	US-08-902-853-2	Sequence 2, Appli	c 618	14	2.0	1767	2	US-08-431-333-5	Sequence 5, Appli
547	14	2.0	1548	3	US-08-665-259-28	Sequence 28, Appl	c 620	14	2.0	1767	5	PCT-US91-02321-1	Sequence 1, Appli
548	14	2.0	1548	3	US-08-762-500-28	Sequence 28, Appl	c 621	14	2.0	1767	5	PCT-US91-02321-5	Sequence 5, Appli
549	14	2.0	1556	2	US-08-881-857-1	Sequence 1, Appli	c 622	14	2.0	1782	2	US-08-308-952-6	Sequence 6, Appli
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551	14	2.0	1571	5	PCT-US94-12912-2	Sequence 2, Appli	c 624	14	2.0	1810	1	US-07-755-573C-7	Sequence 7, Appli
552	14	2.0	1575	3	US-08-957-302A-1	Sequence 1, Appli	c 625	14	2.0	1831	4	US-09-484-970B-84	Sequence 84, Appl
553	14	2.0	1575	4	US-09-542-403-1	Sequence 1, Appli	c 626	14	2.0	1833	3	US-09-120-365-6	Sequence 6, Appli
c 554	14	2.0	1590	4	US-09-323-195A-7	Sequence 7, Appli	c 627	14	2.0	1833	4	US-09-515-039-6	Sequence 6, Appli
555	14	2.0	1600	1	US-08-073-384C-12	Sequence 12, Appl	c 628	14	2.0	1844	1	US-07-872-644-26	Sequence 26, Appl
556	14	2.0	1600	1	US-08-254-359A-12	Sequence 12, Appl	c 629	14	2.0	1844	1	US-08-297-494-26	Sequence 26, Appl
557	14	2.0	1600	1	US-08-483-043-12	Sequence 12, Appl	c 630	14	2.0	1844	1	US-08-297-510-26	Sequence 26, Appl
558	14	2.0	1600	1	US-08-481-238-12	Sequence 12, Appl	c 631	14	2.0	1844	1	US-08-479-532-26	Sequence 26, Appl
559	14	2.0	1600	2	US-08-471-066B-12	Sequence 12, Appl	c 632	14	2.0	1844	1	US-08-455-526-26	Sequence 26, Appl
560	14	2.0	1600	2	US-08-484-956-12	Sequence 12, Appl	c 633	14	2.0	1844	1	US-08-455-525-26	Sequence 26, Appl
561	14	2.0	1600	2	US-08-757-653-12	Sequence 12, Appl	c 634	14	2.0	1844	3	US-09-139-491-26	Sequence 26, Appl
562	14	2.0	1600	2	US-08-539-491-12	Sequence 12, Appl	c 635	14	2.0	1844	5	PCT-US92-03222-26	Sequence 26, Appl
563	14	2.0	1600	2	US-08-756-386-12	Sequence 12, Appl	c 636	14	2.0	1858	4	US-09-336-536-56	Sequence 56, Appl
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565	14	2.0	1600	3	US-08-682-853A-12	Sequence 12, Appl	c 638	14	2.0	1863	4	US-09-421-491-1	Sequence 1, Appli
566	14	2.0	1600	3	US-08-759-038-12	Sequence 12, Appl	c 639	14	2.0	1863	4	US-09-637-118B-1	Sequence 1, Appli
567	14	2.0	1600	3	US-08-758-314-12	Sequence 12, Appl	c 640	14	2.0	1869	4	US-09-336-536-26	Sequence 26, Appl
568	14	2.0	1600	4	US-09-350-309-12	Sequence 12, Appl	c 641	14	2.0	1889	3	US-09-187-050-1	Sequence 1, Appli
569	14	2.0	1600	4	US-08-520-946-12	Sequence 12, Appl	c 642	14	2.0	1894	4	US-07-912-122-3	Sequence 3, Appli
c 570	14	2.0	1602	4	US-09-153-804-9	Sequence 9, Appli	c 643	14	2.0	1894	5	PCT-US93-06404-3	Sequence 3, Appli
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c 580	14	2.0	1642	1	US-07-999-280A-3	Sequence 3, Appli	c 653	14	2.0	1950	1	US-08-592-126-93	Sequence 93, Appl
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c 586	14	2.0	1642	3	US-08-425-876-3	Sequence 3, Appli	c 659	14	2.0	1984	4	US-08-937-067-5	Sequence 5, Appli
c 587	14	2.0	1642	3	US-08-426-243-3	Sequence 3, Appli	c 660	14	2.0	1990	4	US-09-149-476-281	Sequence 281, App
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589	14	2.0	1642	4	US-09-328-314-1	Sequence 1, Appli	c 662	14	2.0	2018	2	US-08-557-973-1	Sequence 1, Appli
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591	14	2.0	1659	2	US-08-943-087-47	Sequence 47, Appl	c 664	14	2.0	2038	4	US-08-810-712-11	Sequence 11, Appl
592	14	2.0	1660	4	US-09-637-367-21	Sequence 21, Appl	c 665	14	2.0	2041	4	US-09-149-476-131	Sequence 131, App
593	14	2.0	1662	4	US-09-370-398-1	Sequence 1, Appli	c 666	14	2.0	2051	2	US-08-530-569B-13	Sequence 13, Appl
c 595	14	2.0	1677	4	US-09-153-804-10	Sequence 10, Appl	c 667	14	2.0	2055	4	US-09-232-160-9	Sequence 9, Appli
c 596	14	2.0	1679	4	US-09-271-437-3	Sequence 3, Appli	c 668	14	2.0	2055	4	US-09-812-484-3	Sequence 3, Appli
c 597	14	2.0	1680	1	US-08-234-783-3	Sequence 3, Appli	c 669	14	2.0	2057	2	US-08-820-170A-42	Sequence 42, Appl
598	14	2.0	1680	5	PCT-US95-05523-3	Sequence 3, Appli	c 670	14	2.0	2057	3	US-09-055-699-42	Sequence 42, Appl
599	14	2.0	1682	3	US-09-096-399-1	Sequence 3, Appli	c 671	14	2.0	2057	4	US-09-273-565-42	Sequence 42, Appl
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c 605	14	2.0	1721	4	US-09-420-915-16	Sequence 16, Appl	c 677	14	2.0	2073	2	US-08-691-814B-5	Sequence 5, Appli
c 606	14	2.0	1726	4	US-09-232-160-14	Sequence 14, Appl	c 678	14	2.0	2080	2	US-08-878-563A-2	Sequence 2, Appli
c 607	14	2.0	1726	4	US-09-812-484-11	Sequence 11, Appl	c 680	14	2.0	2089	1	US-08-270-117-2	Sequence 2, Appli
c 608	14	2.0	1734	4	US-09-182-145-17	Sequence 17, Appl	c 681	14	2.0	2093	1	US-08-441-139-13	Sequence 13, Appl
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c 610	14	2.0	1752	4	US-09-360-779-1	Sequence 1, Appli	c 683	14	2.0	2112	4	US-09-232-160-12	Sequence 12, Appl
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687	14	2.0	2126	3	US-09-058-725B-1	Sequence 1, Appli	760	14	2.0	2499	4	US-09-777-538-1	Sequence 1, Appli
688	14	2.0	2126	3	US-09-232-857-1	Sequence 1, Appli	761	14	2.0	2499	5	PCT-US91-07035-1	Sequence 21, Appli
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706	14	2.0	2265	2	US-08-940-332-1	Sequence 1, Appli	779	14	2.0	2505	2	US-08-757-653-189	Sequence 189, App
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711	14	2.0	2285	3	US-08-473-673-9	Sequence 9, Appli	784	14	2.0	2505	3	US-08-759-038-129	Sequence 129, App
712	14	2.0	2290	2	US-08-933-821-1	Sequence 1, Appli	785	14	2.0	2505	3	US-08-759-038-131	Sequence 131, App
713	14	2.0	2290	3	US-08-960-507-1	Sequence 1, Appli	786	14	2.0	2505	3	US-08-758-314-106	Sequence 106, App
714	14	2.0	2290	4	US-09-136-828-1	Sequence 1, Appli	787	14	2.0	2505	3	US-08-758-314-129	Sequence 129, App
715	14	2.0	2290	4	US-09-332-928A-1	Sequence 1, Appli	788	14	2.0	2505	3	US-08-758-314-131	Sequence 131, App
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717	14	2.0	2290	4	US-09-332-929-1	Sequence 1, Appli	790	14	2.0	2506	1	US-08-254-359A-1	Sequence 1, Appli
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726	14	2.0	2302	1	US-08-401-013-1	Sequence 1, Appli	799	14	2.0	2506	3	US-08-759-038-1	Sequence 1, Appli
727	14	2.0	2302	3	US-08-426-570-1	Sequence 1, Appli	800	14	2.0	2506	3	US-08-758-314-1	Sequence 1, Appli
728	14	2.0	2302	3	US-08-426-570-1	Sequence 1, Appli	801	14	2.0	2506	4	US-09-350-309-1	Sequence 1, Appli
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734	14	2.0	2313	1	US-07-648-796A-16	Sequence 16, Appli	807	14	2.0	2511	4	US-09-422-869-19	Sequence 19, Appli
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736	14	2.0	2329	4	US-08-956-322-1	Sequence 1, Appli	809	14	2.0	2538	4	US-09-126-121-1	Sequence 1, Appli
737	14	2.0	2334	1	US-08-406-070-1	Sequence 1, Appli	810	14	2.0	2559	4	US-09-118-408-43	Sequence 43, Appli
738	14	2.0	2377	4	US-08-556-627A-3	Sequence 3, Appli	811	14	2.0	2559	4	US-09-506-855-43	Sequence 43, Appli
739	14	2.0	2395	4	US-09-724-864-24	Sequence 24, Appli	812	14	2.0	2565	2	US-08-619-554-5	Sequence 5, Appli
740	14	2.0	2400	1	US-07-648-796A-15	Sequence 15, Appli	813	14	2.0	2580	2	US-08-887-798-1	Sequence 1, Appli
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743	14	2.0	2419	4	US-09-624-693A-12	Sequence 12, Appli	816	14	2.0	2626	1	US-08-156-020-1	Sequence 1, Appli
744	14	2.0	2430	4	US-09-232-160-16	Sequence 16, Appli	817	14	2.0	2626	1	US-08-156-020-3	Sequence 3, Appli
745	14	2.0	2453	5	PCT-US95-07180-1	Sequence 1, Appli	818	14	2.0	2626	1	US-08-156-020-5	Sequence 5, Appli
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833	14	2.0	2744	3	US-09-369-618-1	Sequence 1, Appli	906	14	2.0	3484	1	US-08-906-517-105	Sequence 105, App
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839	14	2.0	2766	4	US-08-617-785-13	Sequence 13, Appli	912	14	2.0	3517	4	US-09-199-534-20	Sequence 20, Appli
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847	14	2.0	2864	4	US-09-409-180A-2	Sequence 2, Appli	920	14	2.0	3567	2	US-09-166-203-1	Sequence 1, Appli
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851	14	2.0	2946	3	US-08-369-683A-6	Sequence 6, Appli	924	14	2.0	3627	2	US-09-025-583-7	Sequence 7, Appli
852	14	2.0	2946	4	US-09-297-928-2	Sequence 2, Appli	925	14	2.0	3651	4	US-07-852-132A-13	Sequence 13, Appli
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857	14	2.0	3016	3	US-08-814-095-5	Sequence 5, Appli	930	14	2.0	3684	4	US-09-659-084-17	Sequence 17, Appli
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872	14	2.0	3141	4	US-09-199-637A-12	Sequence 12, Appli	945	14	2.0	4131	1	US-08-485-588-4	Sequence 4, Appli
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878	14	2.0	3358	4	US-09-553-736-2	Sequence 2, Appli	951	14	2.0	4131	2	US-08-943-986-4	Sequence 4, Appli
879	14	2.0	3375	4	US-09-511-625B-67	Sequence 67, Appli	952	14	2.0	4131	2	US-08-943-986-4	Sequence 4, Appli
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881	14	2.0	3416	2	US-08-451-822A-15	Sequence 15, Appli	954	14	2.0	4131	3	US-08-353-784-4	Sequence 4, Appli
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883	14	2.0	3444	4	US-09-178-252-1	Sequence 1, Appli	956	14	2.0	4131	3	US-08-484-719B-4	Sequence 4, Appli
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885	14	2.0	3453	1	US-07-813-593-1	Sequence 1, Appli	958	14	2.0	4131	4	US-08-484-159-4	Sequence 4, Appli
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887	14	2.0	3453	1	US-07-946-507-1	Sequence 1, Appli	960	14	2.0	4134	4	US-09-196-387-1	Sequence 1, Appli
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891	14	2.0	3453	1	US-09-021-324-1	Sequence 1, Appli	964	14	2.0	4220	4	US-09-183-846A-11	Sequence 11, Appli
892	14	2.0	3453	5	PCT-US92-02750-1	Sequence 1, Appli	965	14	2.0	4220	4	US-08-961-578C-11	Sequence 11, Appli
893	14	2.0	3453	5	PCT-US92-05401-1	Sequence 1, Appli	966	14	2.0	4264	2	US-08-784-649A-1	Sequence 1, Appli
894	14	2.0	3453	5	PCT-US92-09893-1	Sequence 1, Appli	967	14	2.0	4264	2	US-08-784-649A-5	Sequence 5, Appli
895	14	2.0	3460	2	US-08-751-305-1	Sequence 1, Appli	968	14	2.0	4296	4	US-09-060-410-3	Sequence 3, Appli
896	14	2.0	3466	1	US-08-468-036-38	Sequence 38, Appli	969	14	2.0	4317	4	US-08-961-527-124	Sequence 124, App
897	14	2.0	3466	2	US-08-376-843-38	Sequence 38, Appli	970	14	2.0	4339	4	US-09-484-970B-164	Sequence 164, App
898	14	2.0	3468	4	US-09-178-252-13	Sequence 13, Appli	971	14	2.0	4415	4	US-09-486-580A-1	Sequence 1, Appli
899	14	2.0	3468	4	US-09-178-252-14	Sequence 14, Appli	972	14	2.0	4480	3	US-09-191-171-7	Sequence 7, Appli
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903	14	2.0	3478	4	US-08-506-517-1	Sequence 1, Appli	976	14	2.0	4526	2	US-08-308-887A-4	Sequence 4, Appli

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C 982 14 2.0 4657 4 US-09-196-387-9
C 983 14 2.0 4659 4 US-09-221-017B-823
C 984 14 2.0 4669 2 US-08-583-276-18
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C 988 14 2.0 4698 4 US-09-439-261-34
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C 992 14 2.0 4758 4 US-09-540-153-1
C 993 14 2.0 4776 2 US-08-852-401-1
C 994 14 2.0 4817 1 US-07-951-715A-18
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C 996 14 2.0 4817 3 US-08-459-595A-18
C 997 14 2.0 4817 3 US-08-459-504B-18
C 998 14 2.0 4817 3 US-08-459-444-18
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1000 14 2.0 4894 4 US-09-505-785-702

ALIGNMENTS

RESULT 1
US-08-759-581B-3/c
; Sequence 3, Application US/08759581B
; Patent No. 5876945

GENERAL INFORMATION:

; APPLICANT: CHISHOLM, DEXTER A.

; APPLICANT: DINER, BRUCE A.

; APPLICANT: DONALDSON, GAIL K.

; APPLICANT: HERSHEY, HOWARD P.

; APPLICANT: JORDAN, DOUGLAS B.

; APPLICANT: TANG, XIAO-SONG

; APPLICANT: TROST, JEFFREY T.

; APPLICANT: WANG, SHAOJIE

; APPLICANT: WARREN, PATRICK V.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING HERBICIDAL AGENTS THAT INHIBIT D1 PROTEIN

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: U.S.A.

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 3.1

; SOFTWARE: MICROSOFT WORD 2.0C

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/759,581B

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: FLOYD, LINDA AXAMETHY

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: CR-9964

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-892-8112

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1680 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

Sequence 4, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 823, Appl
Sequence 18, Appl
Sequence 1, Appl
Sequence 1, Appl
Patent No. 5206352
Sequence 34, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
GENERAL INFORMAT
Sequence 702, App

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: SCENEDESMUS GENE
US-08-759-581B-3

Query Match 2.5%; Score 18; DB 2; Length 1680;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 CTGAGCGGAGGCTGTGC 164
Db 1124 CTGAGCGGAGGCTGTGC 1107

RESULT 2

US-09-304-711-3/c

; Sequence 3, Application US/09304711

; Patent No. 6350573

; GENERAL INFORMATION:

; APPLICANT: DINER, BRUCE A.

; APPLICANT: CHISHOLM, DEXTER A.

; APPLICANT: DONALDSON, GAIL K.

; APPLICANT: HERSHEY, HOWARD P.

; APPLICANT: JORDAN, DOUG B.

; APPLICANT: TANG, XIAO SONG

; APPLICANT: WANG, SHAOJIE

; APPLICANT: TROST, JEFFREY T.

; APPLICANT: WARREN, PATRICK V.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING HERBICIDAL AGENTS THAT

; FILE REFERENCE: CR-9964-C

; CURRENT APPLICATION NUMBER: US/09/304,711

; CURRENT FILING DATE: 1999-05-04

; EARLIER APPLICATION NUMBER: 08/759,581

; EARLIER FILING DATE: DECEMBER 5, 1996

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: MICROSOFT OFFICE 97

; SEQ ID NO 3

; LENGTH: 1680

; TYPE: DNA

; ORGANISM: SCENEDESMUS

US-09-304-711-3

Query Match 2.5%; Score 18; DB 4; Length 1680;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 CTGAGCGGAGGCTGTGC 164
Db 1124 CTGAGCGGAGGCTGTGC 1107

RESULT 3

US-09-173-281-3/c

; Sequence 3, Application US/09173281

; Patent No. 644457

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: METHODS FOR IDENTIFYING HERBICIDAL AGENTS THAT INHIBIT D1 PROTEIN

; NUMBER OF SEQUENCES: 29

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD VERSION 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/173,281

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/759,581

; FILING DATE: DECEMBER 5, 1996

ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9964-A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: SCENEDESMUS GENE
US-09-173-281-3

Query Match 2.4%; Score 18; DB 4; Length 1680;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 CTGAGGGCGAGCTGTGC 164
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Db 1124 CTGAGGGCGAGCTGTGC 1107

RESULT 4
US-08-650-275-35/c
Sequence 35, Application US/08650275
Patent No. 5798249
GENERAL INFORMATION:
APPLICANT: Braxton, Scott Michael
TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181.318
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,275
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0067 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1149007
US-09-181-318-35

Query Match 2.4%; Score 17; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 AGGAAAGGCTGGCTCC 35
|||||
Db 58 AGGAAAGGCTGGCTCC 42

RESULT 6
US-08-650-275-1/c
Sequence 1, Application US/08650275
Patent No. 5798249
GENERAL INFORMATION:
APPLICANT: Braxton, Scott Michael
TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,275
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0067 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1493 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
IMMEDIATE SOURCE:
LIBRARY: LUNGN0T04
CLONE: 890200

US-08-650-275-1
Query Match 2.4%; Score 17; DB 1; Length 1493;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 AGGAAAGGCTGGCTCC 35
Db 58 AGGAAAGGCTGGCTCC 42

RESULT 7
US-09-181-318-1/c
Sequence 1, Application US/09181318
Patent No. 6001632
GENERAL INFORMATION:
APPLICANT: Braxton, Scott Michael
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,318
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,275
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0067 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1493 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
IMMEDIATE SOURCE:
LIBRARY: LUNGN0T04
CLONE: 890200

US-09-181-318-1

Query Match 2.4%; Score 17; DB 3; Length 1493;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 AGGAAAGGCTGGCTCC 35
Db 58 AGGAAAGGCTGGCTCC 42

RESULT 8
US-08-663-566A-10
Sequence 10, Application US/08663566A
Patent No. 5853733
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,566A
FILING DATE: June 13, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1734 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1734

US-08-663-566A-10

Query Match 2.4%; Score 17; DB 2; Length 1734;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 CCACGGAGACAGAGAA 23
Db 761 CCACGGAGACAGAGAA 777

RESULT 9
US-08-023-610-10
; Sequence 10, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Richard D
; APPLICANT: Macdonald Ph.D., Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1734 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1734
US-08-023-610-10

Query Match 2.4%; Score 17; DB 2; Length 1734;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGAA 23
Db 761 CCACGGAGACAGAGAA 777

RESULT 10
US-08-065A-10
; Sequence 10, Application US/08288065A
; Patent No. 5961982
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
; TITLE OF INVENTION: HVT-050 and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,065A
; FILING DATE: Aug-09-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1734 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1734
US-08-288-065A-10

Query Match 2.4%; Score 17; DB 2; Length 1734;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGAA 23
Db 761 CCACGGAGACAGAGAA 777

RESULT 11
US-08-362-240A-10
; Sequence 10, Application US/08362240A
; Patent No. 5965138
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Junker, David
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,240A
; FILING DATE: Dec-22-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 10:

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1804 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 365...490
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: 740...791
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: 1558...1569
OTHER INFORMATION:
US-08-850-910A-42

Query Match 2.4%; Score 17; DB 2; Length 1804;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 TGGCTCCCCCTCCCCAG 45
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Db 1015 TGGCTCCCCCTCCCCAG 1031

RESULT 15

US-07-820-154A-29
Sequence 29, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1907 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Newcastle disease virus
STRAIN: B1
IMMEDIATE SOURCE:
CLONE: 137-23.803 (PSY1142)
POSITION IN GENOME:
MAP POSITION: -50%
UNITS: %G
FEATURE:
NAME/KEY: CDS
LOCATION: 92...1822 /codon_start= 92
OTHER INFORMATION: /product= "NDV heamagglutinin-Neuraminidase"
OTHER INFORMATION: /gene= "HN"
OTHER INFORMATION: /number= 1
US-07-820-154A-29

Query Match 2.4%; Score 17; DB 1; Length 1907;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGGAA 23
|||||
Db 852 CCACGGAGACAGAGGAA 868

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Job time : 58.9887 secs

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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 75.5878 Seconds
(without alignments)
13697.491 Million cell updates/sec

Title: US-09-513-888c-1_COPY_7806_8520
Perfect score: 715
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1029858 seqs, 72403093 residues

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Post-processing: Listing first 1000 summaries

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- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
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- 12: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	74	10.3	470	9 US-09-918-995-27892	Sequence 27892, A
3	19	2.7	2739	9 US-10-098-841-80	Sequence 80, Appl
4	19	2.7	2916	9 US-10-098-841-81	Sequence 81, Appl
C 5	18	2.5	486	9 US-09-918-995-2699	Sequence 2699, Ap
C 6	18	2.5	492	10 US-09-783-590-10224	Sequence 10224, A
7	18	2.5	848	9 US-10-198-846-10677	Sequence 10677, A
8	18	2.5	893	9 US-10-198-846-1071	Sequence 1071, Ap
9	18	2.5	2144	10 US-09-822-830A-8	Sequence 8, Appli
10	18	2.5	2662	10 US-09-925-301-2	Sequence 2, Appli
11	18	2.5	11336	9 US-09-764-868-1440	Sequence 1440, Ap
C 12	18	2.5	536165	9 US-09-939-964-1	Sequence 1, Appli
C 13	17	2.4	335	10 US-09-783-590-2233	Sequence 2233, Ap
C 14	17	2.4	350	9 US-09-803-719-1712	Sequence 1712, Ap
C 15	17	2.4	425	9 US-09-933-797-145	Sequence 145, App
C 16	17	2.4	439	10 US-09-960-352-4713	Sequence 4713, Ap
C 17	17	2.4	467	9 US-10-091-504-448	Sequence 448, App
C 18	17	2.4	467	10 US-09-764-869-448	Sequence 448, App
19	17	2.4	482	9 US-10-206-901B-3	Sequence 3, Appli

Sequence 31139, A	Sequence 31139	526	2.4	17	9 US-09-918-995-31139
Sequence 13523, A	Sequence 13523	543	2.4	17	10 US-09-864-761-13523
Sequence 9133, Ap	Sequence 9133	731	2.4	17	9 US-10-198-846-9133
Sequence 233, App	Sequence 233	967	2.4	17	9 US-09-925-299-233
Sequence 233, App	Sequence 233	967	2.4	17	10 US-09-925-299-233
Sequence 35, Appl	Sequence 35	1264	2.4	17	10 US-09-739-907-35
Sequence 82, Appl	Sequence 82	1409	2.4	17	9 US-10-012-542-82
Sequence 15, Appl	Sequence 15	1558	2.4	17	9 US-09-892-877-15
Sequence 15, Appl	Sequence 15	1558	2.4	17	9 US-09-948-783-15
Sequence 49, Appl	Sequence 49	1898	2.4	17	10 US-09-789-561-49
Sequence 33, Appl	Sequence 33	2112	2.4	17	9 US-10-004-551-33
Sequence 346, App	Sequence 346	2528	2.4	17	9 US-09-992-598-346
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Sequence 346, App	Sequence 346	2528	2.4	17	9 US-10-123-261-461
Sequence 346, App	Sequence 346	2528	2.4	17	9 US-10-140-921-461
Sequence 346, App	Sequence 346	2528	2.4	17	9 US-10-140-928-461
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94	17	2.4	2528	9	US-10-123-292-461	Sequence 461, App	167	17	2.4	2528	9	US-10-146-729-461	Sequence 461, App
95	17	2.4	2528	9	US-10-123-903-461	Sequence 461, App	168	17	2.4	2528	9	US-10-146-791-461	Sequence 461, App
96	17	2.4	2528	9	US-10-124-819-461	Sequence 461, App	169	17	2.4	2528	9	US-10-147-484-461	Sequence 461, App
97	17	2.4	2528	9	US-10-124-822-461	Sequence 461, App	170	17	2.4	2528	9	US-10-147-492-461	Sequence 461, App
98	17	2.4	2528	9	US-10-140-925-461	Sequence 461, App	171	17	2.4	2528	9	US-10-147-508-461	Sequence 461, App
99	17	2.4	2528	9	US-10-160-498-461	Sequence 461, App	172	17	2.4	2528	9	US-10-147-512-461	Sequence 461, App
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101	17	2.4	2528	9	US-09-993-583-346	Sequence 346, App	174	17	2.4	2528	9	US-10-175-735-461	Sequence 461, App
102	17	2.4	2528	9	US-10-121-041-461	Sequence 461, App	175	17	2.4	2528	9	US-09-997-333-346	Sequence 346, App
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104	17	2.4	2528	9	US-10-121-047-461	Sequence 461, App	177	17	2.4	2528	9	US-10-123-905-461	Sequence 461, App
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109	17	2.4	2528	9	US-10-123-910-461	Sequence 461, App	182	17	2.4	2528	9	US-10-127-821A-461	Sequence 461, App
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118	17	2.4	2528	9	US-10-127-839A-461	Sequence 461, App	191	17	2.4	2528	9	US-10-127-834A-461	Sequence 461, App
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122	17	2.4	2528	9	US-10-131-818A-461	Sequence 461, App	195	17	2.4	2528	9	US-10-128-687A-461	Sequence 461, App
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249	17	2.4	10828	10	US-09-942-325A-2	Sequence 2, Appli	322	16	2.2	999	10	US-09-876-527-26	Sequence 26, Appl
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c 301	16	2.2	507	9	US-09-918-995-31641	Sequence 31641, A	c 374	16	2.2	2586	9	US-09-906-700-235	Sequence 235, App
c 302	16	2.2	516	10	US-09-864-864-216	Sequence 216, App	c 375	16	2.2	2586	9	US-09-902-903-235	Sequence 235, App
c 303	16	2.2	524	10	US-09-864-761-8130	Sequence 8130, Ap	c 376	16	2.2	2586	9	US-09-903-749A-235	Sequence 235, App
c 304	16	2.2	553	9	US-09-918-995-13390	Sequence 13390, A	c 377	16	2.2	2586	9	US-09-903-786-235	Sequence 235, App
c 305	16	2.2	568	10	US-10-076-816-58	Sequence 58, Appl	c 378	16	2.2	2586	9	US-09-902-736-235	Sequence 235, App
c 306	16	2.2	568	10	US-09-734-017A-27	Sequence 27, Appl	c 379	16	2.2	2586	9	US-09-904-119-235	Sequence 235, App
c 307	16	2.2	569	10	US-09-864-761-9420	Sequence 9420, Ap	c 380	16	2.2	2586	9	US-09-904-956-235	Sequence 235, App
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c 309	16	2.2	579	9	US-09-738-626-1029	Sequence 1029, Ap	c 382	16	2.2	2586	9	US-10-063-518-7	Sequence 7, Appli
c 310	16	2.2	590	10	US-09-864-761-8014	Sequence 8014, Ap	c 383	16	2.2	2586	9	US-10-063-598-7	Sequence 7, Appli
c 311	16	2.2	594	10	US-09-864-761-16540	Sequence 16540, A	c 384	16	2.2	2586	9	US-10-227-693-7	Sequence 7, Appli

C 385	16	2.2	2586	9	US-09-902-692-235	Sequence 235, App	458	16	2.2	40645	9	US-10-216-441-3	Sequence 3, Appli
C 386	16	2.2	2586	9	US-09-903-520-235	Sequence 235, App	459	16	2.2	40645	10	US-09-818-656A-3	Sequence 3, Appli
C 387	16	2.2	2586	9	US-09-903-943-235	Sequence 235, App	C 460	16	2.2	48841	9	US-09-844-653-32	Sequence 32, Appl
C 388	16	2.2	2586	9	US-09-904-462-235	Sequence 235, App	C 461	16	2.2	60153	9	US-10-222-334-7	Sequence 7, Appli
C 389	16	2.2	2586	9	US-09-905-056-235	Sequence 235, App	C 462	16	2.2	65608	9	US-09-954-531-180	Sequence 180, App
C 390	16	2.2	2586	9	US-09-907-925-235	Sequence 235, App	C 463	16	2.2	65608	10	US-09-962-436-292	Sequence 292, App
C 391	16	2.2	2586	9	US-09-904-553-235	Sequence 235, App	C 464	16	2.2	65608	10	US-09-962-833-119	Sequence 119, App
C 392	16	2.2	2586	9	US-09-905-331-235	Sequence 235, App	C 465	16	2.2	66686	10	US-09-736-960-86	Sequence 86, Appl
C 393	16	2.2	2586	9	US-09-909-084-235	Sequence 235, App	C 466	16	2.2	73467	9	US-10-237-859-3	Sequence 3, Appli
C 394	16	2.2	2586	9	US-10-063-567-7	Sequence 7, Appli	C 467	16	2.2	108359	9	US-10-151-807-3	Sequence 3, Appli
C 395	16	2.2	2586	9	US-09-905-088-235	Sequence 235, App	C 468	16	2.2	110096	10	US-09-880-107-1542	Sequence 1542, Ap
C 396	16	2.2	2586	9	US-09-907-575-235	Sequence 235, App	C 469	16	2.2	111282	12	US-10-094-989-3	Sequence 3, Appli
C 397	16	2.2	2586	9	US-09-902-759-235	Sequence 235, App	C 470	16	2.2	116840	9	US-10-020-141-3	Sequence 3, Appli
C 398	16	2.2	2586	9	US-09-905-075-235	Sequence 235, App	C 471	16	2.2	130427	9	US-10-175-523-87	Sequence 87, Appl
C 399	16	2.2	2586	9	US-10-063-599-7	Sequence 7, Appli	C 472	16	2.2	150474	9	US-10-026-188-6	Sequence 6, Appli
C 400	16	2.2	2586	9	US-09-902-634-235	Sequence 235, App	C 473	16	2.2	170834	10	US-09-835-232-7	Sequence 7, Appli
C 401	16	2.2	2586	9	US-09-902-713-235	Sequence 235, App	C 474	16	2.2	249487	9	US-10-026-188-3	Sequence 3, Appli
C 402	16	2.2	2586	9	US-09-907-979-235	Sequence 235, App	C 475	16	2.2	513509	9	US-09-754-853A-4	Sequence 4, Appli
C 403	16	2.2	2586	9	US-10-063-595-7	Sequence 7, Appli	C 476	16	2.2	1691139	9	US-10-067-514-1	Sequence 1, Appli
C 404	16	2.2	2586	9	US-09-902-615-235	Sequence 235, App	C 477	16	2.2	3309400	9	US-09-738-626-1	Sequence 1, Appli
C 405	16	2.2	2586	9	US-09-903-925-235	Sequence 235, App	C 478	16	2.2	3309400	9	US-09-738-626-1	Sequence 1, Appli
C 406	16	2.2	2586	9	US-09-906-760A-235	Sequence 235, App	C 479	15	2.1	24	9	US-09-920-923-46	Sequence 46, Appl
C 407	16	2.2	2586	9	US-10-223-085-49	Sequence 49, Appl	C 480	15	2.1	24	10	US-09-547-267-17	Sequence 17, Appl
C 408	16	2.2	2586	9	US-10-223-085-49	Sequence 49, Appl	C 481	15	2.1	30	9	US-09-923-327-233	Sequence 233, App
C 409	16	2.2	2586	9	US-09-907-652-235	Sequence 235, App	C 482	15	2.1	30	10	US-09-989-441-5	Sequence 5, Appli
C 410	16	2.2	2586	9	US-10-063-580-7	Sequence 7, Appli	C 483	15	2.1	96	10	US-09-864-761-20608	Sequence 20608, A
C 411	16	2.2	2586	9	US-10-223-084-49	Sequence 49, Appl	C 484	15	2.1	112	7	US-08-781-986A-2875	Sequence 2875, Ap
C 412	16	2.2	2586	9	US-10-223-088-49	Sequence 49, Appl	C 485	15	2.1	123	9	US-10-060-036-2755	Sequence 2755, Ap
C 413	16	2.2	2586	9	US-10-223-090-49	Sequence 49, Appl	C 486	15	2.1	139	10	US-09-969-708-76	Sequence 76, Appl
C 414	16	2.2	2586	10	US-09-909-320-235	Sequence 235, App	C 487	15	2.1	139	10	US-09-969-347-71	Sequence 71, Appl
C 415	16	2.2	2586	10	US-09-909-088B-235	Sequence 235, App	C 488	15	2.1	156	10	US-09-864-761-26492	Sequence 26492, A
C 416	16	2.2	2586	12	US-10-006-867-7	Sequence 7, Appli	C 489	15	2.1	167	10	US-09-864-761-26492	Sequence 26492, A
C 417	16	2.2	2721	10	US-09-822-860-1	Sequence 1, Appli	C 490	15	2.1	171	10	US-09-783-590-9562	Sequence 9562, Ap
C 418	16	2.2	2785	9	US-09-764-891-7798	Sequence 7798, Ap	C 491	15	2.1	205	9	US-09-918-995-14196	Sequence 14196, A
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C 420	16	2.2	2985	10	US-09-764-853-221	Sequence 221, App	C 493	15	2.1	216	9	US-09-736-457-1210	Sequence 1210, Ap
C 421	16	2.2	3102	10	US-09-888-615-16	Sequence 16, Appl	C 494	15	2.1	216	9	US-09-902-941-941	Sequence 941, App
C 422	16	2.2	3201	9	US-10-198-846-9810	Sequence 9810, Ap	C 495	15	2.1	216	9	US-09-902-941-1210	Sequence 1210, Ap
C 423	16	2.2	3282	10	US-09-864-864-298	Sequence 298, App	C 496	15	2.1	216	9	US-09-849-626-941	Sequence 941, App
C 424	16	2.2	3287	10	US-09-876-527-15	Sequence 15, Appl	C 497	15	2.1	216	9	US-09-849-626-1210	Sequence 1210, Ap
C 425	16	2.2	4203	9	US-09-764-891-7800	Sequence 7800, Ap	C 498	15	2.1	216	9	US-10-017-754-941	Sequence 941, App
C 426	16	2.2	4203	9	US-09-764-891-7801	Sequence 7801, Ap	C 499	15	2.1	216	9	US-10-017-754-1210	Sequence 1210, Ap
C 427	16	2.2	4465	9	US-09-984-842-1	Sequence 1, Appli	C 500	15	2.1	226	10	US-09-974-300-7706	Sequence 7706, Ap
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C 429	16	2.2	5087	10	US-09-931-704-3	Sequence 3, Appli	C 502	15	2.1	226	9	US-10-015-219-1594	Sequence 1594, Ap
C 430	16	2.2	5306	9	US-10-079-854-318	Sequence 318, Appl	C 503	15	2.1	226	10	US-09-777-564-1411	Sequence 1411, Ap
C 431	16	2.2	5306	10	US-09-764-878-318	Sequence 318, App	C 504	15	2.1	226	10	US-09-777-564-1594	Sequence 1594, Ap
C 432	16	2.2	6193	10	US-09-880-107-2197	Sequence 2197, Ap	C 505	15	2.1	227	9	US-10-244-633-38	Sequence 38, Appl
C 433	16	2.2	7175	9	US-09-764-891-5642	Sequence 5642, Ap	C 506	15	2.1	229	10	US-09-864-761-30009	Sequence 30009, A
C 434	16	2.2	7718	9	US-10-175-523-192	Sequence 192, App	C 507	15	2.1	242	10	US-09-983-965-4811	Sequence 4811, Ap
C 435	16	2.2	8232	9	US-10-198-846-10976	Sequence 10976, A	C 508	15	2.1	245	10	US-09-983-965-2704	Sequence 2704, Ap
C 436	16	2.2	12930	9	US-10-214-023-4	Sequence 4, Appli	C 509	15	2.1	260	10	US-09-864-761-19724	Sequence 19724, A
C 437	16	2.2	15186	9	US-09-741-744A-134	Sequence 134, App	C 510	15	2.1	264	10	US-09-983-965-3103	Sequence 3103, Ap
C 438	16	2.2	15186	10	US-09-822-860-3	Sequence 3, Appli	C 511	15	2.1	270	9	US-09-104-408-2	Sequence 2, Appli
C 439	16	2.2	19025	9	US-10-274-878-3	Sequence 3, Appli	C 512	15	2.1	270	9	US-10-074-095-166	Sequence 166, App
C 440	16	2.2	21535	9	US-10-103-313-609	Sequence 609, App	C 513	15	2.1	270	10	US-09-764-860-166	Sequence 166, App
C 441	16	2.2	23580	9	US-10-074-095-990	Sequence 990, App	C 514	15	2.1	273	9	US-10-074-095-918	Sequence 918, App
C 442	16	2.2	23580	10	US-09-764-860-990	Sequence 990, App	C 515	15	2.1	273	9	US-10-074-095-919	Sequence 919, App
C 443	16	2.2	31168	9	US-09-764-868-1464	Sequence 1464, Ap	C 516	15	2.1	273	10	US-09-764-860-918	Sequence 918, App
C 444	16	2.2	31348	9	US-10-091-504-1259	Sequence 1259, Ap	C 517	15	2.1	273	10	US-09-764-860-919	Sequence 919, App
C 445	16	2.2	31348	10	US-09-764-869-1259	Sequence 1259, Ap	C 518	15	2.1	283	9	US-10-244-633-37	Sequence 37, Appl
C 446	16	2.2	32192	9	US-10-092-1416	Sequence 1416, Ap	C 519	15	2.1	286	10	US-09-853-386-116	Sequence 116, App
C 447	16	2.2	32192	9	US-09-764-891-7945	Sequence 7945, Ap	C 520	15	2.1	299	10	US-09-867-701-3557	Sequence 3557, Ap
C 448	16	2.2	32192	9	US-09-764-891-8220	Sequence 8220, Ap	C 521	15	2.1	303	10	US-09-864-761-30389	Sequence 30389, A
C 449	16	2.2	32192	9	US-09-764-891-8319	Sequence 8319, Ap	C 522	15	2.1	309	9	US-09-796-692-6122	Sequence 6122, Ap
C 450	16	2.2	32192	10	US-09-764-847-1416	Sequence 1416, Ap	C 523	15	2.1	309	9	US-10-040-862-6122	Sequence 6122, Ap
C 451	16	2.2	32195	9	US-10-091-504-1605	Sequence 1605, App	C 524	15	2.1	310	9	US-09-918-995-18892	Sequence 18892, A
C 452	16	2.2	32195	9	US-10-125-540-611	Sequence 611, App	C 525	15	2.1	313	9	US-09-104-408-1	Sequence 1, Appli
C 453	16	2.2	32195	9	US-10-125-540-617	Sequence 617, App	C 526	15	2.1	313	10	US-09-867-701-3354	Sequence 3354, Ap
C 454	16	2.2	32195	10	US-09-764-870-611	Sequence 611, App	C 527	15	2.1	321	10	US-09-822-830A-353	Sequence 353, App
C 455	16	2.2	32195	10	US-09-764-870-617	Sequence 617, App	C 528	15	2.1	327	10	US-09-867-701-3464	Sequence 3464, Ap
C 456	16	2.2	32195	10	US-09-764-869-1605	Sequence 1605, Ap	C 529	15	2.1	331	10	US-09-912-447-19	Sequence 19, Appl
C 457	16	2.2	33023	10	US-09-880-107-3350	Sequence 3350, Ap	C 530	15	2.1	334	9	US-09-912-935-2	Sequence 2, Appli

C 531	15	2.1	341	9	US-09-764-891-1901	Sequence 1901, Ap	C 604	15	2.1	455	9	US-09-918-995-26972	Sequence 26972, A
C 532	15	2.1	341	10	US-09-983-965-3557	Sequence 3557, Ap	C 605	15	2.1	455	10	US-09-864-761-5426	Sequence 5426, Ap
C 533	15	2.1	344	10	US-09-294-903B-109	Sequence 109, Ap	C 606	15	2.1	455	10	US-09-864-761-13822	Sequence 13822, A
C 534	15	2.1	349	9	US-09-918-995-18085	Sequence 18085, A	C 607	15	2.1	458	9	US-09-918-995-13792	Sequence 13792, A
C 535	15	2.1	353	10	US-09-983-965-304	Sequence 304, App	C 608	15	2.1	458	9	US-09-918-995-14980	Sequence 14980, A
C 536	15	2.1	362	9	US-10-078-623-184	Sequence 184, App	C 609	15	2.1	458	9	US-09-918-995-26443	Sequence 26443, A
C 537	15	2.1	363	9	US-09-918-995-30092	Sequence 30092, A	C 610	15	2.1	458	10	US-09-864-761-364	Sequence 364, App
C 538	15	2.1	366	9	US-09-912-935-1	Sequence 1, Appl	C 611	15	2.1	459	9	US-09-918-995-12482	Sequence 12482, A
C 539	15	2.1	367	9	US-09-918-995-30228	Sequence 30228, A	C 612	15	2.1	463	9	US-09-918-995-11839	Sequence 11839, A
C 540	15	2.1	368	10	US-09-983-965-38856	Sequence 38856, Ap	C 613	15	2.1	463	10	US-09-864-761-14576	Sequence 14576, A
C 541	15	2.1	371	10	US-09-864-761-250	Sequence 250, App	C 614	15	2.1	463	10	US-09-878-574-4262	Sequence 4262, Ap
C 542	15	2.1	372	9	US-09-918-995-37696	Sequence 37696, A	C 615	15	2.1	464	9	US-09-918-995-28838	Sequence 28838, A
C 543	15	2.1	376	10	US-09-960-352-585	Sequence 585, App	C 616	15	2.1	464	9	US-09-918-995-32373	Sequence 32373, A
C 544	15	2.1	379	10	US-09-864-761-2943	Sequence 2943, Ap	C 617	15	2.1	465	9	US-09-796-692-3819	Sequence 3819, Ap
C 545	15	2.1	384	9	US-09-918-995-34217	Sequence 34217, A	C 618	15	2.1	465	9	US-10-040-862-3819	Sequence 3819, Ap
C 546	15	2.1	387	9	US-09-918-995-23224	Sequence 23224, A	C 619	15	2.1	467	9	US-09-907-969-526	Sequence 526, App
C 547	15	2.1	389	10	US-09-960-352-5350	Sequence 5350, Ap	C 620	15	2.1	468	9	US-10-101-464A-30	Sequence 30, Appl
C 548	15	2.1	397	9	US-09-764-868-402	Sequence 402, App	C 621	15	2.1	468	9	US-09-907-969-557	Sequence 557, App
C 549	15	2.1	397	9	US-09-918-995-6014	Sequence 6014, Ap	C 622	15	2.1	469	9	US-09-918-995-2440	Sequence 2440, Ap
C 550	15	2.1	397	9	US-10-198-846-12103	Sequence 12103, A	C 623	15	2.1	469	9	US-09-918-995-2804	Sequence 2804, Ap
C 551	15	2.1	401	9	US-09-946-807-917	Sequence 917, App	C 624	15	2.1	469	9	US-09-918-995-22877	Sequence 22877, A
C 552	15	2.1	401	10	US-09-795-668-917	Sequence 917, App	C 625	15	2.1	470	9	US-09-907-969-525	Sequence 525, App
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C 554	15	2.1	402	9	US-09-738-626-1420	Sequence 1420, Ap	C 627	15	2.1	470	10	US-09-864-761-6468	Sequence 6468, Ap
C 555	15	2.1	405	9	US-10-060-036-3325	Sequence 3325, Ap	C 628	15	2.1	472	10	US-09-918-995-31690	Sequence 31690, A
C 556	15	2.1	406	9	US-09-918-995-37082	Sequence 37082, A	C 629	15	2.1	475	9	US-10-101-464A-434	Sequence 434, App
C 557	15	2.1	407	9	US-10-060-036-2835	Sequence 2835, Ap	C 630	15	2.1	476	9	US-09-918-995-26779	Sequence 26779, A
C 558	15	2.1	408	9	US-09-918-995-10555	Sequence 10555, A	C 631	15	2.1	477	9	US-09-918-995-26526	Sequence 26526, A
C 559	15	2.1	409	10	US-09-867-701-1147	Sequence 1147, Ap	C 632	15	2.1	477	10	US-09-864-761-593	Sequence 593, App
C 560	15	2.1	410	9	US-09-918-995-3946	Sequence 3946, Ap	C 633	15	2.1	478	10	US-09-864-761-456	Sequence 456, App
C 561	15	2.1	410	9	US-10-060-036-2134	Sequence 2134, Ap	C 634	15	2.1	482	9	US-09-918-995-34979	Sequence 34979, A
C 562	15	2.1	410	10	US-09-783-590-8693	Sequence 8693, Ap	C 635	15	2.1	482	9	US-09-918-995-31211	Sequence 31211, A
C 563	15	2.1	410	10	US-09-867-701-5316	Sequence 5316, Ap	C 636	15	2.1	482	9	US-10-146-574-5	Sequence 5, Appl
C 564	15	2.1	412	9	US-09-736-457-1047	Sequence 1047, Ap	C 637	15	2.1	484	9	US-10-091-483-66	Sequence 66, Appl
C 565	15	2.1	412	9	US-09-902-941-1047	Sequence 1047, Ap	C 638	15	2.1	484	9	US-10-079-854-220	Sequence 220, App
C 566	15	2.1	412	9	US-09-849-626-1047	Sequence 1047, Ap	C 639	15	2.1	484	10	US-09-764-878-220	Sequence 220, App
C 567	15	2.1	412	9	US-10-017-754-1047	Sequence 1047, Ap	C 640	15	2.1	484	10	US-09-764-878-222	Sequence 222, App
C 568	15	2.1	416	9	US-09-918-995-1517	Sequence 1517, Ap	C 641	15	2.1	484	10	US-09-764-846-66	Sequence 66, Appl
C 569	15	2.1	416	9	US-09-918-995-6441	Sequence 6441, Ap	C 642	15	2.1	484	10	US-09-764-846-66	Sequence 66, Appl
C 570	15	2.1	418	9	US-09-796-692-5872	Sequence 5872, Ap	C 643	15	2.1	485	9	US-09-907-969-544	Sequence 544, App
C 571	15	2.1	418	9	US-10-040-862-5872	Sequence 5872, Ap	C 644	15	2.1	485	9	US-09-918-995-1436	Sequence 1436, Ap
C 572	15	2.1	418	9	US-10-198-846-3352	Sequence 3352, Ap	C 645	15	2.1	487	10	US-09-864-761-3465	Sequence 3465, Ap
C 573	15	2.1	419	9	US-09-796-692-7030	Sequence 7030, Ap	C 646	15	2.1	489	10	US-09-918-995-401	Sequence 401, App
C 574	15	2.1	419	10	US-10-040-862-7030	Sequence 7030, Ap	C 647	15	2.1	491	10	US-09-880-107-1399	Sequence 1399, Ap
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C 576	15	2.1	421	9	US-09-918-995-35355	Sequence 35355, A	C 649	15	2.1	493	9	US-09-918-995-14197	Sequence 14197, A
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; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_FL_genes Version 1.0
```

```
; SEQ ID NO 81
; LENGTH: 2916
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (483)..(1787)
US-10-098-841-81

Query Match          2.7%; Score 19; DB 9; Length 2916;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 GGCCTGAGCGGAGGCTG 161
      |||||
DB 554 GGCCTGAGCGGAGGCTG 572

RESULT 5
US-09-918-995-2699/c
; Sequence 2699, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2699
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(486)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2699

Query Match          2.5%; Score 18; DB 9; Length 486;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 CCACTGCTCTGCCTCAGA 104
      |||||
DB 373 CCACTGCTCTGCCTCAGA 356

RESULT 6
US-09-783-590-10224/c
; Sequence 10224, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16-2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10224
```

```
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (18)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (178)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (284)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (322)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (337)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (339)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (341)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (345)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (351)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (352)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (357)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (364)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (368)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (370)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (371)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (380)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (385)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (399)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (408)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (418)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc feature
; LOCATION: (420)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (430)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (437)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (441)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (447)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (451)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (454)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (482)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-10224
```

```
Query Match 2.5%; Score 18; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 497 CCTGGCCCCAGGCCCCAG 514
Db 278 CCTGGCCCCAGGCCCCAG 261
```

RESULT 7

```
US-10-198-846-10677
; Sequence 10677, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10677
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 829, 845, 846, 847, 848
; OTHER INFORMATION: n = A,T,C or G
; US-10-198-846-10677
```

```
Query Match 2.5%; Score 18; DB 9; Length 848;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 288 CAGATGTTCTCCCTGGGC 305
Db 206 CAGATGTTCTCCCTGGGC 223
```

RESULT 8
US-10-198-846-1071
; Sequence 1071, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1071
; LENGTH: 893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3, 5, 6, 7, 10, 28, 348, 429, 469, 517, 539, 573, 576, 583,
; LOCATION: 593, 616, 645, 685, 718, 761, 769, 773, 791, 800, 821, 825,
; LOCATION: 828, 836, 845, 850, 858, 860, 867, 879, 881, 884, 886, 889,
; LOCATION: 893
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-1071

Query Match 2.5%; Score 18; DB 9; Length 893;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 CAGATGCTCTCCCTGGGC 305
DB 104 CAGATGCTCTCCCTGGGC 121

RESULT 9
US-09-822-830A-8
; Sequence 8, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 2144
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-8

Query Match 2.5%; Score 18; DB 10; Length 2144;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 CAGATGCTCTCCCTGGGC 305
DB 2127 CAGATGCTCTCCCTGGGC 2144

RESULT 10
US-09-925-301-2
; Sequence 2, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2662)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-2

Query Match 2.5%; Score 18; DB 10; Length 2662;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 489 GCACAGAGCCTGGCCCCA 506
DB 1184 GCACAGAGCCTGGCCCCA 1201

RESULT 11
US-09-764-868-1440
; Sequence 1440, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1440
; LENGTH: 11336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4205)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-1440

Query Match 2.5%; Score 18; DB 9; Length 11336;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTGGCCCCAGGCCCA 513
DB 1073 GCCTGGCCCCAGGCCCA 1090

RESULT 12

```
US-09-939-964-1/c
; Sequence 1, Application US/09939964
; Publication No. US20030054522A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; FILE REFERENCE: Plasmid
; CURRENT APPLICATION NUMBER: US/09/939,964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214,808
; PRIOR FILING DATE: 1999-08-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1

Query Match      2.5%; Score 18; DB 9; Length 536165;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      632 CGCATCACCCTCACCAGG 649
Db      360500 CGCATCACCCTCACCAGG 360483

RESULT 13
US-09-783-590-2233
; Sequence 2233, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2233
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (82)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (99)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
```

```
; LOCATION: (192)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (205)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (259)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (274)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (303)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (308)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (309)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (318)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-2233
```

```
Query Match      2.4%; Score 17; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      495 AGCCTGGCCCCAGGCC 511
Db      39 AGCCTGGCCCCAGGCC 55
```

RESULT 14

```
US-09-803-719-1712/c
; Sequence 1712, Application US/09803719
; Publication No. US20030044783A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Human Genes and Gene Products
; FILE REFERENCE: 1624.002
; CURRENT APPLICATION NUMBER: US/09/803,719
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,609
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 2396
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1712
```


; LENGTH: 350
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-719-1712

Query Match 2.4%; Score 17; DB 9; Length 350;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 527 TCCTGCCCTTCCTCTG 543
|||||
Db 217 TCCTGCCCTTCCTCTG 201

RESULT 15

US-09-933-797-145/c
; Sequence 145, Application US/09933797
; Patent No. US20020155119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; PRIOR FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 145
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-145

Query Match 2.4%; Score 17; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 CCAGCGCGCCGATG 252
|||||
Db 391 CCAGCGCGCCGATG 375

Search completed: June 17, 2003, 09:59:46
Job time : 87.5878 secs

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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 812.5 Seconds
(without alignments)
14252.028 Million cell updates/sec

Title: US-09-513-888C-1_COPY_7806_8520
Perfect score: 715
Sequence: 1 actgcccacagagacagag.....ttccctcctagctctccag 715

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
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- 7: em_estro:*
- 8: em_htc:*
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- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	278	38.9	925	12	BF338502
2	260	36.4	848	9	AL566277
3	155	21.7	326	9	AL047147
4	150	21.0	622	10	AV751885
5	142	19.9	448	14	R88008
6	99	13.8	495	14	N42784

80	19	2.7	684	10	BB866290	BB866290	BB866290	153	18	2.5	438	9	AI751163	AI751163	cn08b03.x
81	19	2.7	684	10	BE309763	BE309763	601094030	154	18	2.5	439	12	BG691697	BG691697	340973 BA
82	19	2.7	694	10	BE313024	BE313024	601150380	155	18	2.5	439	13	BI014521	BI014521	CN3-ET009
83	19	2.7	721	13	BI912351	BI912351	603067696	156	18	2.5	434	13	BI285833	BI285833	CM3-ET009
84	19	2.7	722	12	BG820499	BG820499	602782819	157	18	2.5	456	10	BE292083	BE292083	601085811
85	19	2.7	722	17	AO371661	AO371661	RPCI11-14	158	18	2.5	458	12	BF229412	BF229412	MR1-CI002
86	19	2.7	726	13	BI59897	BI59897	603246847	159	18	2.5	461	13	BJ273862	BJ273862	BJ273862
87	19	2.7	744	17	AG187426	AG187426	Pan trogl	160	18	2.5	465	14	RO1367	RO1367	ye81e06.r1
88	19	2.7	747	17	BH024855	BH024855	RPCI-24-3	161	18	2.5	466	17	AQ667259	AQ667259	HS-2109 A
89	19	2.7	760	17	AG032084	AG032084	Pan trogl	162	18	2.5	472	12	BF394965	BF394965	UI-R-CA0-
90	19	2.7	788	12	BG163536	BG163536	602338563	163	18	2.5	479	17	AQ112930	AQ112930	CIT-HSP-2
91	19	2.7	851	14	BQ948941	BQ948941	AGENCOURT	164	18	2.5	481	13	BJ201155	BJ201155	CIT-HSP-2
92	19	2.7	870	12	BG395237	BG395237	602457748	165	18	2.5	493	9	AL045237	AL045237	DKZP4341
93	19	2.7	880	14	QO213511	QO213511	AGENCOURT	166	18	2.5	491	17	AQ522959	AQ522959	HS-5202 A
94	19	2.7	884	12	BG396457	BG396457	602459175	167	18	2.5	504	17	AQ212184	AQ212184	HS-3073 A
95	19	2.7	884	10	BE231225	BE231225	HVSMG001	168	18	2.5	505	17	AQ055922	AQ055922	CIT-HSP-2
96	19	2.7	896	14	BQ215113	BQ215113	AGENCOURT	169	18	2.5	508	10	BE106768	BE106768	unm33d04.Y
97	19	2.7	901	14	BQ679778	BQ679778	AGENCOURT	170	18	2.5	510	10	BE480668	BE480668	165861 BA
98	19	2.7	906	12	BG330663	BG330663	602430070	171	18	2.5	515	10	BE430822	BE430822	SUN006.B0
99	19	2.7	920	14	QO888031	QO888031	AGENCOURT	172	18	2.5	517	12	BF591215	BF591215	7b43e12.x
100	19	2.7	923	14	EQ927585	EQ927585	AGENCOURT	173	18	2.5	519	12	BF192274	BF192274	244037 MA
101	19	2.7	929	12	BG174319	BG174319	602336327	174	18	2.5	519	13	BI345001	BI345001	373677 MA
102	19	2.7	945	14	BQ649665	BQ649665	AGENCOURT	175	18	2.5	519	17	AQ810155	AQ810155	HS-4787 A
103	19	2.7	949	12	BF314376	BF314376	601901125	176	18	2.5	526	13	BJ273905	BJ273905	RPCI-11-3
104	19	2.7	966	14	BQ668492	BQ668492	AGENCOURT	177	18	2.5	526	17	AQ544183	AQ544183	BJ273905
105	19	2.7	1019	12	BG565019	BG565019	602583807	178	18	2.5	527	9	AL041355	AL041355	DKZP434A
106	19	2.7	1088	12	BF345938	BF345938	602017942	179	18	2.5	536	10	AW049386	AW049386	UI-M-BH1-
107	19	2.7	1094	12	BF314647	BF314647	601900678	180	18	2.5	537	12	BG512838	BG512838	dad63a09.
108	19	2.7	1107	12	BF311014	BF311014	601988330	181	18	2.5	537	17	AZ626768	AZ626768	1M0467007
109	19	2.7	1118	12	BF348179	BF348179	602022085	182	18	2.5	539	12	BF705614	BF705614	228134 MA
110	18	2.5	125	17	AZ252472	AZ252472	RPCI-23-2	183	18	2.5	540	13	BI010491	BI010491	MR2-EN009
111	18	2.5	189	14	F15970	F15970	HSP000446 H	184	18	2.5	543	13	BJ194728	BJ194728	BJ194728
112	18	2.5	191	14	EQ380476	EQ380476	RC3-UT008	185	18	2.5	544	9	AL672947	AL672947	AL672947
113	18	2.5	243	9	AU059880	AU059880	AU059880	186	18	2.5	544	14	BQ211679	BQ211679	UI-R-DZ1-
114	18	2.5	253	10	AW823661	AW823661	uf57c11.x	187	18	2.5	546	10	AW951566	AW951566	EST363636
115	18	2.5	264	10	BE579462	BE579462	BB579462	188	18	2.5	549	12	BF705694	BF705694	244538 MA
116	18	2.5	275	17	AO637463	AO637463	RPCI-11-4	189	18	2.5	549	17	AQ174681	AQ174681	HS-3205 B
117	18	2.5	288	10	BE202421	BE202421	BB202421	190	18	2.5	550	17	AZ298218	AZ298218	RPCI-23-1
118	18	2.5	297	10	BE031980	BE031980	130769 MA	191	18	2.5	550	17	AZ467636	AZ467636	1M0279H10
119	18	2.5	298	10	AW242848	AW242848	xn26904.x	192	18	2.5	553	9	AL676383	AL676383	AL676383
120	18	2.5	308	9	AW789342	AW789342	vv93a09.r	193	18	2.5	554	13	BJ169644	BJ169644	BJ169644
121	18	2.5	312	10	AW076439	AW076439	683018C04	194	18	2.5	555	12	BE845925	BE845925	232597 BA
122	18	2.5	313	10	BB549601	BB549601	BB549601	195	18	2.5	555	13	BJ424293	BJ424293	BJ424293
123	18	2.5	314	10	BB194657	BB194657	BB194657	196	18	2.5	555	13	AQ925729	AQ925729	RPCI-23-2
124	18	2.5	323	9	AA372341	AA372341	ESR84490	197	18	2.5	555	17	AQ321266	AQ321266	RPCI11-10
125	18	2.5	341	9	AI324098	AI324098	mh06g10.x	198	18	2.5	569	13	BJ396817	BJ396817	BJ396817
126	18	2.5	341	9	AA344167	AA344167	EST50077	199	18	2.5	572	12	BG512119	BG512119	GR025e12.
127	18	2.5	345	10	AW183341	AW183341	xj76c12.x	200	18	2.5	579	13	BI342716	BI342716	370643 MA
128	18	2.5	353	10	AW336125	AW336125	23681 MAR	201	18	2.5	579	13	BJ005471	BJ005471	BJ005471
129	18	2.5	353	17	AQ018416	AQ018416	CIT-HSP-2	202	18	2.5	579	13	BJ172742	BJ172742	BJ172742
130	18	2.5	359	9	AL628789	AL628789	AL628789	203	18	2.5	582	17	AZ653781	AZ653781	1M0527C10
131	18	2.5	365	13	BI040069	BI040069	CM4-N7028	204	18	2.5	586	13	BJ009877	BJ009877	BJ009877
132	18	2.5	374	13	BM432599	BM432599	IUEJ11F3.	205	18	2.5	590	17	BH036367	BH036367	RPCI-24-2
133	18	2.5	375	13	BM431973	BM431973	IUEJ11F3.	206	18	2.5	592	9	AL682686	AL682686	AL682686
134	18	2.5	375	13	BM432641	BM432641	IUEJ112B7.	207	18	2.5	593	9	AL595604	AL595604	AL595604
135	18	2.5	377	13	BM481901	BM481901	534522 MA	208	18	2.5	593	17	AQ544199	AQ544199	RPCI-11-3
136	18	2.5	387	13	BI334653	BI334653	602998609	209	18	2.5	595	13	BI849747	BI849747	477676 MA
137	18	2.5	395	10	BE592140	BE592140	WS185.A0	210	18	2.5	597	17	AQ162155	AQ162155	mgx00011L
138	18	2.5	399	9	AI503281	AI503281	vn13d09.x	211	18	2.5	600	17	AQ473623	AQ473623	CITBI-EI-
139	18	2.5	400	17	AQ090077	AQ090077	HS-3000 B	212	18	2.5	601	10	BE588741	BE588741	194358 BA
140	18	2.5	400	17	BH366290	BH366290	CH230-75H	213	18	2.5	603	12	BG908756	BG908756	TaIR1171A
141	18	2.5	402	10	BE480670	BE480670	165863 BA	214	18	2.5	611	13	BI966577	BI966577	id56a04.x
142	18	2.5	405	13	BM461118	BM461118	1113GR.ab	215	18	2.5	627	12	BF530123	BF530123	602040302
143	18	2.5	405	17	AZ261683	AZ261683	RPCI-23-1	216	18	2.5	629	13	BI159785	BI159785	602863520
144	18	2.5	406	12	BF870809	BF870809	CM3-ET009	217	18	2.5	632	9	AA625525	AA625525	af72f06.r
145	18	2.5	407	17	AQ082223	AQ082223	RPCI11-55	218	18	2.5	637	9	AL683185	AL683185	AL683185
146	18	2.5	412	9	BF955446	BF955446	MR4-NN018	219	18	2.5	639	14	BQ195125	BQ195125	UI-R-CN1-
147	18	2.5	413	9	AA027233	AA027233	zj99a12.s	220	18	2.5	642	10	AV733321	AV733321	AV733321
148	18	2.5	428	10	AW297549	AW297549	UI-H-EW0-	221	18	2.5	642	17	BH109550	BH109550	RPCI-24-2
149	18	2.5	431	9	AL044298	AL044298	DKFZp434N	222	18	2.5	644	17	BH350360	BH350360	CH230-320
150	18	2.5	432	10	BE487382	BE487382	176094 BA	223	18	2.5	647	9	AI147208	AI147208	qa89b12.x
151	18	2.5	433	17	FR0017362	FR0017362	F.rubripe	224	18	2.5	654	13	BJ243844	BJ243844	BJ243844
152	18	2.5	435	13	BI065452	BI065452	pgf1n.pk0	225	18	2.5	657	12	BG770038	BG770038	602745156

C	226	18	2.5	660	10	AVG10110		AVG10110	AV610110		C	299	18	2.5	921	17	CNS049VL	AL291082	Tetraodon
	227	18	2.5	663	9	AL790318		AL790318	AL790318			300	18	2.5	924	12	BQ35921	BQ35921	AGENCOURT
	228	18	2.5	663	13	BJ168051		BJ168051	BJ168051			301	18	2.5	924	14	BQ68965	BQ68965	AGENCOURT
	229	18	2.5	666	17	AZ120164	RPCI-23-4	AZ120164	RPCI-23-4			302	18	2.5	928	13	BM453383	BM453383	AGENCOURT
	230	18	2.5	668	13	BJ273890		BJ273890	BJ273890			303	18	2.5	930	14	BQ644914	BQ644914	AGENCOURT
	231	18	2.5	675	10	BB383556		BB383556	BB383556			304	18	2.5	930	14	BQ939534	BQ939534	AGENCOURT
	232	18	2.5	675	10	BE615267		BE615267	601280826			305	18	2.5	931	12	BG742213	BG742213	AGENCOURT
	233	18	2.5	676	12	BG333222		BG333222	602430939			306	18	2.5	932	12	BG109806	BG109806	AGENCOURT
	234	18	2.5	687	13	BM007737		BM007737	603617185			307	18	2.5	935	14	BQ675120	BQ675120	AGENCOURT
	235	18	2.5	687	17	AZ716197	RPCI-24-1	AZ716197	RPCI-24-1			308	18	2.5	935	14	BQ923647	BQ923647	AGENCOURT
	236	18	2.5	687	17	AG121604	Pan trogl	AG121604	Pan trogl			309	18	2.5	938	12	BQ386273	BQ386273	AGENCOURT
	237	18	2.5	688	10	BB619790		BB619790	BB619790			310	18	2.5	938	12	BQ891229	BQ891229	AGENCOURT
	238	18	2.5	691	12	BG762768		BG762768	602734685			311	18	2.5	950	17	CNS04NMV	AL298275	Tetraodon
	239	18	2.5	694	10	BS570835		BS570835	601329336			312	18	2.5	950	12	BF339803	BF339803	AGENCOURT
	240	18	2.5	695	10	BB344077		BB344077	BB344077			313	18	2.5	960	14	BQ951227	BQ951227	AGENCOURT
	241	18	2.5	697	9	AL653433		AL653433	AL653433			314	18	2.5	961	13	BF299687	BF299687	AGENCOURT
	242	18	2.5	700	12	BE917382		BE917382	601664213			315	18	2.5	965	12	BF475657	BF475657	AGENCOURT
	243	18	2.5	700	13	BI1116671		BI1116671	602868349			316	18	2.5	965	13	BI411929	BI411929	AGENCOURT
	244	18	2.5	704	12	BG748190		BG748190	602705814			317	18	2.5	972	14	BQ891229	BQ891229	AGENCOURT
	245	18	2.5	719	13	BM016518		BM016518	603642144			318	18	2.5	977	14	BQ933450	BQ933450	AGENCOURT
	246	18	2.5	720	17	AZ9611286		AZ9611286	602229111			319	18	2.5	983	14	BQ936084	BQ936084	AGENCOURT
	247	18	2.5	728	13	BI857728		BI857728	603388360			320	18	2.5	993	12	BG330768	BG330768	AGENCOURT
	248	18	2.5	734	10	BE273443		BE273443	601143138			321	18	-2.5	1012	14	BM917847	BM917847	AGENCOURT
	249	18	2.5	736	17	AZ721209	RPCI-24-9	AZ721209	RPCI-24-9			322	18	2.5	1015	13	BM559810	BM559810	AGENCOURT
	250	18	2.5	738	12	BG392323		BG392323	602410477			323	18	2.5	1020	14	BQ054393	BQ054393	AGENCOURT
	251	18	2.5	745	9	AU1116843		AU1116843	AU1116843			324	18	2.5	1022	14	BM806168	BM806168	AGENCOURT
	252	18	2.5	751	12	BG478754		BG478754	602525681			325	18	2.5	1023	14	BQ058335	BQ058335	AGENCOURT
	253	18	2.5	752	12	BG824539		BG824539	602728436			326	18	2.5	1042	12	BF306771	BF306771	AGENCOURT
	254	18	2.5	761	12	BG743862		BG743862	602722617			327	18	2.5	1050	14	BQ066272	BQ066272	AGENCOURT
	255	18	2.5	762	13	BI686675		BI686675	603312902			328	18	2.5	1051	14	BQ059399	BQ059399	AGENCOURT
	256	18	2.5	772	9	AL521157		AL521157	AL521157			329	18	2.5	1056	14	BQ051964	BQ051964	AGENCOURT
	257	18	2.5	775	17	BH312500	CH230-119	BH312500	CH230-119			330	18	2.5	1071	12	BF690553	BF690553	AGENCOURT
	258	18	2.5	776	17	CNS02Y2Q		AL219131	Tetraodon			331	18	2.5	1081	14	BM916591	BM916591	AGENCOURT
	259	18	2.5	779	12	BG871365		BG871365	602790543			332	18	2.5	1082	14	BQ054920	BQ054920	AGENCOURT
	260	18	2.5	781	12	BF342396		BF342396	602013192			333	18	2.5	1088	17	CNS05MB6	AL344427	Tetraodon
	261	18	2.5	782	17	AZ520242		AZ520242	RPCI-11-2			334	18	2.5	1100	14	BM917087	BM917087	AGENCOURT
	262	18	2.5	784	9	AU119143		AU119143	AU119143			335	18	2.5	1115	14	BQ059011	BQ059011	AGENCOURT
	263	18	2.5	792	12	BE733718		BE733718	601568230			336	18	2.5	1149	12	BF971937	BF971937	AGENCOURT
	264	18	2.5	797	12	BG863913		BG863913	602797171			337	18	2.5	1168	17	CNS06TIA	AL413972	T3 end of
	265	18	2.5	798	17	CNS04YD6		AL306339	Tetraodon			338	18	2.5	1194	14	BQ893053	BQ893053	AGENCOURT
	266	18	2.5	799	10	AW045021		AW045021	um16506.Y			339	18	2.5	1221	13	BM564098	BM564098	AGENCOURT
	267	18	2.5	801	12	BG761029		BG761029	602717539			340	18	2.5	1324	14	BM806169	BM806169	AGENCOURT
	268	18	2.5	801	10	BE613560		BE613560	601504325			341	18	2.5	1493	12	BG622685	BG622685	AGENCOURT
	269	18	2.5	811	9	AL521158		AL521158	AL521158			342	18	2.5	1612	14	BM927011	BM927011	AGENCOURT
	270	18	2.5	813	13	BI261586		BI261586	602953653			343	17	2.4	82	17	AZ777035	AZ777035	2M0011J12
	271	18	2.5	823	13	BM018838		BM018838	603646757			344	17	2.4	100	9	AA542233	AA542233	vk28b02.r
	272	18	2.5	826	12	BG675934		BG675934	602622286			345	17	2.4	133	17	BH324346	BH324346	CH230-133
	273	18	2.5	830	14	BQ961311		BQ961311	AGENCOURT			346	17	2.4	136	13	BQ479338	BQ479338	BJ479338
	274	18	2.5	838	12	BF678125		BF678125	602085177			347	17	2.4	141	12	BF857780	BF857780	QV1-F7020
	275	18	2.5	840	17	AQ745383	HS 2276 A	AQ745383	HS 2276 A			348	17	2.4	154	10	BE158193	BE158193	MR2-HT038
	276	18	2.5	842	12	BG490860	602520044	BG490860	602520044			349	17	2.4	156	12	BF411739	BF411739	UI-R-BT1-
	277	18	2.5	848	12	BE781631		BE781631	601467488			350	17	2.4	157	14	T23990	T23990	seq2146 NHB
	278	18	2.5	853	17	CNS04HTT		AL291586	Tetraodon			351	17	2.4	158	17	AZ730710	AZ730710	RPCI-24-1
	279	18	2.5	855	14	BQ642584		BQ642584	AGENCOURT			352	17	2.4	159	17	CNS04ETP	AL287494	Tetraodon
	280	18	2.5	855	14	BQ924903		BQ924903	AGENCOURT			353	17	2.4	183	13	BI751683	BI751683	Ta01_13c0
	281	18	2.5	858	9	AA203200	zx57a04.r	AA203200	zx57a04.r			354	17	2.4	183	13	BI751784	BI751784	Ta01_12b1
	282	18	2.5	863	12	BG763365		BG763365	602735427			355	17	2.4	183	14	BQ901380	BQ901380	Ta02_18h0
	283	18	2.5	871	12	BE961683		BE961683	601647959			356	17	2.4	183	14	BQ901459	BQ901459	Ta02_15f0
	284	18	2.5	877	12	BE900734		BE900734	601673902			357	17	2.4	183	14	BQ901772	BQ901772	Ta02_11f0
	285	18	2.5	879	14	BQ721722		BQ721722	AGENCOURT			358	17	2.4	183	14	BQ902249	BQ902249	Ta02_06f0
	286	18	2.5	883	12	BG479515		BG479515	602526046			359	17	2.4	192	9	AA038584	AA038584	mi85e09.r
	287	18	2.5	885	14	BQ962515		BQ962515	AGENCOURT			360	17	2.4	192	14	BQ901457	BQ901457	Ta02_19h0
	288	18	2.5	887	13	BI870592		BI870592	603394077			361	17	2.4	203	12	BF63978	BF63978	CM0-CS004
	289	18	2.5	889	14	BQ227906		BQ227906	AGENCOURT			362	17	2.4	208	10	BE158194	BE158194	MR2-HT038
	290	18	2.5	893	17	CNS02UOI		AL214731	Tetraodon			363	17	2.4	212	12	BF752577	BF752577	RCO-BN041
	291	18	2.5	896	14	BQ898880		BQ898880	AGENCOURT			364	17	2.4	214	10	BB227412	BB227412	B9227412
	292	18	2.5	900	14	BQ723195		BQ723195	AGENCOURT			365	17	2.4	215	17	AZ733211	AZ733211	RPCI-24-1
	293	18	2.5	902	13	BM451269		BM451269	AGENCOURT			366	17	2.4	217	17	AZ774967	AZ774967	2M0004A20
	294	18	2.5	907	14	BQ051460		BQ051460	AGENCOURT			367	17	2.4	222	10	BE523092	BE523092	B8523092
	295	18	2.5	911	12	BG762117		BG762117	602717704			368	17	2.4	223	12	BF899962	BF899962	7h20h09.x
	296	18	2.5	914	14	BQ653698		BQ653698	AGENCOURT			369	17	2.4	224	12	BF800062	BF800062	MRI-C1002
	297	18	2.5	915	12	BF306251		BF306251	601893310			370	17	2.4	225	9	A1566424	A1566424	tr195d01.x
	298	18	2.5	918	14	BQ720407		BQ720407	AGENCOURT			371	17	2.4	231	10	AW407398	AW407398	UI-HF-BM0

C 372	17	2.4	233	10	BB169472	BB169472	BB169472	445	17	2.4	354	13	BM253857	BM253857	515063 MA
C 373	17	2.4	236	9	AV241776	AV241776	AV241776	446	17	2.4	355	9	AA863865	AA863865	vx15b10.r
C 374	17	2.4	237	9	AV229732	AV229732	AV229732	C 447	17	2.4	356	9	AU161496	AU161496	BM253857
C 375	17	2.4	238	10	AV377039	AV377039	AV377039	C 448	17	2.4	357	12	BG907360	BG907360	TALR1159D
C 376	17	2.4	238	10	AW376284	AW376284	RC3-CT020	C 449	17	2.4	357	12	BF285684	BF285684	EST450275
C 377	17	2.4	240	10	BB178438	BB178438	BB178438	C 450	17	2.4	357	14	BQ749904	BQ749904	SnEST4a73
C 378	17	2.4	241	10	AV376815	AV376815	AV376815	C 451	17	2.4	358	14	BQ337322	BQ337322	IL2-NT018
C 379	17	2.4	243	9	AV105028	AV105028	AV105028	C 452	17	2.4	361	9	AI892038	AI892038	u158d04.y
C 380	17	2.4	249	10	AW563223	AW563223	LGI-204.H	C 453	17	2.4	364	9	AI672996	AI672996	we9c03.x
C 381	17	2.4	256	9	AI872565	AI872565	wm7g07.x	C 454	17	2.4	366	14	BQ659591	BQ659591	H501P21u
C 382	17	2.4	266	10	BB259009	BB259009	BB259009	C 455	17	2.4	367	12	BG313726	BG313726	WHE2057.G
C 383	17	2.4	269	13	BJ459519	BJ459519	BJ459519	C 456	17	2.4	367	12	BG907182	BG907182	TALR1157G
C 384	17	2.4	270	12	BF054374	BF054374	EST439604	C 457	17	2.4	370	13	BI873998	BI873998	963112F12
C 385	17	2.4	272	12	BF799932	BF799932	MR1-CT002	C 458	17	2.4	371	10	BE365951	BE365951	P11.2.E10
C 386	17	2.4	273	9	AI928661	AI928661	wp61b01.x	C 459	17	2.4	372	13	BQ842841	BQ842841	BU042841
C 387	17	2.4	277	12	BF880720	BF880720	QV3-ET017	C 460	17	2.4	373	10	AW820483	AW820483	QV2-ST029
C 388	17	2.4	281	9	AA506315	AA506315	nh45c06.s	C 461	17	2.4	373	12	BG907181	BG907181	TALR1157G
C 389	17	2.4	281	10	BB402834	BB402834	BB402834	C 462	17	2.4	375	10	AW427695	AW427695	64034 MAR
C 390	17	2.4	282	13	BJ451424	BJ451424	BJ451424	C 463	17	2.4	375	12	BG692516	BG692516	342232 BA
C 391	17	2.4	283	10	BB182728	BB182728	BB182728	C 464	17	2.4	376	10	AW478610	AW478610	21191 MAR
C 392	17	2.4	285	9	AA507298	AA507298	nh49b08.s	C 465	17	2.4	377	9	AI180542	AI180542	uc70c11.r
C 393	17	2.4	285	14	BM845045	BM845045	K-EST0123	C 466	17	2.4	377	12	BF016798	BF016798	ux16h07.y
C 394	17	2.4	289	17	BH089789	BH089789	RPCI-24-3	C 467	17	2.4	379	9	AI797513	AI797513	we8h11.x
C 395	17	2.4	291	10	BB038001	BB038001	BB038001	C 468	17	2.4	379	14	BE291545	BE291545	601084356
C 396	17	2.4	291	12	BE722956	BE722956	192237 MA	C 469	17	2.4	379	10	BQ659880	BQ659880	HG01A13u
C 397	17	2.4	291	12	BE722957	BE722957	192238 MA	C 470	17	2.4	380	10	AW406894	AW406894	UT-HF-BK0
C 398	17	2.4	291	14	W79279	W79279	xd80a04.r1	C 471	17	2.4	380	10	BF731935	BF731935	UT-HF-BK0
C 399	17	2.4	292	10	BB607762	BB607762	BB607762	C 472	17	2.4	380	13	BQ457125	BQ457125	BU457125
C 400	17	2.4	293	12	BF711571	BF711571	MI-P-A2-a	C 473	17	2.4	382	9	AV011765	AV011765	AV011765
C 401	17	2.4	294	10	BB555912	BB555912	BB555912	C 474	17	2.4	382	17	AZ509341	AZ509341	1M0352D16
C 402	17	2.4	294	12	BF947188	BF947188	MR3-NN021	C 475	17	2.4	383	10	AW137002	AW137002	UT-H-B11-
C 403	17	2.4	297	12	BF751413	BF751413	203343 MA	C 476	17	2.4	383	13	BI396959	BI396959	K664401.Y
C 404	17	2.4	298	14	F12536	F12536	HSC3BC041.n	C 477	17	2.4	384	10	BB803125	BB803125	BB803125
C 405	17	2.4	299	17	AZ655768	AZ655768	1M0530J21	C 478	17	2.4	384	12	BF095532	BF095532	IL2-UT007
C 406	17	2.4	300	9	AU276116	AU276116	AU276116	C 479	17	2.4	385	9	AA310284	AA310284	EST18111
C 407	17	2.4	300	10	BE401201	BE401201	CNW01P01	C 480	17	2.4	387	10	AW315107	AW315107	12000 MAR
C 408	17	2.4	307	17	B44134	B44134	HS-1058-B2-	C 481	17	2.4	387	12	BG908200	BG908200	TALR1166D
C 409	17	2.4	308	12	BF933677	BF933677	IL5-NT022	C 482	17	2.4	387	17	AQ482414	AQ482414	RPCI-11-2
C 410	17	2.4	310	13	BI002936	BI002936	MR3-HN006	C 483	17	2.4	388	9	AT004167	AT004167	AT004167
C 411	17	2.4	311	12	BF365944	BF365944	IL5-NT007	C 484	17	2.4	391	10	AW907153	AW907153	EST343276
C 412	17	2.4	314	9	AI917235	AI917235	ts53c10.x	C 485	17	2.4	393	9	AI615610	AI615610	V122h01.Y
C 413	17	2.4	317	10	BE638697	BE638697	946012G11	C 486	17	2.4	393	10	BB817236	BB817236	BB817236
C 414	17	2.4	318	13	BI052798	BI052798	RC4-GN033	C 487	17	2.4	393	13	BI053046	BI053046	RCO-GN027
C 415	17	2.4	319	9	AA576259	AA576259	nm62c07.s	C 488	17	2.4	393	12	AQ121303	AQ121303	HS-3075.A
C 416	17	2.4	320	10	BB245363	BB245363	BB245363	C 489	17	2.4	395	12	BF774472	BF774472	284152 MA
C 417	17	2.4	322	12	EG012863	EG012863	CW4-GN036	C 490	17	2.4	396	13	BI360883	BI360883	388961 MA
C 418	17	2.4	323	13	BM286919	BM286919	527142 MA	C 491	17	2.4	396	13	BI360885	BI360885	388963 MA
C 419	17	2.4	324	12	BF991156	BF991156	IL5-GN017	C 492	17	2.4	397	10	AW501800	AW501800	UT-HF-BR0
C 420	17	2.4	324	14	T08803	T08803	EST06695.In	C 493	17	2.4	398	9	AA761019	AA761019	nw08G04.s
C 421	17	2.4	326	10	BM208793	BM208793	BM208793	C 494	17	2.4	398	10	AW406797	AW406797	UT-HF-BL0
C 422	17	2.4	328	10	AW503020	AW503020	UT-HF-BR0	C 495	17	2.4	398	12	BG276868	BG276868	uv08G04.Y
C 423	17	2.4	329	9	AL838282	AL838282	AL838282	C 496	17	2.4	398	13	BU458918	BU458918	BU458918
C 424	17	2.4	330	10	BB101817	BB101817	BB101817	C 497	17	2.4	398	14	BQ661277	BQ661277	HM02M11u
C 425	17	2.4	333	10	AW958256	AW958256	EST370326	C 498	17	2.4	398	17	AQ031485	AQ031485	HS-2223.A
C 426	17	2.4	334	13	BJ454793	BJ454793	BJ454793	C 499	17	2.4	399	12	BG406635	BG406635	g8c14g12.
C 427	17	2.4	335	13	BI536785	BI536785	396166 MA	C 500	17	2.4	399	13	BJ449707	BJ449707	BJ449707
C 428	17	2.4	336	13	EG941480	EG941480	ax13e10.x	C 501	17	2.4	399	14	BQ632668	BQ632668	il26c05.Y
C 429	17	2.4	338	12	BF892520	BF892520	IL0-NT015	C 502	17	2.4	400	9	AL837331	AL837331	AL837331
C 430	17	2.4	338	13	BJ459564	BJ459564	BJ459564	C 503	17	2.4	400	9	AV102465	AV102465	AV102465
C 431	17	2.4	340	9	AA414544	AA414544	vc60a12.s	C 504	17	2.4	401	9	AA758083	AA758083	ah68a03.s
C 432	17	2.4	340	13	BI342660	BI342660	370568 MA	C 505	17	2.4	402	9	AU197751	AU197751	AU197751
C 433	17	2.4	340	17	AZ101591	AZ101591	RPCI-23-3	C 506	17	2.4	402	13	BI799682	BI799682	H138B09.E
C 434	17	2.4	344	12	BF333604	BF333604	MR2-CN003	C 507	17	2.4	402	14	BQ463646	BQ463646	HG01A01r
C 435	17	2.4	344	17	AQ242049	AQ242049	CTIBI-E1-	C 508	17	2.4	403	10	AW282788	AW282788	LGI-290.D
C 436	17	2.4	345	13	BI722762	BI722762	1031064A0	C 509	17	2.4	403	10	AW282931	AW282931	LGI-304.D
C 437	17	2.4	347	13	BG959143	BG959143	PM4-CT080	C 510	17	2.4	403	17	B94209	B94209	CIT-HSP-217
C 438	17	2.4	348	14	BQ657204	BQ657204	HA09E07u	C 511	17	2.4	403	17	AQ341494	AQ341494	RPCI11-12
C 439	17	2.4	349	12	BF737159	BF737159	PM4-KT004	C 512	17	2.4	404	10	AV910267	AV910267	AV910267
C 440	17	2.4	349	14	N44832	N44832	YY39d11.r1	C 513	17	2.4	404	10	AW284719	AW284719	LGI-214.F
C 441	17	2.4	351	10	BB725329	BB725329	BB725329	C 514	17	2.4	404	10	AQ515749	AQ515	

C 518	17	2.4	407	13	BJ447290	RJ447290	BX4747290	C 591	17	2.4	449	13	BM218099	BM218099 C0906D06
C 519	17	2.4	407	17	TAG8G07P	AL452629 T. brucei	AL452629 T. brucei	C 592	17	2.4	450	9	AA612010	AA612010 voo2c12.r
C 520	17	2.4	408	12	BG907840	TAlrlll63B	BG907840 TAlrlll63B	C 593	17	2.4	450	13	BG995163	BG995163 CMO-HTI29
C 521	17	2.4	409	10	AW897233	CNO-NN005	AW897233 CNO-NN005	C 594	17	2.4	450	17	AQ473123	AQ473123 CITBI-E1-
C 522	17	2.4	409	13	BM328261	PICL_23.A	BM328261 PICL_23.A	C 595	17	2.4	451	9	AA253758	AA253758 mw03b07.r
C 523	17	2.4	409	14	BQ659872	HGOlA01U	BQ659872 HGOlA01U	C 596	17	2.4	451	14	BQ908096	BQ908096 T002D10.O
C 524	17	2.4	410	9	AA047661	Zf14a05.B	AA047661 Zf14a05.B	C 597	17	2.4	451	14	R44014	R44014 Y119e03.r1
C 525	17	2.4	411	12	BF725949	BF725949 Bx22a10.Y	BF725949 Bx22a10.Y	C 598	17	2.4	451	17	AQ111777	AQ111777 CIT-HSP-2
C 526	17	2.4	412	10	AW437355	JR763 MAR	AW437355 JR763 MAR	C 599	17	2.4	451	17	AZ950059	AZ950059 ZM021A06
C 527	17	2.4	412	12	BF011939	ug37h09.Y	BF011939 ug37h09.Y	C 600	17	2.4	453	9	AI095114	AI095114 gal9a10.x
C 528	17	2.4	414	17	AZ281849	RPCI-23-1	AZ281849 RPCI-23-1	C 601	17	2.4	453	10	AV910686	AV910686 AV910686
C 529	17	2.4	415	10	AV667195	AV667195	AV667195 AV667195	C 602	17	2.4	453	13	B1359612	B1359612 384209.MA
C 530	17	2.4	415	12	BE816031	EG996752	BE816031 XRO-BN018	C 603	17	2.4	454	10	BB755186	BB755186 BB755186
C 531	17	2.4	415	13	BG996752	EF897207	EF897207 IL2-WT018	C 604	17	2.4	454	12	BF468543	BF468543 UI-N-BH3-
C 532	17	2.4	416	12	BF897207	IL2-WT018	BF897207 IL2-WT018	C 605	17	2.4	455	14	R48905	R48905 Yj69f06.r1
C 533	17	2.4	416	17	AZ3369732	I M0120C02	AZ3369732 I M0120C02	C 606	17	2.4	455	17	AQ338818	AQ338818 HS 3118.B
C 534	17	2.4	417	10	AW204275	UI-H-B11-	AW204275 UI-H-B11-	C 607	17	2.4	456	10	BB751485	BB751485 BB751485
C 535	17	2.4	417	12	BF709310	M1-P-AYO-	BF709310 M1-P-AYO-	C 608	17	2.4	456	12	BP229415	BP229415 MRI-CI002
C 536	17	2.4	418	12	BF229432	XRL-CI002	BF229432 XRL-CI002	C 609	17	2.4	457	9	AA656845	AA656845 vz24603.r
C 537	17	2.4	420	9	AL796516	AL796516	AL796516 AL796516	C 610	17	2.4	457	10	AAW200197	AAW200197 dal2g12.y
C 538	17	2.4	420	12	BF229631	WFHE2216.A	BF229631 WFHE2216.A	C 611	17	2.4	457	10	AZ583746	AZ583746 IM0378F17
C 539	17	2.4	420	14	N30487	yX48f05_r1	N30487 yX48f05_r1	C 612	17	2.4	457	17	BH749768	BH749768 SALK 0301
C 540	17	2.4	420	17	AZ3233358	IM004AO07	AZ3233358 IM004AO07	C 613	17	2.4	458	10	AV910822	AV910822 AV910822
C 541	17	2.4	421	10	AW909828	wr74f10.Y	AW909828 wr74f10.Y	C 614	17	2.4	458	10	BB703108	BB703108 BB703108
C 542	17	2.4	421	12	BF941718	nad92c03..	BF941718 nad92c03..	C 615	17	2.4	459	10	BB795732	BB795732 BB795732
C 543	17	2.4	421	13	BJ458079	BJ458079	BJ458079 BU458079	C 616	17	2.4	460	9	AI060291	AI060291 UI-R-C1-I
C 544	17	2.4	421	14	BQ659923	HGOlDI3u	BQ659923 HGOlDI3u	C 617	17	2.4	460	9	AL822851	AL822851 AL822851
C 545	17	2.4	424	17	TA76H09P	AL460760 T. brucei	AL460760 T. brucei	C 618	17	2.4	460	13	BM038728	BM038728 V009A03.O
C 546	17	2.4	426	10	AW283727	LGI_222.G	AW283727 LGI_222.G	C 619	17	2.4	460	14	BM761644	BM761644 K-EST0042
C 547	17	2.4	426	12	BF810963	CM2-CI017	BF810963 CM2-CI017	C 620	17	2.4	460	17	AQ880723	AQ880723 HS 5058.A
C 548	17	2.4	427	10	BE014084	125664.MA	BE014084 125664.MA	C 621	17	2.4	461	9	AA683338	AA683338 ah51a09.s
C 549	17	2.4	427	14	EQ335141	CM3-MT029	EQ335141 CM3-MT029	C 622	17	2.4	461	10	BE246438	BE246438 TCBAPIE46
C 550	17	2.4	428	9	AU094557	AU094557	AU094557 AU094557	C 623	17	2.4	461	12	BF958307	BF958307 CM2-NN024
C 551	17	2.4	428	12	BF841025	RC3-HT097	BF841025 RC3-HT097	C 624	17	2.4	461	17	AZ741302	AZ741302 RPCI-24-7
C 552	17	2.4	429	12	BF443537	MA	BF443537 261055.MA	C 625	17	2.4	462	9	AI419507	AI419507 LF22a03.x
C 553	17	2.4	429	12	BF800053	MR1-CI002	BF800053 MR1-CI002	C 626	17	2.4	462	14	BQ447189	BQ447189 UI-H-EU1-
C 554	17	2.4	431	9	AA030087	m127C03.r	AA030087 m127C03.r	C 627	17	2.4	462	14	BQ9911	BQ9911 Ym05G02.r1
C 555	17	2.4	431	9	AL827401	AL827401	AL827401 AL827401	C 628	17	2.4	464	10	AW742197	AW742197 up53e10.Y
C 556	17	2.4	431	17	AZ818697	AZ818697	AZ818697 2M0088E24	C 629	17	2.4	464	12	BF880518	BF880518 QV3-ET017
C 557	17	2.4	432	9	A1275074	q165b02.x	A1275074 q165b02.x	C 630	17	2.4	464	10	AW252896	AW252896 UI-R-BJ0-
C 558	17	2.4	432	12	BG360140	dab92h05.	BG360140 dab92h05.	C 631	17	2.4	465	17	B38918	B38918 HS-1048-B1-
C 559	17	2.4	432	12	BE785760	IL3-WT010	BE785760 IL3-WT010	C 632	17	2.4	466	9	AI326502	AI326502 mq34d05.y
C 560	17	2.4	432	14	BQ661772	HP01D15W	BQ661772 HP01D15W	C 633	17	2.4	467	17	TA372F12Q	TA372F12Q T. brucei
C 561	17	2.4	432	14	T49530	30.ya76f09.s1	T49530 ya76f09.s1	C 634	17	2.4	468	10	BE159570	BE159570 MRO-HT040
C 562	17	2.4	435	17	AQ812286	HS 5263.A	AQ812286 HS 5263.A	C 635	17	2.4	468	12	BG313982	BG313982 WHE2065.E
C 563	17	2.4	436	9	AA801029	ESTI90526	AA801029 ESTI90526	C 636	17	2.4	470	9	AA789229	AA789229 a127e01.s
C 564	17	2.4	437	9	AL182542	AL182542	AL182542 AL182542	C 637	17	2.4	470	10	BE247311	BE247311 TCBAPIE37
C 565	17	2.4	438	13	BG986753	CNO-HTI29	BG986753 CNO-HTI29	C 638	17	2.4	470	12	BG275110	BG275110 WHE2117.H
C 566	17	2.4	438	13	BI809216	F002F08.O	BI809216 F002F08.O	C 639	17	2.4	471	12	BF485332	BF485332 WHE2310.C
C 567	17	2.4	438	13	BM087101	AI499771.MA	BM087101 AI499771.MA	C 640	17	2.4	471	13	BJ451959	BJ451959 BJ451959
C 568	17	2.4	439	9	AA310446	ESTI181260	AA310446 ESTI181260	C 641	17	2.4	471	14	W99993	W99993 mg27d06.r1
C 569	17	2.4	439	9	AA611692	6020C04.r	AA611692 6020C04.r	C 642	17	2.4	472	10	AV703800	AV703800 AV703800
C 570	17	2.4	439	12	BF529470	602043223	BF529470 602043223	C 643	17	2.4	472	12	BG905996	BG905996 TaLr11444A
C 571	17	2.4	440	9	AA590179	vm23C01.r	AA590179 vm23C01.r	C 644	17	2.4	474	12	BF811935	BF811935 QV1-CI017
C 572	17	2.4	440	12	BF841033	RC3-HT097	BF841033 RC3-HT097	C 645	17	2.4	474	12	BF293158	BF293158 WHE2315.C
C 573	17	2.4	440	13	BM527026	ea148f06.	BM527026 ea148f06.	C 646	17	2.4	474	14	BM837081	BM837081 K-EST0113
C 574	17	2.4	440	14	R49154	Yg57b10.s1	R49154 Yg57b10.s1	C 647	17	2.4	475	10	BE425743	BE425743 S078A08.S
C 575	17	2.4	441	13	BI806358	BI806358	BI806358 S062B01.S	C 648	17	2.4	475	13	BI806822	BI806822 S078A08.S
C 576	17	2.4	441	17	AQ695578	HS 2148.A	AQ695578 HS 2148.A	C 649	17	2.4	476	9	AI832623	AI832623 at70H05.x
C 577	17	2.4	442	9	AL182488	AU182488	AL182488 AU182488	C 650	17	2.4	476	10	BE206737	BE206737 ba02d01.y
C 578	17	2.4	442	10	AV737548	AV737548	AV737548 AV737548	C 651	17	2.4	476	12	BG907968	BG907968 TaLr1164C
C 579	17	2.4	445	14	W40652	me90c08.r1	W40652 me90c08.r1	C 652	17	2.4	477	12	BE498414	BE498414 WHE0963.H
C 580	17	2.4	445	14	W80014	me90c08.r1	W80014 me90c08.r1	C 653	17	2.4	477	13	BJ455086	BJ455086 BJ455086
C 581	17	2.4	446	14	BM837931	K-EST0114	BM837931 K-EST0114	C 654	17	2.4	477	14	W78309	W78309 me78e12.r1
C 582	17	2.4	446	14	R41549	yf88b06.s1	R41549 yf88b06.s1	C 655	17	2.4	478	9	AA139676	AA139676 mq34d05.r
C 583	17	2.4	446	17	BH590055	BOH0R94TR	BH590055 BOH0R94TR	C 656	17	2.4	478	12	BF776790	BF776790 288513.MA
C 584	17	2.4	447	9	AU182976	AU182976	AU182976 AU182976	C 657	17	2.4	479	10	AW322976	AW322976 uo054g06.y
C 585	17	2.4	448	12	BF442448	BF442448	BF442448 259169.MA	C 658	17	2.4	479	17	AZ338978	AZ338978 IM0070G14
C 586	17	2.4	448	12	BF803570	QV1-CI017	BF803570 QV1-CI017	C 659	17	2.4	480	9	AI901966	AI901966 618013A08
C 587	17	2.4	448	13	BJ450655	BJ450655	BJ450655 BJ450655	C 660	17	2.4	480	10	BE426332	BE426332 WHE0330.A
C 588	17	2.4	448	17	AQ988396	RPCI-23-3	AQ988396 RPCI-23-3	C 661	17	2.4	480	10	BE490097	BE490097 WHE0365.E
C 589	17	2.4	449	9	AU506352	AU506352	AU506352 AU506352	C 662	17	2.4	480	17	AQ148012	AQ148012 HS 3110.A
C 590	17	2.4	449	13	BI021996	CM3-MT029	BI021996 CM3-MT029	C 663	17	2.4	481	9	AI640401	AI640401 tz70d11.x

664	17	2.4	481	13	BG988496	BG988496 RC4-HT109	c 737	17	2.4	511	13	BJ449745	BJ449745
c 665	17	2.4	481	14	T74062	T74062 YC81f01.r1	738	17	2.4	511	14	BM843462	BM843462 K-EST0121
666	17	2.4	481	17	TA253A06Q	AL483062 T. brucei	c 739	17	2.4	511	17	BM895197	BM895197 952070A06
c 667	17	2.4	482	9	A220140	A220140 my01e12.r	740	17	2.4	511	17	AZ381804	AZ381804 1W0138H01
668	17	2.4	482	12	BG560805	BG560805 D108 SSH-	c 741	17	2.4	512	10	AW495543	AW495543 UT-M-BH3-
669	17	2.4	482	14	BM986485	BM986485 EST594079	c 742	17	2.4	512	10	BE496927	BE496927 WHE0762_F
670	17	2.4	482	17	AQ693921	AQ693921 HS_5466_B	c 743	17	2.4	513	10	AV908933	AV908933 AV908933
c 671	17	2.4	483	10	BM971413	BM971413 EST383502	744	17	2.4	513	12	BF812229	BF812229 QV1-C1017
c 672	17	2.4	483	13	B1647003	B1647003 60327877A	c 745	17	2.4	514	13	BM184847	BM184847 L0911F11-
c 673	17	2.4	484	10	BE497071	BE497071 WHE0764_A	746	17	2.4	514	17	AQ302735	AQ302735 HS_3227_A
c 674	17	2.4	484	10	BE499884	BE499884 WHE0799_B	747	17	2.4	515	12	BF812232	BF812232 QV1-C1017
675	17	2.4	485	17	AQ702465	AQ702465 HS_5429_A	c 748	17	2.4	516	13	BJ188837	BJ188837
676	17	2.4	485	17	AQ126178	AQ126178 HS_3035_A	749	17	2.4	516	10	AV667196	AV667196 AV667196
677	17	2.4	487	10	BE246469	BE246469 TCBAP1E47	c 750	17	2.4	518	10	BE235918	BE235918 143546_MA
c 678	17	2.4	487	12	BF777102	BF777102 288923_MA	c 751	17	2.4	518	12	BG268001	BG268001 1000144H1
c 679	17	2.4	487	13	BJ452006	BJ452006 BJ452006	752	17	2.4	518	12	BG906509	BG906509 TAlr1150B
c 680	17	2.4	488	10	BE470874	BE470874 WHE0280_D	c 753	17	2.4	518	12	BG909134	BG909134 TAlr1174D
c 681	17	2.4	488	14	BM765508	BM765508 K-EST0047	c 754	17	2.4	519	13	BM372982	BM372982 Ema04_SO
682	17	2.4	488	14	BM842269	BM842269 K-EST0119	c 755	17	2.4	519	17	AZ873278	AZ873278 2W0187A06
c 683	17	2.4	489	9	A1563022	A1563022 TENS2186	c 756	17	2.4	520	12	BF292970	BF292970 WHE2163_B
c 684	17	2.4	489	9	AA434585	AA434585 zw32c04.r	c 757	17	2.4	520	13	BJ449354	BJ449354
c 685	17	2.4	489	12	BG908126	BG908126 TAlr1165F	758	17	2.4	521	9	AL822711	AL822711 AL822711
c 686	17	2.4	489	14	BQ839316	BQ839316 WHE4164_G	759	17	2.4	521	10	AW040138	AW040138 EST282637
c 687	17	2.4	489	17	AQ513179	AQ513179 HS_5138_B	760	17	2.4	521	10	AW040157	AW040157 EST282656
688	17	2.4	490	10	AV910808	AV910808 AV910808	761	17	2.4	521	10	BE313601	BE313601 601148675
689	17	2.4	490	13	B1399432	B1399432 MI-P-AV1-	c 762	17	2.4	521	12	BF267246	BF267246 HV_C8A001
c 690	17	2.4	491	10	AV879676	AV879676 AV879676	c 763	17	2.4	521	13	BJ448991	BJ448991
c 691	17	2.4	491	13	BJ461240	BJ461240 BJ461240	764	17	2.4	522	9	A1939459	A1939459 tf22a03.x
c 692	17	2.4	491	14	BQ459978	BQ459978 HA07118r	765	17	2.4	522	12	BG909151	BG909151 TAlr1174E
693	17	2.4	491	17	AZ281173	AZ281173 RPCI-23-1	c 766	17	2.4	523	12	BF628124	BF628124 HVSMED000
c 694	17	2.4	492	10	BE080728	BE080728 QV1-BT063	c 767	17	2.4	523	17	BH352603	BH352603 CH230-81J
695	17	2.4	492	12	BF812207	BF812207 QV1-C1017	c 768	17	2.4	524	13	BM037863	BM037863 S113B04_S
c 696	17	2.4	493	10	AV634603	AV634603 AV634603	769	17	2.4	524	14	BM850191	BM850191 K-EST0130
c 697	17	2.4	493	10	AW254267	AW254267 UI-R-BJ0-	c 770	17	2.4	525	10	BE519653	BE519653 HV_CED001
c 698	17	2.4	493	10	BE080717	BE080717 QV1-BT063	c 771	17	2.4	526	10	BE215830	BE215830 HV_CED000
699	17	2.4	493	12	BG298817	BG298817 602396557	c 772	17	2.4	526	14	BQ089682	BQ089682 rc51e03.Y
700	17	2.4	493	13	BJ088595	BJ088595 BJ088595	c 773	17	2.4	527	12	BF326182	BF326182 MG0-AN008
c 701	17	2.4	494	10	AW160878	AW160878 au76h03.Y	774	17	2.4	528	14	N91137	N91137 zb24d02.s1
c 702	17	2.4	494	10	BE598415	BE598415 P11-82.G1	c 775	17	2.4	528	17	AZ6333181	AZ6333181 1M0488H18
703	17	2.4	495	12	BG905537	BG905537 TAlr1140D	c 776	17	2.4	529	13	BI807715	BI807715 B001F05_O
c 704	17	2.4	495	12	BE724155	BE724155 198874_MA	c 777	17	2.4	529	13	BM420244	BM420244 U004H02_O
c 705	17	2.4	495	12	BF367693	BF367693 IL5-GN003	c 778	17	2.4	530	10	AW286342	AW286342 LG1_330_E
706	17	2.4	496	12	BG907264	BG907264 TAlr1158E	c 779	17	2.4	530	13	BJ453024	BJ453024 BJ453024
c 707	17	2.4	496	12	BF351333	BF351333 M83-HT048	780	17	2.4	531	10	AW732164	AW732164 ba06C09.X
c 708	17	2.4	497	14	BM765139	BM765139 K-EST0052	c 781	17	2.4	531	12	BG909679	BG909679 TAlr1107C
709	17	2.4	498	12	BF803433	BF803433 QV1-C1017	c 782	17	2.4	531	13	BM420850	BM420850 U020B06_O
710	17	2.4	498	12	BG908887	BG908887 TAlr1172A	c 783	17	2.4	533	9	AL822710	AL822710 AL822710
711	17	2.4	498	13	BM152131	BM152131 TCBAP1E46	c 784	17	2.4	533	12	BF811738	BF811738 QV1-C1017
c 712	17	2.4	499	10	AW503626	AW503626 UI-HF-BN0	c 785	17	2.4	534	13	BI118788	BI118788 EST176_D1
713	17	2.4	499	13	BJ460573	BJ460573 BJ460573	c 786	17	2.4	535	9	AA919627	AA919627 vz22e11.r
714	17	2.4	500	9	AA630424	AA630424 ac09d07.s	c 787	17	2.4	535	13	BM371505	BM371505 Ema08_SQ
715	17	2.4	500	13	BJ456817	BJ456817 BJ456817	c 788	17	2.4	535	13	BM372942	BM372942 Ema04_SQ
716	17	2.4	501	12	BG834473	BG834473 352708_MA	789	17	2.4	535	14	W48131	W48131 mc85c12.r1
c 717	17	2.4	501	12	AW144714	AW144714 EST290494	790	17	2.4	536	14	BM742197	BM742197 K-EST0014
c 718	17	2.4	503	10	AW286279	AW286279 LG1_329_G	c 791	17	2.4	537	12	BF257139	BF257139 HVSMED001
719	17	2.4	503	12	BF929419	BF929419 IL2-NT020	792	17	2.4	538	9	AL705089	AL705089 DKZP2686E
c 720	17	2.4	503	12	BG907605	BG907605 TAlr1161D	c 793	17	2.4	538	10	AV847661	AV847661 AV847661
721	17	2.4	504	10	AV912217	AV912217 AV912217	c 794	17	2.4	538	13	BM037679	BM037679 S096A06_S
c 722	17	2.4	504	10	AW282476	AW282476 LG1_313_C	c 795	17	2.4	538	13	AZ288564	AZ288564 RPCI-23-1
723	17	2.4	504	14	BM986486	BM986486 EST594080	796	17	2.4	539	17	AQ471290	AQ471290 CITBI-E1-
c 724	17	2.4	504	17	AZ475220	AZ475220 IM0293H14	c 797	17	2.4	540	9	AI605978	AI605978 mu43e02.Y
725	17	2.4	505	10	AV910272	AV910272 AV910272	c 798	17	2.4	540	12	BF266321	BF266321 HV_C8A001
c 726	17	2.4	505	10	AW677599	AW677599 DGI_8_D11	c 799	17	2.4	540	14	BM723671	BM723671 UI-E-EJ0-
c 727	17	2.4	506	10	AW837033	AW837033 QV1-LF003	c 800	17	2.4	541	9	AA214205	AA214205 zq90a08.r
c 728	17	2.4	506	13	BJ469516	BJ469516 BJ469516	c 801	17	2.4	541	10	AW653345	AW653345 101998_MA
c 729	17	2.4	506	13	BM087765	BM087765 500577_MA	c 802	17	2.4	542	10	AW387425	AW387425 M81-ST011
730	17	2.4	506	17	AQ529631	AQ529631 RPCI-11-3	803	17	2.4	543	9	AI905839	AI905839 IL-BT100-
c 731	17	2.4	507	10	AW174019	AW174019 f138d06.Y	804	17	2.4	543	9	AA230820	AA230820 mv52a02.r
c 732	17	2.4	508	10	AW672439	AW672439 LG1_359_C	c 805	17	2.4	543	10	AW653944	AW653944 102884_MA
c 733	17	2.4	508	10	BE494405	BE494405 WHE1254_F	c 806	17	2.4	543	13	BM098112	BM098112 EBPi03_SO
734	17	2.4	508	12	BF023589	BF023589 ux09g12.Y	c 807	17	2.4	544	13	BJ453698	BJ453698
c 735	17	2.4	509	12	BG906788	BG906788 TAlr1152F	c 808	17	2.4	545	10	AV885127	AV885127 AV885127
736	17	2.4	509	13	BJ454911	BJ454911 BJ454911	809	17	2.4	545	12	BG905411	BG905411 TAlr1139E

810	17	2.4	545	13	BI528093	BI528093 1024087D0	883	17	2.4	575	13	BJ460619	BJ460619 BJ460619
C 811	17	2.4	545	13	BM323931	BM323931 P1C1_29_C	884	17	2.4	575	17	AZ402860	AZ402860 1M0170D20
C 812	17	2.4	545	14	BQ907422	BQ907422 P006A06-O	C 885	17	2.4	576	10	AV843663	AV843663 AV843663
C 813	17	2.4	545	17	A2752922	A2752922 RPCI-24-1	C 886	17	2.4	577	9	AA930347	AA930347 v659d11.x
C 814	17	2.4	546	9	AI380373	AI380373 t901c09.x	887	17	2.4	578	10	AV923083	AV923083 AV923083
C 815	17	2.4	546	10	BE504293	BE504293 hv87g02.x	888	17	2.4	578	10	BB649608	BB649608 BB649608
C 816	17	2.4	546	12	BG905995	BG905995 Talr1144A	C 889	17	2.4	578	12	BG907596	BG907596 Talr1161D
C 817	17	2.4	546	13	BJ447081	BJ447081 BJ447081	C 890	17	2.4	578	13	BM328443	BM328443 P1C1_29_C
C 818	17	2.4	546	13	BM485095	BM485095 539317 MA	891	17	2.4	579	13	BJ461725	BJ461725 BJ461725
C 819	17	2.4	547	14	BQ660050	BQ660050 HG01M06u	892	17	2.4	580	17	AZ087286	AZ087286 RPCI-23-2
C 820	17	2.4	548	9	AL826875	AL826875 AL826875	893	17	2.4	581	13	BI344329	BI344329 372774 MA
C 821	17	2.4	548	10	BE497083	BE497083 WHR0764_B	894	17	2.4	581	17	BH082229	BH082229 RPCI-24-3
C 822	17	2.4	549	12	BG072874	BG072874 H3116A04-O	C 895	17	2.4	582	12	BF284106	BF284106 EST748697
C 823	17	2.4	550	13	BJ181586	BJ181586 BJ181586	C 896	17	2.4	582	17	AQ548268	AQ548268 RPCI-11-3
C 824	17	2.4	551	9	A1042721	A1042721 uc76h03.x	897	17	2.4	583	12	BG300966	BG300966 HVSME001
C 825	17	2.4	551	10	AW490542	AW490542 UT-M-BH3-	C 898	17	2.4	586	9	AI649070	AI649070 uk34q12.x
C 826	17	2.4	551	10	AW538279	AW538279 C0105F02-	C 899	17	2.4	586	12	BG638728	BG638728 L034125.3
C 827	17	2.4	551	10	AW657359	AW657359 110165 MA	900	17	2.4	587	12	BF008182	BF008182 1393773 A
C 828	17	2.4	551	12	BG906031	BG906031 Talr1144D	901	17	2.4	588	9	AL800234	AL800234 AL800234
C 829	17	2.4	552	10	AW672349	AW672349 LG1_359_C	902	17	2.4	588	9	AL803418	AL803418 AL803418
C 830	17	2.4	552	10	BE490534	BE490534 WHE0362_E	C 903	17	2.4	588	10	BE366535	BE366535 P11_34_G1
C 831	17	2.4	552	12	BF192395	BF192395 243561 MA	904	17	2.4	588	12	BG908712	BG908712 Talr1170F
C 832	17	2.4	552	13	BI133667	BI133667 UT-M-BH3-	C 905	17	2.4	588	13	BM334442	BM334442 MEST117-B
C 833	17	2.4	552	13	BM258291	BM258291 523058 MA	906	17	2.4	589	12	BG905637	BG905637 Talr1141C
834	17	2.4	553	17	BH273690	BH273690 CH230-70E	907	17	2.4	589	17	AZ421922	AZ421922 1M0200F22
C 835	17	2.4	554	12	BG078019	BG078019 H3022F10-	C 908	17	2.4	591	9	AT004056	AT004056 AT004056
C 836	17	2.4	555	9	A1041552	A1041552 cv82d03.x	909	17	2.4	591	13	BJ457165	BJ457165 BJ457165
C 837	17	2.4	555	12	BG904290	BG904290 Talr1131A	C 910	17	2.4	592	17	AZ647813	AZ647813 1M0514G04
C 838	17	2.4	555	12	BG908108	BG908108 Talr1165E	911	17	2.4	593	14	BM842871	BM842871 K-EST0120
C 839	17	2.4	555	13	BG949015	BG949015 QV1-HB003	912	17	2.4	593	14	AZ893204	AZ893204 RPCI-24-2
840	17	2.4	555	13	BI153794	BI153794 602871466	C 913	17	2.4	594	14	BQ638814	BQ638814 h427h12.Y
841	17	2.4	555	13	BJ314238	BJ314238 BJ314238	914	17	2.4	594	14	BQ743812	BQ743812 WHE4108.D
842	17	2.4	555	14	BQ807500	BQ807500 N1SC_KK04	915	17	2.4	595	10	AW958350	AW958350 AV958350
843	17	2.4	555	17	AQ683167	AQ683167 HS_5378_B	C 916	17	2.4	595	10	AW285583	AW285583 LG1_245_F
C 844	17	2.4	556	10	BE158256	BE158256 M22-HT038	C 917	17	2.4	595	12	BF263226	BF263226 HV_CEA000
845	17	2.4	556	12	BG609411	BG609411 323251 MA	C 918	17	2.4	596	13	BI533023	BI533023 1024126F1
846	17	2.4	557	12	BF313397	BF313397 601899971	919	17	2.4	596	9	AI573726	AI573726 uJ65a08.Y
C 847	17	2.4	557	13	BI735751	BI735751 603357012	C 920	17	2.4	596	12	BF937231	BF937231 fm62d07.Y
C 848	17	2.4	559	10	AW542256	AW542256 C0155R01-	C 921	17	2.4	596	12	BE917653	BE917653 OVI_6.D07
C 849	17	2.4	559	13	BI342041	BI342041 369695 MA	C 922	17	2.4	597	12	BG906508	BG906508 Talr1150B
C 850	17	2.4	559	14	BM707796	BM707796 UT-E-C11-	C 923	17	2.4	597	12	AZ815588	AZ815588 2M0083N19
C 851	17	2.4	560	10	AV908915	AV908915 AV908915	924	17	2.4	597	17	AZ967371	AZ967371 2M0238115
852	17	2.4	560	10	BE067100	BE067100 PM3-BT034	C 925	17	2.4	598	9	AI615267	AI615267 486095H31
C 853	17	2.4	560	12	BF906245	BF906245 IL3-MT026	C 926	17	2.4	598	12	BF977770	BF977770 602148393
C 854	17	2.4	560	12	BG908125	BG908125 Talr1165F	927	17	2.4	598	12	BG905784	BG905784 Talr1142D
855	17	2.4	560	17	TA18A10P	TA18A10P T_brucei	C 928	17	2.4	598	12	BE703960	BE703960 MR0-NN112
C 856	17	2.4	561	10	AW335408	AW335408 S46H7_AGS	C 929	17	2.4	599	14	W62536	W62536 md63d07.r1
857	17	2.4	561	12	BF906250	BF906250 IL3-MT026	C 930	17	2.4	599	17	AG073305	AG073305 Pan trogl
C 858	17	2.4	561	13	BI345711	BI345711 Talr1157C	931	17	2.4	600	12	BG803885	BG803885 0243-06 M
C 859	17	2.4	561	13	BI345711	BI345711 374611 MA	932	17	2.4	600	12	BG805246	BG805246 0614-21 M
860	17	2.4	561	14	W67512	W67512 zd42f07.s1	933	17	2.4	600	12	BG808771	BG808771 2122-12 M
C 861	17	2.4	563	12	BG949010	BG949010 OVI-HB003	C 934	17	2.4	600	14	BQ037925	BQ037925 pgn1c.pk0
C 862	17	2.4	563	12	BF430601	BF430601 OG02F07T3	C 935	17	2.4	601	14	BM700150	BM700150 UT-E-DW1-
C 863	17	2.4	565	12	BG277017	BG277017 uv10c05.Y	C 936	17	2.4	602	10	AW333880	AW333880 S27D10 AG
C 864	17	2.4	565	13	BM506378	BM506378 IL3B05.Y	937	17	2.4	604	12	BG908786	BG908786 Talr1171B
865	17	2.4	565	14	BQ640303	BQ640303 he26g01.Y	938	17	2.4	604	12	BG005554	BG005554 MR3-GN018
C 866	17	2.4	566	10	AW744798	AW744798 LG1_384_A	939	17	2.4	604	14	BQ448544	BQ448544 UT-H-EU1-
C 867	17	2.4	566	14	R60116	R60116 yhl3f07.x1	C 940	17	2.4	605	13	BM373446	BM373446 Esm04 SQ
C 868	17	2.4	567	17	AZ852883	AZ852883 2M0155D20	C 941	17	2.4	605	17	AZ784383	AZ784383 2M0027K18
C 869	17	2.4	568	12	BG061500	BG061500 L0907C10-	942	17	2.4	606	9	AL674152	AL674152 AL674152
C 870	17	2.4	568	17	AQ737666	AQ737666 HS_2194_A	943	17	2.4	606	12	BG909309	BG909309 Talr1175H
871	17	2.4	569	14	BQ619641	BQ619641 Talr1176B	944	17	2.4	607	10	AW842840	AW842840 MR2-CN003
872	17	2.4	570	17	AZ948448	AZ948448 2M0211E04	C 945	17	2.4	607	10	BE199270	BE199270 use6a09.X
C 873	17	2.4	571	10	BE489540	BE489540 WHE1060_A	C 946	17	2.4	607	12	BG826936	BG826936 602751033
C 874	17	2.4	571	12	BF478906	BF478906 WHE2015_B	C 947	17	2.4	607	13	BI400260	BI400260 MI-P-Ayl-
C 875	17	2.4	572	12	BG737774	BG737774 f095h05.Y	948	17	2.4	608	12	BG062760	BG062760 L0957E05-
C 876	17	2.4	572	12	BE915961	BE915961 601669452	949	17	2.4	608	17	AZ394045	AZ394045 1M0517L19
C 877	17	2.4	573	10	BE122408	BE122408 894019G08	950	17	2.4	608	17	AZ394045	AZ394045 1M0517L19
878	17	2.4	573	13	BI848101	BI848101 470430 MA	C 951	17	2.4	608	17	BH098442	BH098442 RPCI-24-2
879	17	2.4	573	17	AZ402862	AZ402862 1M0170D22	952	17	2.4	609	12	BG908755	BG908755 Talr1171A
880	17	2.4	575	17	AW563208	AW563208 LG1_204_H	953	17	2.4	609	14	BQ416283	BQ416283 1153b12.Y
C 881	17	2.4	575	12	BF079494	BF079494 230109 MA	C 954	17	2.4	610	12	BG906718	BG906718 Talr1152A
C 882	17	2.4	575	12	BF079494	BF079494 230109 MA	C 955	17	2.4	610	13	BI957347	BI957347 HVSME000

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 161 a 230 c 294 g 161 t 2 others
ORIGIN

Query Match 36.4%; Score 260; DB 9; Length 848;
Best Local Similarity 99.3%; Pred. No. 3.7e-101;
Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 303 GGCTGCCACACAGCCCCCGCCAGAGTGGCCACCGTGGCACTAGATGCAAGTATCTCTG 362
Db 799 GGCTGCCACACAGCCCCCGCCAGAGTGGCCACCGTGGCACTAGATGCAAGTATCTCTG 740
Qy 363 CGACTCTTGCAACCTCACCCTTCTGTGGGTGTTCTTCTGCGCTGTCCAAAGCGCCCTC 422
Db 739 CGACTCTTGCAACCTCACCCTTCTGTGGGTGTTCTTCTGCGCTGTCCAAAGCGCCCTC 680
Qy 423 ACTATTCTTGACCATGCGCATCTGCTCTCTGGAAGAGGCTCTGGACAGCAGAGC 482
Db 679 ACTATTCTTGACCATGCGCATCTGCTCTCTGGAAGAGGCTCTGGACAGCAGAGC 620
Qy 483 CTCAAGCAGACAGCTGGCCCGCCAGGCCCCAGACAGAGGTGGCTCTGCGCTCTCCCTCT 542
Db 619 CTCAAGCAGACAGCTGGCCCGCCAGGCCCCAGACAGAGGTGGCTCTGCGCTCTCCCTCT 560
Qy 543 GGGCAGCGCTCTGGCCGACCACTGACCCACTCGGATGGACCACTCTGTGCCCA 602
Db 559 GGGCAGCGCTCTGGCCGACCACTGACCCACTCGGATGGACCACTCTGTGCCCA 500
Qy 603 AAGCAGCGCTCGAGGAGAGCAGCAGCTCCGCATCACCTCACCAGGATCGGACTCTGCC 662
Db 499 AAGCAGCGCTCGAGGAGAGCAGCAGCTCCGCATCACCTCACCAGGATCGGACTCTGCC 440
Qy 663 CCTGACCTGGAGACGACTGACTGTACGGGGTTCCTCTAGTCTCCAG 715
Db 439 CCTGACCTGGAGACGACTGACTGTACGGGGTTCCTCTAGTCTCCAG 387

RESULT 3
AL047147
LOCUS AL047147 326 bp mRNA linear EST 29-FEB-2000
DEFINITION DKFZp586E1518 r1 586 (synonym: hute1) Homo sapiens cDNA clone
ACCESSION DKFZp586E1518 5', mRNA sequence.
VERSION AL047147.1 GI:5435179
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 326)
AUTHORS Kohrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Kohrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Koehler K
MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFZp586E1518) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

1..326
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp586E1518"
/clone_lib="586 (synonym: hute1)"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/note="vector: pSPORT1; Site_1: NotI; Site_2: SalI/MluI"
64 a 110 c 67 t 1 others

Query Match 21.7%; Score 155; DB 9; Length 326;
Best Local Similarity 100.0%; Pred. No. 4.8e-56;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 54 CCCCCCACTCCAGAAAGAGCAGTCAGAGTCCAGTCTCTGCTCAGACGTTGCCCTG 113
Db 140 CCCCCCACTCCAGAAAGAGCAGTCAGAGTCCAGTCTCTGCTCAGACGTTGCCCTG 199
Qy 114 AGAAGAAGTGGCTCCACACCCAGGGAAGCCCTGAGGCGGAGGCTGTGCTCGCCATG 173
Db 200 AGAAGAAGTGGCTCCACACCCAGGGAAGCCCTGAGGCGGAGGCTGTGCTCGCCATG 259
Qy 174 GTGTCCCGGTACCTTCCATACACAGAGGAGTGACAG 208
Db 260 GTGTCCCGGTACCTTCCATACACAGAGGAGTGACAG 294

RESULT 4
AV751885
LOCUS AV751885 622 bp mRNA linear EST 19-OCT-2000
DEFINITION AV751885 NPD Homo sapiens cDNA clone NPDBHA02 5', mRNA sequence.
ACCESSION AV751885
VERSION AV751885.1 GI:10909733
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 622)
AUTHORS Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu,
W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Zhang, Q.,
Han, Z., Chen, Z., Hu, R. and Chen, J.
TITLE Homo sapiens NPD library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mbshi@ms.stn.sh.cn

This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers
1..622
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NPDBHA02"
/clone_lib="NPD"
/tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
/note="vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

FEATURES
source

130 a 214 c 158 g 120 t
ORIGIN

Query Match 13.3%; Score 95; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;

Query Match 13.3%; Score 95; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;

Qy	54	CCCCCCCCTCCAGAAAGACGAGTCAGAGTCAAGTGCTCTGCCTCAGACGTTGCCTG	113
Db	143	CCCCCCCCTCCAGAAAGACGAGTCAGAGTCAAGTGCTCTGCCTCAGACGTTGCCTG	202

QY 114 AGAAGAATGCTGCTGCACACCCAGGGAGGCCCT 148

RESULT	8
R18912	
R18912	
LOCUS	
R18912	357 bp
	mRNA
	linear
	EST 14-APR-1995

DEFINITION	Yq17d11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32837 5', mRNA sequence.
ACCESSION	R18912

VERSION R18912.1 GI:772522
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

ORGANISM

nomio sapientis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 357)

AUTHORS

Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rafkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENTS

CONTACT: WILSON KN
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 285 1810
Email: est@watson.wustl.edu
Insert Size: 1468

High quality sequence stops: 247 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 High quality sequence stop: 247.
 Location/Qualifiers
 Seq primer: M13RP1
 Insert Length: 1468 Std Error: 0.00

```
source
1. .357
/organism="Homo sapiens"
/db xref="GDB:405184"
```

```
/db xref="taxon:9606"  
/clone="IMAGE:32837"  
/clone_lib="Soares infant brain INIB"
```

```

/dev stage="73 days post natal"
/lab host="DH10B (ampicillin resistant)"
/notes="organ: whole brain; Vector: Latmid BA; Site 1: Not
/sex="female"

```

I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGAAGATTCGCGCCGACGGAATTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lacmid EA vector.

BASE COUNT	66 a	109 c	97 g	78 t	7 others
ORIGIN	Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."				

ORIGIN	Query Match	12.2%	Score 87;	DB 14;	Length 357;
--------	-------------	-------	-----------	--------	-------------

Best Local Similarity 100.0%; Pred. No. 7.7e-27;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 CCCCCCACTCCAGGAAGAGCAGTCCAGTCCAGTCCCTCCAGACGTTGCGTG 113
Db CCCCCCACTCCAGGAAGAGCAGTCCAGTCCAGTCCCTCCAGACGTTGCGTG 201

Qy 114 AGAAGAAGTGGCTGCCACACCCAGGGG 140
Db AGAAGAAGTGGCTGCCACACCCAGGGG 228

RESULT 9
BG009363
LOCUS BG009363 401 bp mRNA linear EST 24-JAN-2001
DEFINITION PMI-GN0305-011200-001-002 GN0305 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG009363
VERSION BG009363.1 GI:12455309
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1. (bases 1 to 401)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922

Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&t2=PM1-GN0305-
011200-001-d02&t3=2000-12-01&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 20

High quality sequence stop: 401.

Location/Qualifiers

FEATURES

source

1. .401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0305"
/dev_stage="Adult"

/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI
; Site 2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 83 a 126 c 113 g 79 t

ORIGIN

Query Match 11.7%; Score 84; DB 12; Length 401;

Best Local Similarity 100.0%; Pred. No. 1.5e-25;

Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 615 AGGAGAGCAGCAGTCCGCATCACCACCAAGATCGGACTCGCCCTGGACCTGGG 674

Db AGGAGAGCAGCAGTCCGCATCACCACCAAGATCGGACTCGCCCTGGACCTGGG 124

Qy 675 AACGACTGGAGTGTCAACGGGGTTC 698
Db AACGACTGGAGTGTCAACGGGGTTC 148

RESULT 10
BF690171/c

LOCUS BF690171 712 bp mRNA linear EST 22-DEC-2000
DEFINITION 602186505T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298593 3',
mRNA sequence.

ACCESSION BF690171

VERSION BF690171.1 GI:11975579

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1. (bases 1 to 712)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-x@mail.nih.gov

Tissue Procurement: ATCC/DCTP/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI154 row: j column: 02

High quality sequence stop: 365.

Location/Qualifiers

FEATURES

source

1. .712

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4298593"

/clone_lib="NIH_MGC_49"

/tissue_type="melanotic melanoma, high MDR (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

into EcoRI; cDNA made by oligo-dT priming. Directionally cloned

GGCAGCAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH_MGC

Library."

BASE COUNT 101 a 207 c 264 g 140 t

ORIGIN

Query Match 7.8%; Score 56; DB 12; Length 712;

Best Local Similarity 100.0%; Pred. No. 1.6e-13;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 660 GCCCTGGAGCTGGGACGAGTGGAGTGTCAACGGGGTTCCTCTAGCTCTCCAG 715

Db GCCCTGGAGCTGGGACGAGTGGAGTGTCAACGGGGTTCCTCTAGCTCTCCAG 209

RESULT 11

BI027772/c

LOCUS BI027772 471 bp mRNA linear EST 14-JUN-2001

DEFINITION MR4-MT0255-140201-203-c09 MT0255 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI027772

VERSION BI027772.1 GI:14434402

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1. (bases 1 to 471)

AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
MEDLINE
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-WT0255-
140201-203-c09&t3=2001-02-14&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 471.

FEATURES
source
1..471
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="WT0255"
/dev_stages="Adult"
/note="Organ: marrow; Vector: puc18; Site:1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT
ORIGIN
98 a 144 c 140 g 87 t 2 others

Query Match 7.1%; Score 51; DB 13; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 665 TGGACCTGGGAACGACTGTGCACGGGGTTCCTCTAGCTCTCCAG 715
|||||
|||||

Db 454 TGGACCTGGGAACGACTGTGCACGGGGTTCCTCTAGCTCTCCAG 404
|||||
|||||

RESULT 12
Fl1822
LOCUS
DEFINITION HSC32A091 normalized infant brain cDNA Homo sapiens CDNA clone
c-32a09, mRNA sequence.
Fl1822
ACCESSION
VERSION Fl1822.1 GI:706134
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 302)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
,M.D., Duprat,S., Houllatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
Michell,H., Marriage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastien-Kabaktchis,C. and Tessier,A.
TITLE IMAGE: molecular integration of the analysis of the human genome
and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534
COMMENT Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain

1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr

Single read
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-32a09
Seq primer: (-21)M13_universal.
Location/Qualifiers
1..302
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="c-32a09"
/tissue="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stages="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;
Site 2: NotI; sex:female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain
; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B. Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

BASE COUNT
ORIGIN
67 a 97 c 65 g 72 t 1 others

Query Match 4.6%; Score 33; DB 14; Length 302;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTGCCCCACGACAGACAGAGGAGGGCTGGCT 33
|||||
|||||

Db 270 ACTGCCCCACGACAGACAGAGGAGGGCTGGCT 302
|||||
|||||

RESULT 13
N31948/c
LOCUS
DEFINITION YV22g12.s1 Soares melanocyte 2NDHM Homo sapiens CDNA clone
IMAGE:272038 3', mRNA sequence.
N31948
ACCESSION
VERSION N31948.1 GI:1152347
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 599)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 345
Source: IMAGE Consortium LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 345.

FEATURES
source
1..599
/organism="Homo sapiens"
/db_xref="GDB:3881680"
/db_xref="taxon:9606"
/clone="IMAGE:272038"

```

/clone_lib="Soares melanocyte 2N6HM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: p77T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGCGCGCGAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p77T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      159 a 162 c 159 g 116 t
ORIGIN
Query Match      4.2%; Score 30; DB 14; Length 599;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 665 TGGACCTGGGAACGACTGACTGCACGGG 694
|||||
Db 574 TGGACCTGGGAACGACTGACTGCACGGG 545

RESULT 14
BM471442      1044 bp mRNA linear EST 05-FEB-2002
LOCUS      AGENCOURT 6478304 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5563262
DEFINITION      5' mRNA sequence.
ACCESSION      BM471442
VERSION      BM471442.1 GI:18520484
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1044)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12293 row: p column: 15
High quality sequence stop: 238.
Location/Qualifiers
1..1044
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5563262"
/clone_lib="NIH MGC 72"
/tissue_type="melanocyte melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT      251 a 326 c 266 g 196 t 5 others
ORIGIN
Query Match      3.8%; Score 27; DB 13; Length 1044;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 CCCTCCCGGCTGGAGACCCCC 61

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Db 225 CCCTCCCGGCTGGAGACCCCC 251
|||||
RESULT 15
BE014383      541 bp mRNA linear EST 09-JUL-2000
LOCUS      125972 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
DEFINITION      BE014383
ACCESSION      BE014383
VERSION      BE014383.1 GI:8275324
KEYWORDS      EST.
SOURCE      pig.
ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE      1 (bases 1 to 541)
AUTHORS      Stone,R.T., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Fahrenkrug,S.C., Preking,W.M., Bennett,G.A., Laegreid,W.W.,
and Keele,J.W.
TITLE      Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL      Unpublished (2000)
COMMENT      Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 53 row: N column: 21
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1..541
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      110 a 188 c 132 g 111 t
ORIGIN
Query Match      2.9%; Score 21; DB 10; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 CCTCCCGGCTGGAGACCC 57
|||||
Db 380 CCTCCCGGCTGGAGACCC 400
|||||
Search completed: June 17, 2003, 06:27:15
Job time : 863.75 secs

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